Bangladesh J. Bot. **55**(2): 363-369, 2026 (June) DOI: https://doi.org/10.3329/bjb.v55i2.90981

ASSESSMENT OF GENETIC VARIABILITY AND CHARACTER ASSOCIATION FOR YIELD IMPROVEMENT IN SUNFLOWER

SAURABH GODARA AND R KALAIYARASI*

Department of Oil Seeds, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore-641 003, (Tamil Nadu)

Keywords: Sunflower, Variability, Heritability, Principal component analysis

Abstract

Genetic variability and character association were studied in 45 sunflower genotypes to identify trait-specific variability for yield and yield related traits. Significant variation was found among genotypes for all traits. High genotypic coefficients of variation were observed for single plant yield, hundred seed weight, and head diameter. High heritability and genetic advance indicated the impact of additive gene action and promoting selection. Single plant yield positively correlated with head diameter, hundred seed weight, hull content, and plant height, but negatively with days to maturity. Principal component (PC) analysis identified three major components PC 1, 2 and 3 cumulative variation (68.96%) and these were only with eigenvalue greater than 1. The study indicates significant variability among the genotypes, which is valuable for identifying diverse genotypes through genetic diversity analysis and could be utilized as parents for sunflower yield improvement.

Introduction

The sunflower (*Helianthus annuus* L.) is a major oilseed crop that thrives in arid and semi-arid climatic conditions. The genus *Helianthus* belongs tocompositae consists of 51 species (Seiler and Gulya 2005). Sunflower is a diploid plant with an inflorescence of distinctive composite blooms. Sunflowers are primarily cultivated for their edible oil, constituting 40-52% of the seed. Sunflower oil is rich in polyunsaturated fatty acids, which helpto lower blood cholesterol levels and reduce the risk of coronary heart disease. Additionally, sunflower seeds contain 33.9% protein, 65.4% lipid, and 18 mineral elements. Beyond its dietary uses, sunflower oil is utilized in biofuel, soap, detergents, and as a supplement in the chemical and pharmaceutical sectors.

Globally, sunflowers are cultivated on 26.66 million hectares, with an estimated production of 50.7 million tons (FAO 2022). In India, sunflower cultivation covers 3.64 lakh hectares, producing 3.63 lakh tons and productivity of 996 kg/ha (India Stat 2023). India accounts for 13-15% of the global oilseed cultivation area and contributes 4% to the worldwide production of edible oils (Narayan 2016).

The present study was undertaken to assess the genetic variability, character association, and their influence on yield and its contributing traits, along with oil content, in sunflower.

Materials and Methods

The study was conducted at the Department of Oilseeds, Tamil Nadu Agricultural University, Coimbatore, during the rabi season of 2023-24. Forty sunflower genotypes and five checks (PB 1384,1389, 1390, 1392, 1409, 1410, 1421, CSFI 1532, 1533, 1538, 1540, 1544, 1543,1542, 13004, 13010, 13012, 13025, 13026, 13035, RSLP 98, IB 11-3, AKSFI 21, 37-4, GMU 1032, CSFI 8002, RCR 72, RHA 850, OPH 92, GMU 689, RHA 378, RHA 1232, 120 R, IB 80, GMU 500, IL 44, GMU 313, GPR 58R, REC 441, and P 147R, experimental checks : CSFI 99, IR 6,

---

*Author for correspondence: <kalaiyarasi_2002@yahoo.com>.

COSF 12B, CMS 335 B, and LTRR 341) were raised in a randomized complete block design (RCBD) with three replications. Each genotype was planted in 4-meter rows with 60 cm × 30 cm spacing.

Data were collected from five randomly selected plants per accession for nine quantitative traits i.e.,days to 50% flowering (DF), days to maturity (DM), plant height (PH), head diameter (HD), volume weight (VW), hundred seed weight (HSW), hull content (HC), single plant yield (SPY), and oil content (OC).

PhenotypicCoefficient of Variability (PCV) and GenotypicCoefficient of Variability (GCV)were calculated following Burton and DeVane (1953). Broad-sense heritability (h^2) and genetic advance were estimated using the methods of Johnson *et al.* (1955).Principal Component Analysis (PCA) and biplots were generated using R version 3.1.3 with "FactoMineR" and "ggplot2" packages(Lê *et al.* 2008,de Mendiburu2023).

Results and Discussion

The analysis of variance indicates highly significant variation ($P<0.01$) for all characters (Table 1). Notably, IB 80 recorded a high oil yield of 44.20%, followed by GPR 58R with 41.45%. In terms of single plant yield, GMU 500 achieved 49.84g, while REC 441 produced 45.91g. The mean, range,PCV and GCV, heritability (h^2), and genetic advance for the respective characters are mentioned in Table 2. PCVranged from 5.40 to 40.55% and GCV ranged from 4.87% to 37.79%. Broad-sense heritability estimates were highest for oil content (90.51%), and high for hundred seed weight (88.77%), days to 50% flowering (87.41%), plant height (87.07%), single plant yield (86.84%), volume weight (84.09%), days to maturity (78.59%), head diameter (78.47%) and hull content (70.41%). Genetic advance as a percentage of the mean (GAM) was highest for single plant yield (72.55%), followed by hundred seed weight (49.07%), with other traits showing high to moderate genetic advance. High PCV and GCV estimates were notably observed for single plant yield, head diameter, and hundred seed weight, suggesting a promising scope for enhancement in these traits through selection (Riaz *et al.* 2019, Dudhe*et al.* 2020). Moderate levels of PCV and GCV were found in plant height, volume weight, hull content, and oil content, consistent with the findings of Singh *et al.* (2019).

Table 1. Analysis of variance for seed yield and its component characters in sunflower genotypes.

Source of variation	df	Replication2	Genotype44	Error88
Days to 50% flowering (days)		0.455	88.467**	4.0503
Days to maturity(days)		3.163	62.937**	5.238
Plant height (cm)		289.751	1365.940**	64.376
Head diameter (cm)		8.7438	15.065**	1.262
Hundred seed weight (g)		0.123	3.863**	0.156
Seed Volume weight (g/100ml)		3.90	53.50**	3.172
Hull content (%)		8.33	40.47**	4.97
Oil content (%)		1.16	53.26**	1.79
Single plant yield (g)		11.152	309.672**	14.879

df: Degrees of freedom, *, ** : Significance at 5 and 1% level.

Heritability in the broad sense is the ratio of genotypic variation to total variance in populations. Oil content (90.51%) had the highest estimate of broad-sense heritability, followed by hundred seed weight (88.77%), plant height (87.07%), and single plant yield (86.84%). High heritability estimates for all traits suggest the presence of additive genetic effects, making these traits particularly amenable to improve through selection (Allard 1960). The significant magnitude of heritability suggests a high level of reliability, indicating a strong likelihood that the genotype can be accurately identified by its phenotypic expression. These results indicate that environmental influences had little to no effect on the phenotypic variance of these features, consistent with findings from other researchers. In sunflowers, broad-sense high heritability estimates would be an effective tool for selection, especially when they are accompanied by a substantial genetic advance as a percentage of the mean. High heritability combined with a high genetic advance as a percentage of the mean was recorded for single plant yield, hundred seed weight, head diameter, plant height, oil content, and volume weight, indicating minimal environmental influence and a significant role of additive gene action. Selection of genotypes based on these traits would be effective. Previous studies have also reported high heritability along with GAM estimates for single-plant yield (Lakshman *et al.* 2021). In the current study, high heritability with low genetic advance for days to 50% flowering, hull content, and days to maturity suggests that these traits are not effectively improved through selection (Umarani *et al.* 2022). Low genetic advance, regardless of whether heritability is high or low, indicates non-additive gene action, suggesting that improving such traits through simple selection may not be effective.

Table 2. Range, mean, coefficients of variation, heritability, and genetic advance performance of sunflower genotypes for nine quantitative traits.

Traits	Mean±SE	CV (%)	Min.	Max.	PCV (%)	GCV (%)	h^2 (%)	GA	GAM (%)
DF	59.22±1.16	3.39	46.33	71.00	9.57	8.95	87.41	10.21	17.24
DM	91.59±1.32	2.49	80.33	102.00	5.40	4.78	78.59	8.00	8.74
PH	122.71±4.63	6.53	80.66	169.95	18.18	16.97	87.07	40.04	32.62
HD	10.85±0.64	10.61	5.24	14.56	22.88	20.26	78.47	3.91	36.98
HSW	4.39±0.228	8.99	2.01	7.26	26.83	25.28	88.77	2.15	49.07
VW	37.19±1.028	4.78	28.41	44.03	12.00	11.01	84.09	7.73	20.80
HC	35.86±1.28	6.21	28.41	43.38	11.42	9.59	70.41	5.94	16.57
OC	34.38±0.774	3.89	22.29	44.20	12.66	12.04	90.51	8.11	23.60
SPY	26.22±2.227	14.70	7.98	49.84	40.55	37.79	86.84	19.03	72.55

CV: Co-efficient of variation, PCV: Phenotypic coefficient of variation, GCV: Genotypic coefficient of variation, h^2: Heritability, GA: Genetic advance, GAM: Genetic advance as percent of the mean, DF: Days to 50% flowering, DM: Days to maturity, PH: Plant height (cm), HD: Head diameter (cm), HSW: Hundred seed weight (g), VW: Seed volume weight (g/100ml), HC: Hull content (%), OC: Oil content (%) and SPY: Single plant yield (g).

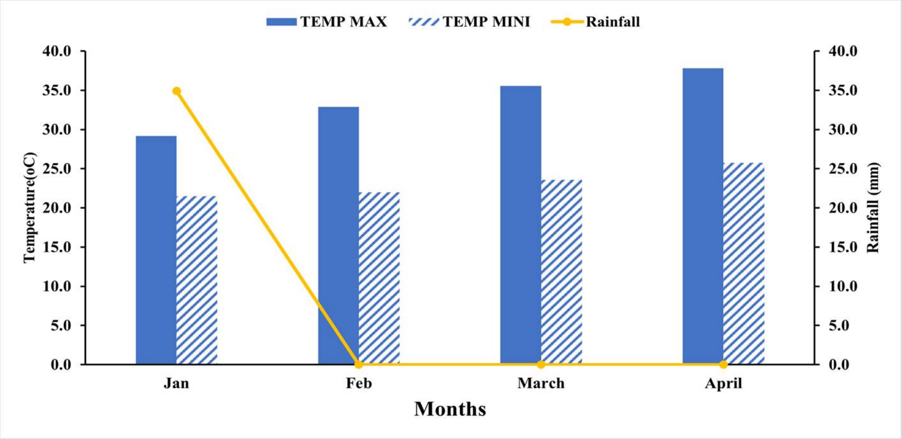
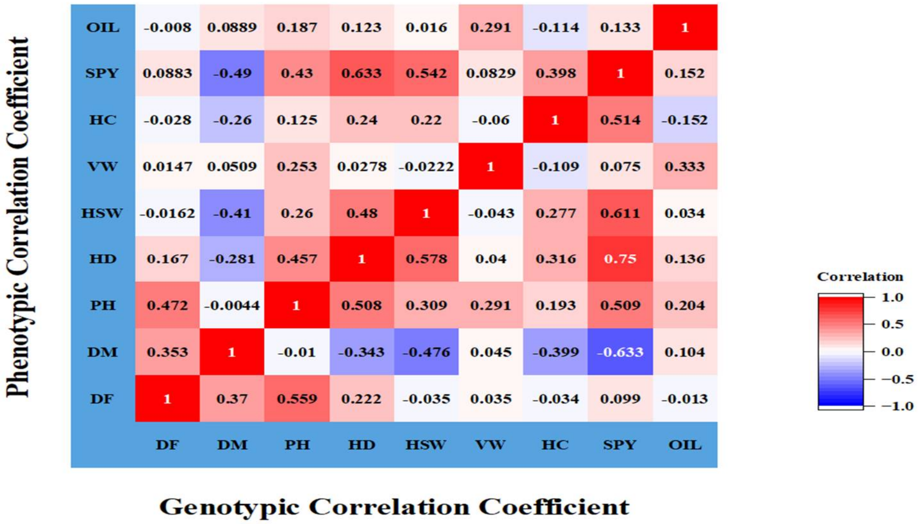


Fig. 1. Monthly average temperature and rainfall during crop session 2023-2024.



OIL	-0.008	0.0889	0.187	0.123	0.016	0.291	-0.114	0.133	1
SPY	0.0883	-0.49	0.43	0.633	0.542	0.0829	0.398	1	0.152
HC	-0.028	-0.26	0.125	0.24	0.22	-0.06	1	0.514	-0.152
VW	0.0147	0.0509	0.253	0.0278	-0.0222	1	-0.109	0.075	0.333
HSW	-0.0162	-0.41	0.26	0.48	1	-0.043	0.277	0.611	0.034
HD	0.167	-0.281	0.457	1	0.578	0.04	0.316	0.75	0.136
PH	0.472	-0.0044	1	0.508	0.309	0.291	0.193	0.509	0.204
DM	0.353	1	-0.01	-0.343	-0.476	0.045	-0.399	-0.633	0.104
DF	1	0.37	0.559	0.222	-0.035	0.035	-0.034	0.099	-0.013
	DF	DM	PH	HD	HSW	VW	HC	SPY	OIL

Fig. 2. Heat map showing phenotypic and genotypic correlation coefficients among nine traits.

The correlations among nine characters at both phenotypic and genotypic levels were calculated to determine the nature of their associations. The significant correlations at thelevels are discussed. The outcomes are shown in heat map (Fig.2).Phenotypic correlation revealed that among the nine characteristics studied, single plant yield had a significant positive association with head diameter (rp = 0.633), hundred seed weight (rp = 0.542), plant height (rp = 0.430), and hull content (rp = 0.398), while a significant negative association with days to maturity was observed (rp = -0.490). Oil content had a positive significant correlation with volume weight (rp = 0.291).Genotypic correlation (rg) of single plant yield with other major traits showed a positive significant correlation with head diameter (rg = 0.750), hundred seed weight (rg = 0.611), hull content (rg = 0.514), and plant height (rg = 0.509), and a significant negative correlation with days to maturity (rg = -0.633). Oil content had a significant positive association with volume weight (rg = 0.333).Selection efficiency is enhanced by understanding the relationship between seed yield and its component traits, as well as the interrelationships among the components themselves. A strongly significant negative correlation was found between days to maturity and single plant yield. Additionally, days to maturity exhibited negative correlations with hundred seed weight and head diameter. This suggests that selecting early maturity genotypes could result in higher yield and larger head diameter. Correlation analysis revealed a strong significant positive correlation among traits such as head diameter, hundred seed weight, hull content, and plant height with single plant yield, which are crucial for enhancing single-plant yield in sunflowers. A significant positive correlation was observed between plant height and single-plant yield. Numerous researchers have documented a positive correlation between single-plant yield and head diameter, hundred-seed weight, and plant height (Hladni *et al.* 2015) Generally, taller sunflower plants tend to have a greater number of leaves, potentially enhancing total biomass production by increasing carbon fixation, which in turn promotes reproductive organ development and higher yield. Based on these observations, an ideal high-yielding sunflower plant is characterized by its height, capacity to sustain maximum leaf area, and ability to support large heads capable of holding numerous filled seeds. In sunflower, oil production is the most valuable output, making it essential to comprehend its relationships with other traits to enhance oil yield. In this research, oil content showed positive correlations with all traits examined, although significant associations were observed specifically with volume weight. This presents an opportunity for concurrent enhancement of oil content alongside these traits, and vice versa. By leveraging these correlations and understanding the genetic underpinnings of these traits, breeding programs can more effectively select for high-yielding and high-oil content sunflower varieties, thereby improving overall productivity and quality(Singh *et al.*2019).

Table 3. Principal component analysis showing eigenvalues, the proportion of variance and unrotated loadings.

Parameter	Principal component axis								
	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9
Eigenvalue	3.043	1.89	1.275	0.797	0.676	0.463	0.381	0.298	0.178
Percentage of variance (%)	33.807	20.995	14.165	8.852	7.507	5.144	4.235	3.313	1.982
Cumulative variance (%)	33.807	54.801	68.967	77.818	85.325	90.469	94.705	98.018	100

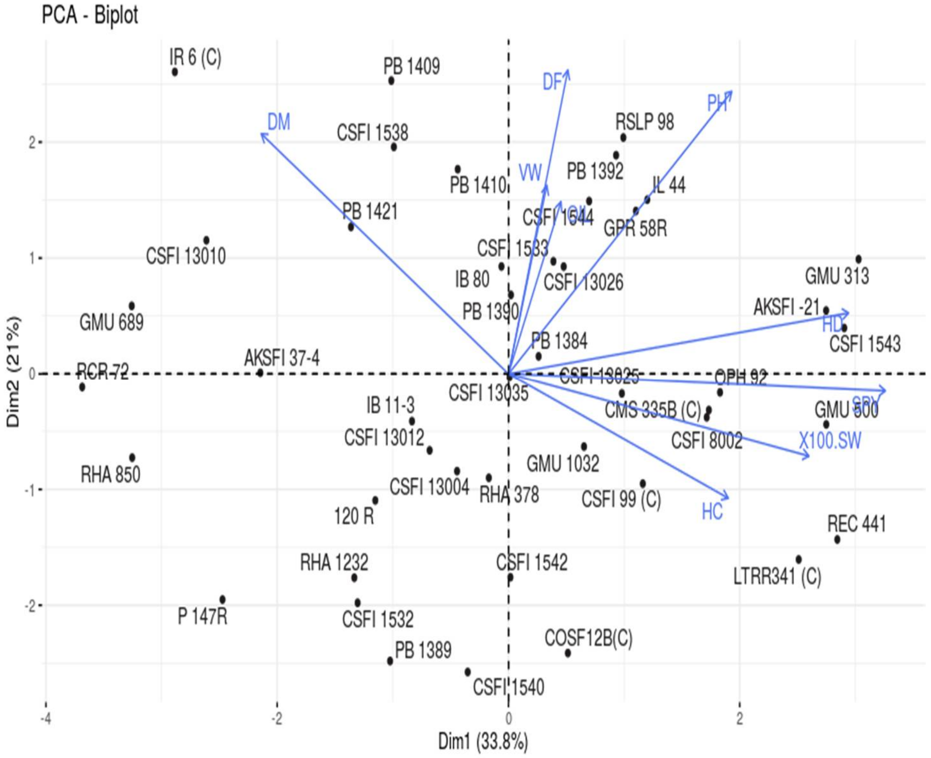


Fig. 3. A biplot illustrating the contributions of various factors to the variance between PC 1 and 2.

The PCA resulted in nine independent principal components with a cumulative explained variance of 100%. The significance of important characters for each PC can be determined by examining their associated eigenvalues. The PCA revealed that the first three components, with an eigenvalue greater than 1, accounted for about 68.96% of the total variability in 45 genotypes (Table 3). The first principal component (PC1) accounted for 33.807% of the total variation in the population. The second principal component (PC2) accounted for 20.99% of the total variation in the population. Together, PC1 and PC2 accounted for more than 50% of the total variability. The third principal component (PC3) accounted for 14.16% of the total variation in the population.The angles of vectors in the biplot diagram are crucial to consider, volume weight, days to 50% flowering, and plant heighthad a small angle with each other in Fig. 3(Hussain*et al.* 2017,Lagiso*et al.* 2021). PCA is a non-parametric method used to extract meaningful information from complex datasets by reducing dimensionality and eliminating interrelationships among components(Ibrar*et al.* 2022).

The present study revealed significant genetic variability among sunflower genotypes for seed yield and related traits, supporting their effective utilization in recombination breeding programs. High heritability coupled with substantial genetic advance for key traits indicates the predominance of additive gene action, enabling efficient selection. The positive association of seed yield with head diameter, hundred seed weight, and plant height highlights their importance as selection criteria, while the negative association with days to maturity suggests the advantage of early maturing genotypes. Principal component analysis further confirmed the contribution of major traits to overall variability. The genetically diverse and superior germplasm identified can serve as valuable donors for developing inbred lines and trait-specific heterotic gene pools, ultimately aiding in the development of high-yielding, oil-rich, and adaptable sunflower varieties.

References

Allard RW 1960. Principles of Plant Breeding. Wiley, New York. 485 pp.

Burton GWand DeVaneEH1953. Estimating heritability in tall Fescue (*Festuca arundinacea*) from replicatedclonalmaterial. Agron. J.**45**(10):478-481.

Dudhe MY, Mulpuri S, Meena HP, Ajjanavara RRG, Kodeboyina VS and Adala VR 2020. Genetic variability, diversity and identification of trait-specificaccessions from the conservedsunflowergermplasm for exploitation in the breedingprogramme. Agric. Res.**9**(1):9-22.

FAO 2022. Faostat, Food and Agriculture Organization of the United Nations. FAOSTAT Statistical Database, Rome.

de MendiburuF2023. Agricolae: Statistical Procedures for Agricultural Research. Published by International Potato Center, FAO AGRIS.

HussainF, RafiqM, GhiasM, QamarR, Razzaq MK, Hameed A, Habib S and Mustafa HSB 2017. Genetic diversity for seedyield and its componentsusing principalcomponent and clusteranalysis in sunflower (*Helianthus annuus* L.). Life Sci. J.**14**(5):71-78.

Hladni N, Miklic V, Mijic A, Jocic S and Miladinovic D2015. Correlation and path coefficient analysis for protein yield in confectionery sunflower (*Helianthus annuus* L.). Genetika**47**(3):811-818.

Ibrar D, Khan S, Mahmood T, Bakhsh A, Aziz I, Rais A and Hasnain Z 2022. Molecular markers-based DNA fingerprinting coupled with morphological diversity analysis for prediction of heterotic grouping in sunflower (*Helianthus annuus* L.). Front. Plant Sci.**13**:916845.

India Stat 2023. Agriculture selectedstate, season-wise area production yield.https://www.indiastat.com /table/agriculture/selected-state-season-wise-area-production-product/1457082

JohnsonHW, Robinson HF and Comstock RE 1955. Estimates of genetic and environmental variability in soybeans. Agronomy J.**47**(7):314-318.

Lagiso TM, Singh BCS and Weyessa B2021. Evaluation of sunflower (*Helianthus annuus* L.) genotypes for quantitative traits and character association of seed yield and yield components at Oromia region, Ethiopia. Euphytica**217**(2):1-13.

LakshmanSS, Chakraborty NR, Debnath S and Kant A 2021. Genetic variability, character association and divergence studies in sunflower (*Helianthus annuus* L.) for improvement in oil yield. Afr. J.Biol. Sci.**3**(1):129-145.

Lê S, Josse J and Husson F 2008. FactoMineR : An *R* Package for Multivariate Analysis. J. Statistical Software**25**(1):1-18.

Narayan P 2016. Recent demand-supply and growth of oilseeds and edibleoil in India: an analyticalapproach. Int. J. Adv. Engin. Res. Sci. **4**(1):32-46.

Riaz A, Nadeem Tahir MH, Rizwan M, Fiaz S, Chachar S, Razzaq K, Riaz B and Sadia H2019. Developing a selection criterionusing correlation and pathcoefficientanalysis in sunflower (*Helianthus Annuus* L.). Helia**42**(70):85-99.

Seiler GJ and Gulya TJ2005. Collection of rare, endangered, threatened, and interesting wild *Helianthus* species for the USDA-ARS sunflowergenebank. *In*: 10th Technical Consultation of the FAO-European Cooperative Research Network on Sunflower 17-20 July, Novi Sad, Serbia and Montenegro.

SinghVK, Sheoran RK, Chander S and SharmaB2019. Genetic variability, evaluation and characterization of sunflower (*Helianthus annuus* L.) germplasm. Bangladesh J. Bot.**48**(2):253-263.

Umarani E, Saritha A and Ramanjaneyulu AV 2022. Estimation of geneticparameters in sunflower (*Helianthus annuus* L.) germplasmlines for yield and itscontributingtraits. Int.J. Environ. Clim. Chan.**12**(12):936-942.

(Manuscript received on 20 February, 2026; revised on 06 April, 2026)