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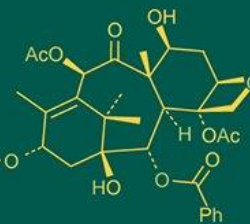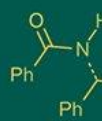
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Evaluation of genetic variability, yield attributes and character association in pre-release sunflower hybrids under Odisha agro-climatic conditions

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Abstract
The present study was conducted at the AICRP Sunflower research plot, Instructional Farm, OUAT, Bhubaneswar, to assess genetic variability, character association, and the direct and indirect effects of yield-attributing traits through path analysis. The study comprised 23 pre-release hybrids and two check varieties evaluated in a Randomized Block Design with two replications for eleven morphological and yield-related traits. Observations from five representative plants per replication were statistically analysed to estimate parameters such as mean, range, PCV, GCV, heritability, and genetic advance. Analysis of variance revealed significant differences among hybrids for all characters, confirming substantial genetic variability. Higher PCV than GCV across traits indicated environmental influence, although both were notably high for plant height, head diameter, oil yield, plot yield, and seed yield per plant. Seed yield per plant exhibited high heritability coupled with high genetic advance, suggesting predominance of additive gene action. Significant positive phenotypic and genotypic correlations were observed between seed yield and plant height, head diameter, number of leaves per plant, oil yield, and plot yield. Promising hybrids identified for plot yield (>20 q/ha) included IOSH-1321, IOSH-1327, IOSH-1329, IOSH-1331, IOSH-1335, IOSH-1336, and IOSH-1346, while hybrids superior in oil yield (>800 kg/ha) were IOSH-1326, IOSH-1329, IOSH-1331, IOSH-1335, IOSH-1336, and IOSH-1346. The study highlights key traits for effective selection in sunflower yield improvement.

Keywords: Genetic variability; heritability; genetic advance; character association; correlation; path analysis; yield attributes; oil yield; pre-release hybrids

Introduction
Sunflower (*Helianthus annuus* L.) is an important global oilseed crop cultivated for its high-quality edible oil, nutritional value and wide adaptability across diverse production environments. In India, sunflower contributes significantly to addressing the edible oil demand, and the development of superior hybrids with high yield and oil percentage remains a primary breeding objective (Seetharam *et al*., 2011) [11]. Effective crop improvement requires the presence of adequate genetic variability, as variability forms the basis for selection and genetic advancement (Allard, 1999) [1]. Understanding the magnitude of variability and the genetic parameters associated with key traits enables plant breeders to identify promising genotypes and design efficient breeding strategies.

Yield in sunflower is a complex polygenic trait influenced by interactions among multiple morphological, physiological and biochemical characters. Therefore, studying trait interrelationships through correlation and path analysis is essential for identifying traits that exert substantial direct or indirect contributions to seed yield (Dewey & Lu, 1959) [5]. While correlation analysis provides the direction and strength of association between traits, path coefficient analysis allows partitioning these correlations to reveal their underlying cause-effect relationships (Wright, 1921) [26]. Such information is critical for determining reliable selection criteria for yield improvement. Environmental variation may alter the expression of yield and its component traits; hence, evaluating new hybrids under specific agro-climatic conditions is vital (Falconer & Mackay, 1996) [6]. Odisha's rabi season conditions moderate temperatures, residual soil moisture and variable climatic patterns, present a unique environment for sunflower cultivation. Assessing pre-release hybrids under these conditions

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helps determine their suitability, stability and adaptability. Genotypes expressing desirable levels of genetic variability, high heritability and substantial genetic advance offer greater potential for improvement through selection (Johnson *et al*., 1955) [13].

The present study was undertaken to estimate the extent of genetic variability, quantify key genetic parameters and analyse correlations and path coefficients for yield-related traits. Twenty-three pre-release sunflower hybrids along with two standard checks were evaluated for eleven quantitative traits, including phenological traits, growth parameters, seed attributes, oil content and yield measures. Understanding how these traits interact and contribute to performance under Odisha conditions will facilitate the identification of superior hybrids and key yield-determining traits. Overall, the study aims to provide essential information for sunflower breeding programmes, offering a scientific basis for selecting high-yielding, early-maturing and high-oil hybrids suitable for cultivation in eastern Indian agro-ecologies.

Materials and Methods
The study was conducted during 2020 at the AICRP Sunflower research plot, Instructional Farm, OUAT, Bhubaneswar (20.2671°N, 85.8106°E; 25.9 m above mean sea level.). The experimental material comprised 23 pre-release sunflower hybrids and two checks (DRSH-1 and KBSH-44) obtained from IIOR, Hyderabad. The trial was laid out in a Randomized Block Design with two replications, sown on 15 January 2020 in 5.4 m² plots with 60×30 cm spacing. Recommended agronomic practices were followed. Five randomly selected plants per plot were tagged for recording observations on 11 morphological and yield traits, and mean values were used for analysis.

Characters Studied
Observations were recorded on eleven characters. Days to 50% flowering was noted as days from sowing to 50% plants flowering. Plant height was measured from the base to the capitulum. Days to maturity denoted days from sowing to physiological maturity. Number of leaves per plant was counted at full bloom. Head diameter was measured as the mean of two diagonal axes. 100-seed weight and 100-volume weight were recorded in grams. Oil content (%) was estimated using an NMR spectrometer at IIOR, Hyderabad. Oil yield (kg/ha) was computed from plot yield and oil percentage. Seed yield per plant and plot yield were recorded from harvested, cleaned and dried seeds.

Table 1: List of pre-release hybrids of Sunflower

Sl. No.	Genotype	Source
1	IOSH-1307	IIOR, Hyderabad
2	IOSH-1309	IIOR, Hyderabad
3	IOSH-1310	IIOR, Hyderabad
4	IOSH-1311	IIOR, Hyderabad
5	IOSH-1315	IIOR, Hyderabad
6	IOSH-1317	IIOR, Hyderabad
7	IOSH-1319	IIOR, Hyderabad
8	IOSH-1320	IIOR, Hyderabad
9	IOSH-1321	IIOR, Hyderabad
10	IOSH-1325	IIOR, Hyderabad
11	IOSH-1326	IIOR, Hyderabad
12	IOSH-1327	IIOR, Hyderabad
13	IOSH-1329	IIOR, Hyderabad
14	IOSH-1330	IIOR, Hyderabad
15	IOSH-1331	IIOR, Hyderabad
16	IOSH-1335	IIOR, Hyderabad
17	IOSH-1336	IIOR, Hyderabad
18	IOSH-1337	IIOR, Hyderabad
19	IOSH-1338	IIOR, Hyderabad
20	IOSH-1340	IIOR, Hyderabad
21	IOSH-1341	IIOR, Hyderabad
22	IOSH-1345	IIOR, Hyderabad
23	IOSH-1346	IIOR, Hyderabad
24	DRSH-1 (Check)	IIOR, Hyderabad
25	KBSH-44 (Check)	UAS, Bengaluru

Statistical Analysis
Data were analysed using OPSTAT and R software to estimate mean, range, standard error, critical difference, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, and genetic advance.

ANOVA and Test of Significance
The analysis of variance (ANOVA) for yield-related traits was conducted following the method proposed by Steel and Torrie (1960), using MSTAT-C software. The significance of differences among treatments was evaluated at the 5% and 1% probability levels. Both parental lines and hybrids were subjected to ANOVA, which revealed significant differences for all evaluated traits. The Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV), calculated as per Hallauer *et al*. (2010) [7], indicated substantial variability among the genotypes for all studied characters. Genetic advance and heritability (h²) estimates were derived following the procedures described by Hanson *et al*. (1956) [9]. Principal Component Analysis (PCA) was performed using PAST software (Hammer *et al*. (2001) [8] to reduce dimensionality and highlight major data trends, while pie charts were generated using the same software. Correlation analysis based on the Pearson

coefficient was conducted using IBM SPSS 20 (IBM Corp., 2011).

ANOVA was conducted as per RBD using the model: Yij = M + gi + rj + eij. Where Yij is observation, M is general mean, gi is genotype effect, rj replication effect, and eij is error. Variance components were estimated using mean sum of squares (Table 2).

Table 2: ANOVA with expected mean sum of squares

Source of Variation	Degrees of Freedom (d. f.)	Sum of Squares (SS)	Mean Sum of Squares (MSS)	Expected Mean Sum of Squares (EMS)	F-value
Replication	(r − 1)	(1/gi) Σ yj² − CF	MSr	σ²e + g σ²r	MSr / MSe
Genotypes	(g − 1)	(1/rj) Σ yi² − CF	MSg	σ²e + r σ²g	MSg / MSe
Error	(r − 1) (g − 1)	By subtraction	MSe	σ²e	
Total	(rg − 1)	Σ yi²j − CF			

Where:

r = Number of replications
g = Number of genotypes
MSr = Mean sum of squares due to replications
MSg = Mean sum of squares due to genotypes
MSe = Mean sum of squares due to error

Variance Components

Variance Type	Formula
Error variance	σ²e = MSe
Genotypic variance	σ²g = (MSg − MSe) / r
Phenotypic variance	σ²p = σ²g + σ²e

Estimation of Mean, Range, SE$_m$, SE$_d$ and CD

Standard formulas were used to compute mean, range, standard error of mean (SE$_m$), standard error of difference (SE$_d$), and critical difference (CD) at 5% significance level.

Heritability and Genetic Advance (Brief)

Broad-sense heritability (h²) was estimated following Hanson *et al*. (1956) [9], Lush (1949) and Burton & De Vane (1953) using:

$$h_{bs}^2 = \frac{\sigma_g^2}{\sigma_p^2}$$

where σg² and σp² denote genotypic and phenotypic variances, respectively. Genetic advance (GA) was computed as per Johnson *et al*. (1955) [13]:

$$GA = K \times h^2 \times \sigma_p$$

And expressed as percentage of the mean.

Correlation Studies

Genotypic and phenotypic correlations among traits were estimated using variance and covariance components. Covariance components were derived through ANCOVA as per Al-Jibouri *et al*.. Genotypic, phenotypic and environmental correlations were calculated using:

$$r_p = \frac{\sigma_p(xy)}{\sigma_p(x)\sigma_p(y)}, r_g = \frac{\sigma_g(xy)}{\sigma_g(x)\sigma_g(y)}, r_e = \frac{\sigma_e(xy)}{\sigma_e(x)\sigma_e(y)}$$

Standard errors were computed using:

$$SE(r) = \sqrt{\frac{1 - r^2}{(g - 2)}}$$

and significance was tested using the *t*-test with appropriate degrees of freedom.

Results and Discussion
Study of genetic variability

The study was conducted at the AICRP Sunflower research plot, Instructional Farm, OUAT, Bhubaneswar to evaluate genetic variability, character association and the direct and indirect effects of yield-attributing traits through path analysis. The experiment was laid out in a Randomized Block Design with two replications, using observations from five representative plants per replication. Eleven characters such as days to 50% flowering, plant height, head diameter, number of leaves per plant, days to maturity, 100-seed weight, 100-volume weight, oil content, oil yield, seed yield per plant and plot yield were recorded, and the mean values were used for statistical analysis.

The study of genetic variability was undertaken to assess the potential for improving traits through selection. Analysis of variance (Table 3) revealed that mean sum of squares due to treatments was highly significant (1% level) for all the quantitative characters examined, indicating the presence of substantial genetic variability among the hybrids. This confirmed that ample scope exists for selecting promising genotypes for yield and related traits.

Further assessment of variability, based on mean performance, range, coefficient of variation and genetic parameters (PCV and GCV), is presented in Tables 4 and 5. A wide range of variation was observed for most characters, reflecting considerable diversity among the genotypes. These estimates provide valuable insight into the extent of genetic variability and the relative influence of genetic and environmental factors on trait expression.

Table 3: Analysis of variance for 11 quantitative characters in 25 genotypes of sunflower

Sl. No.	Characters	Replication (1)	Treatments (24)	Error (24)
1	Days to 50% flowering	2.420	6.167**	1.170
2	Plant height (cm)	1,019.713	322.048**	64.362
3	Head diameter (cm)	1.411	6.647**	2.898
4	No. of leaves/plant	0.080	9.377**	2.732
5	Days to maturity	0.320	13.878**	1.195

6	100-seed weight (g)	0.024	0.825**	0.261
7	Volume weight (g/100 ml)	16.474	10.180**	2.576
8	Oil content (%)	1.267	8.088**	2.675
9	Oil yield	5,593.913	41,984.26**	15,310.988
10	Seed yield (g/plant)	66.586	102.451**	31.755
11	Plot yield	7.896	29.594**	8.480

* Significant at P = 0.05, ** Significant at P = 0.01

The evaluation of 25 sunflower genotypes revealed substantial variation across all eleven quantitative traits studied. Days to 50% flowering showed significant differences among genotypes, with values ranging from 55 days in DRSH-1 to 63 days in IOSH-1338, and an overall average of 57.30 days. DRSH-1 flowered earlier than KBSH-44, while several genotypes such as IOSH-1329, IOSH-1338 and IOSH-1345 showed significantly delayed flowering compared to both checks. This variation indicates ample scope for selecting early- or late-flowering hybrids based on breeding objectives. Plant height also exhibited significant variability, with the shortest genotype being IOSH-1311 (119.30 cm) and the tallest being IOSH-1337 (174.60 cm), against a general mean of 150.49 cm. Several entries, including IOSH-1311, IOSH-1319 and IOSH-1321, were significantly shorter than both checks, while genotypes such as IOSH-1346, IOSH-1338 and IOSH-1337 were significantly taller than DRSH-1. However, none surpassed the height of the national check KBSH-44 significantly. The broad range observed suggests considerable genetic diversity for plant height, facilitating selection for dwarf or tall plant types depending on agronomic suitability. Head diameter ranged from 16.40 cm in IOSH-1311 to 25.00 cm in IOSH-1329, with an overall mean of 21.68 cm. Most genotypes were comparable to the checks, except IOSH-1329 and IOSH-1330, which exhibited significantly larger heads, and IOSH-1311, which had a significantly smaller head diameter. As head diameter directly influences seed production potential, these differences highlight valuable variability for improvement. Number of leaves per plant showed a wide range between 20.20 (IOSH-1309) and 28.40 (IOSH-1336). Several genotypes, including IOSH-1309 and IOSH-1311, produced significantly fewer leaves than both checks, while IOSH-1336 and IOSH-1338 produced significantly more leaves. A few genotypes also exceeded DRSH-1 in leaf number, although none surpassed KBSH-44, which recorded one of the highest leaf counts. This variation indicates differential photosynthetic potential among genotypes. Days to maturity ranged from 85 days (IOSH-1335) to 95 days (IOSH-1338), with a mean of 89.28 days. DRSH-1 was the earliest to mature, whereas KBSH-44 matured at 94 days. Most hybrids matured earlier than KBSH-44 but later than DRSH-1, suggesting variability in maturity duration suitable for different cropping systems or climatic conditions. Hundred-seed weight ranged between 5.61 g in IOSH-1311 and 8.53 g in IOSH-1337, with an

average of 7.30 g. IOSH-1337 and IOSH-1345 recorded significantly higher seed weights than the overall mean, while IOSH-1311 and IOSH-1320 recorded significantly lower values than both checks. Only IOSH-1337 showed superiority over DRSH-1 for this trait. The observed differences imply scope for enhancing seed size through selection. For 100-volume weight, genotypes varied from 37.36 g (IOSH-1311) to 48.74 g (DRSH-1), with a mean of 44.32 g. IOSH-1325 recorded significantly higher values than the mean, while IOSH-1311 and IOSH-1341 were significantly lower than both checks. This parameter reflects seed density and indirectly seed quality, and the variability observed offers room for improvement. Oil content varied from 33.87% (KBSH-44) to 42.27% (IOSH-1326), with a general mean of 37.89%. Many entries showed significantly higher oil content than KBSH-44, and IOSH-1326 was the only genotype superior to DRSH-1. The wide range highlights valuable diversity for developing high-oil hybrids. Oil yield exhibited considerable variation, ranging from 345.248 kg/ha in IOSH-1317 to 898.94 kg/ha in IOSH-1335, with a mean of 693.425 kg/ha. Although no genotype surpassed both checks, some entries performed comparably, while hybrids such as IOSH-1309, IOSH-1311 and IOSH-1317 recorded significantly lower oil yields. This trait, being a function of both seed yield and oil content, reflects cumulative performance and is crucial for commercial sunflower production. Seed yield per plant ranged from 24.6 g (IOSH-1309) to 56.1 g (IOSH-1326), with a mean of 42.890 g. IOSH-1326 showed the highest seed yield and significantly exceeded the general mean. IOSH-1309 and IOSH-1311 recorded significantly lower values. Many other genotypes performed on par with the checks. This variation demonstrates substantial potential for selecting high-yielding hybrids. Plot yield ranged from 9.445 q/ha (IOSH-1317) to 24.105 q/ha (IOSH-1329), with an overall mean of 18.245 q/ha. Three genotypes IOSH-1309, IOSH-1311 and IOSH-1317 produced significantly lower yields than both checks, while none exceeded the check varieties significantly. The remaining hybrids performed similarly to the standard checks, suggesting stable performance under the tested conditions. Overall, the results indicate wide genetic variability among the sunflower hybrids across all traits, providing strong opportunities for effective selection and breeding for improved flowering behaviour, maturity duration, seed traits, oil content and yield performance.

Table 4: Mean performance of 25 genotypes of sunflower for 11 quantitative characters

Sl. No.	Genotypes	DFF	PH (cm)	HD (cm)	NLP	DM	100-SW (g)	VW (g/100 ml)	OC (%)	OY (kg/ha)	SYP (g/plant)	PY (q/ha)
1	IOSH-1307	57	139.25	21.4	23.1	90	8.075	42.81	37.96	580.365	40.8	15.295
2	IOSH-1309	57.5	137.6	22.6	20.200*	90	7.367	45.56	37.53	387.515*	24.600*	10.325*
3	IOSH-1310	58	142.95	20.4	23.2	90	7.237	46.7	31.11	669.806	37.1	17.13
4	IOSH-1311	58	119.300*	16.400*	20.300*	91	5.605*	37.360*	38.975	425.122*	24.750*	10.790*
5	IOSH-1315	58.5	141.8	20.6	24.3	91	7.516	44.48	40.92	790.367	45.6	19.17
6	IOSH-1317	56.5	147.7	21.9	23.9	89	7.81	43.88	36.575	345.248*	40.05	9.445*
7	IOSH-1319	55.5	134.000*	21	22	88	6.98	45.43	38.785	657.507	38.2	16.945
8	IOSH-1320	56	145.1	20.3	25.1	88	6.170*	45.715	40.945	727.736	42.6	17.795

9	IOSH-1321	56.5	134.300*	19.3	21.9	88	6.88	44.42	37.435	762.557	42.75	20.37
10	IOSH-1325	57.5	149.35	22.3	23.6	90	6.906	47.485	40.265	662.087	40.2	16.405
11	IOSH-1326	56.5	150.2	22	23.1	88	6.85	45.8	42.270**	820.386	56.1	19.46
12	IOSH-1327	56	148.75	22.6	23.9	86.5	7.87	43.275	36.535	755.253	47.5	20.555
13	IOSH-1329	59.5	151.7	25.000**	27.1	90.5	6.827	44.185	35.735	865.754	50.1	24.105
14	IOSH-1330	56.5	158.6	24.500**	24.4	88	6.931	45.805	37.35	684.048	42.7	18.245
15	IOSH-1331	55.5	152.95	23.3	24.1	86	7.326	42.53	35.9	829.009	47.3	23.15
16	IOSH-1335	56.5	147.2	21.2	25.4	85	7.151	44.975	38.165	898.94	50.5	23.52
17	IOSH-1336	58	166.3	20.4	28.4	90	6.823	43.63	38.635	809.831	44.4	20.975
18	IOSH-1337	56.5	174.6	24.4	26.5	88	8.533	43	35.86	530.799	43.1	14.815
19	IOSH-1338	63.00**	169.95	21.1	27.8	95	7.985	43.285	34.625	644.572	41.3	18.66
20	IOSH-1340	56.5	155.3	20.3	25.1	88	7.358	43.525	37.215	693.733	39.6	18.615
21	IOSH-1341	56	151.7	21.8	23.6	88	7.422	41.210*	36.49	711.269	40.9	19.535
22	IOSH-1345	61.00**	160.3	23.3	27.2	95	8.295	45.69	38.135	757.568	44.5	19.845
23	IOSH-1346	57.5	168.7	23.3	25.3	90	7.333	42.515	39.695	850.426	52.2	21.425
24	DRSH-1 (Check)	55	152.3	21.5	23.7	85	7.63	48.74	38.26	749.84	46.5	19.585
25	KBSH-44 (Check)	58.5	162.4	21.1	27.4	94	7.691	46.165	33.87	725.888	48.9	21.435

**significantly higher than highest check, *significantly lower than lowest check

Genetic parameters of yield and its attributing characters

The genetic parameters of yield and its attributing traits were assessed using mean data of 23 sunflower hybrids and two checks. Key genetic statistics including mean, range, phenotypic and genotypic coefficients of variation (PCV and GCV), heritability and genetic advance were analyzed to understand trait variability and the extent of genetic control. Traits were classified into low, medium and high categories for PCV, GCV, heritability and genetic advance based on established criteria by Johnson et al. (1955) [13].

The coefficients of variation (CV) showed that days to maturity had the lowest variation (1.224%), while oil yield exhibited the highest (17.844%). Most traits recorded CV values below 15%, except oil yield and plot yield, indicating relatively uniform experimental conditions. PCV ranged from 3.075% for days to maturity to 23.837% for plot yield. High PCV was noted for oil yield, seed yield and plot yield, suggesting substantial phenotypic variation. Traits such as days to 50% flowering, plant height, days to maturity, 100-volume weight and oil content exhibited low PCV values, indicating limited environmental influence. Medium PCV (10-15%) was recorded for traits such as head diameter and 100-seed weight. GCV values ranged from 2.758% (days to 50% flowering) to 17.751% (plot yield). High GCV was detected for oil yield, seed yield and plot yield, demonstrating strong inherent genetic variability for these traits. Lower GCV was recorded for most characters, including plant height, head diameter, number of leaves per plant, days to maturity and oil content. The moderate GCV values observed in some traits further indicated a combination of genetic and environmental influence. In all cases, PCV values exceeded GCV values, suggesting environmental effects on trait expression. However, the small differences between PCV and GCV for most traits indicate that genetic factors predominantly govern variability, except in oil content, oil yield and plot yield, where environmental sensitivity appears greater.

Heritability and Genetic Advance

Broad-sense heritability estimates revealed that days to maturity (84.144%) had the highest heritability, while head diameter (39.277%) had the lowest. High heritability (>60%) was recorded for days to 50% flowering, plant height, days to maturity and seed yield per plant. Medium heritability (30-60%) was observed for head diameter,

number of leaves per plant, 100-seed weight, 100-volume weight, oil content, oil yield and plot yield. These results suggest that some traits, particularly seed yield, maturity duration and flowering time, are more genetically controlled and therefore can be effectively improved through selection. Genetic advance as a percentage of mean ranged from 4.690% for days to 50% flowering to 27.230% for plot yield. High genetic advance (>20%) was observed for oil yield, seed yield per plant and plot yield, indicating strong additive gene action and high potential for improvement through selection. Moderate genetic advance (10-20%) was observed for plant height, number of leaves per plant and 100-seed weight. Low genetic advance values were recorded for traits such as days to 50% flowering, days to maturity, oil content and head diameter, indicating possible non-additive gene action or environmental influence. High heritability coupled with high genetic advance for seed yield per plant suggested that selection would be highly effective. Traits exhibiting high heritability but low genetic advance, such as days to 50% flowering and days to maturity, may require hybridization and recurrent selection to capitalize on both additive and non-additive genetic effects. Medium heritability combined with low genetic advance in traits like head diameter and oil content suggested limited scope for direct selection. Meanwhile, traits with moderate heritability and high genetic advance, such as oil yield and plot yield, indicated substantial additive gene control and strong selection potential.

The analysis of variance revealed highly significant differences among the 25 sunflower hybrids for all eleven quantitative traits, confirming the presence of substantial genetic variability. Such significant mean sum of squares for treatments has been widely reported in sunflower improvement programmes and is considered a prerequisite for effective selection (Singh et al., 2021; Hussain et al., 2022) [22, 10]. The magnitude of differences observed across traits such as days to 50% flowering, plant height, head diameter and yield components indicates the existence of both early- and late-maturing types, dwarf and tall genotypes, along with high-yielding and high-oil lines that could be exploited in future breeding.

Days to 50% flowering and days to maturity exhibited relatively narrow ranges but high significance across genotypes, suggesting that even modest variation in phenology can be genetically meaningful. The PCV and GCV values for these traits were moderate, while

heritability estimates were high (68.10% and 84.14%, respectively), indicating strong additive genetic control. Similar findings were reported by Kumar *et al.* (2020) and more recently by Reddy and Shankar (2023) [20], who also observed high heritability and moderate genetic advance for flowering and maturity traits in diverse sunflower hybrids. These traits are essential for adaptation to varying agro-climatic zones, and the presence of variability in the present material opens scope for developing hybrids suited to early or late planting windows. Plant height showed wide variability (119.30-174.60 cm), accompanied by moderate GCV (7.54%) and heritability of 66.68%. Comparable patterns have been documented by Kandel *et al.* (2022) [14], who noted similar PCV-GCV proximity for plant height, indicating limited environmental influence. The presence of both short and tall statured genotypes can be beneficial for tailoring hybrids for lodging resistance or mechanical harvesting suitability. Number of leaves per plant also showed considerable diversity with moderate heritability (54.88%), indicating scope for improvement. Leaf production influences canopy structure and photosynthetic efficiency, and similar magnitudes of variability were reported by Azeem *et al.* (2021) [2] and Patel & Chandel (2024) [18].

Head diameter exhibited moderate PCV and GCV along with lower heritability (39.28%), indicating stronger environmental influence. Such trends were also found by Verma *et al.* (2023) [25], who reported that head diameter may not respond rapidly to selection due to its polygenic nature and environmental responsiveness. A moderate degree of variability was also found for 100-seed weight and volume weight. The moderate heritability and genetic advance observed for these traits align with earlier reports (Mankar *et al.*, 2021; Jat & Sharma, 2023) [17, 12], indicating that improvement is possible through multi-season selection. Oil content ranged from 31.11% to 42.27% with moderate heritability (50.29%), consistent with the findings of Das *et al.* (2022) [4], who also reported moderate heritability due to the complexity of oil biosynthesis pathways. The identification of genotypes surpassing checks (such as IOSH-1326) indicates important opportunities for improving oil concentration in future hybrids.

Seed yield per plant and plot yield showed wide ranges and moderate to high PCV and GCV values, indicating significant genetic diversity. Heritability values were moderate to high (63.19% and 55.45%, respectively), suggesting that additive genetic effects contribute substantially to their expression. High genetic advance for seed yield (21.24%) and plot yield (27.23%) indicates that direct selection would be effective. Similar trends have been

reported by Tiwari *et al.* (2022) [24], Yadav *et al.* (2023) [27], and most recently by Bhattarai & Pant (2024) [3], all of whom noted that yield traits in sunflower commonly exhibit moderate to high heritability coupled with high genetic advance. Oil yield exhibited considerable variability and moderately high PCV and GCV, though with lower heritability (46.55%). Since oil yield is a composite trait influenced by both seed yield and oil content, this pattern is consistent with previous research (Rani *et al.*, 2022) [19]. The present results suggest that selection for oil yield should be indirect, via its major contributing traits. The presence of substantial genetic variability across all characters indicates strong potential for genetic improvement in sunflower. The moderate to high heritability combined with high genetic advance for key traits such as seed yield, plot yield, plant height, and days to maturity suggests that additive gene effects predominate, making these traits amenable to direct selection. Traits with moderate heritability but lower genetic advance, such as head diameter and oil content, may require multi-environment evaluation or selection indexing to enhance their improvement. The results collectively agree with recent findings across sunflower breeding research, reinforcing the importance of genetic variability as the foundation for developing climate-resilient, high-yielding, and high-oil hybrids.

Character Association

Correlation analysis at phenotypic and genotypic levels revealed valuable information for trait-based selection. Among 55 correlation estimates, 22 were positive and significant at the phenotypic level, while 25 were significant and 38 positives at the genotypic level. Eight significant correlations at the genotypic level were negative. Seed yield per plant showed strong, positive and significant correlations with plant height, head diameter, number of leaves per plant, oil yield and plot yield at both phenotypic and genotypic levels, indicating these traits are key contributors to seed yield. A significant positive phenotypic correlation was also observed between 100-seed weight and seed yield. Days to flowering and maturity showed negative but non-significant correlations with seed yield, suggesting minimal direct influence. Oil yield demonstrated significant positive correlations with plant height and number of leaves per plant at both levels, and additionally with 100-volume weight at the genotypic level, highlighting the importance of vegetative vigour and seed characteristics in determining oil productivity. Oil content exhibited significant negative associations with plant height, number of leaves per plant, head diameter and 100-seed weight, suggesting a trade-off between oil percentage and plant size or seed weight.

Table 5: Genetic parameters of variability for eleven quantitative characters in sunflower

Sl. No.	Characters	Mean	Range (Min-Max)	CV (%)	PCV (%)	GCV (%)	h² (Broad sense) (%)	Genetic advance	Genetic advance as % of Mean
1	Days to 50% flowering	57.300	55 - 63	1.887	3.343	2.758	68.105	2.687	4.690
2	Plant height (cm)	150.492	119.30 - 174.60	5.330	9.236	7.543	66.687	19.095	12.688
3	Head diameter (cm)	21.680	16.40 - 25.00	7.852	10.076	6.315	39.277	1.768	8.153
4	No. of leaves/plant	24.424	20.20 - 28.40	6.767	10.074	7.463	54.881	2.782	11.390
5	Days to maturity	89.280	85 - 95	1.224	3.075	2.821	84.144	4.759	5.330
6	100-seed weight (g)	7.303	5.61 - 8.53	6.995	10.092	7.269	51.886	0.788	10.786
7	Volume weight (g/100 ml)	44.327	37.36 - 48.74	3.620	5.697	4.459	61.206	3.101	6.996
8	Oil content (%)	37.890	31.11 - 42.27	4.316	6.122	4.342	50.294	2.403	6.343
9	Oil yield (kg/ha)	693.425	345.248 - 898.94	17.844	24.409	16.654	46.554	162.319	23.408
10	Seed yield (g/plant)	42.890	24.60 - 56.10	13.138	19.099	15.183	63.190	9.110	21.240
11	Plot yield (q/ha)	18.304	9.45 - 24.11	15.898	23.837	17.751	55.453	4.984	27.230
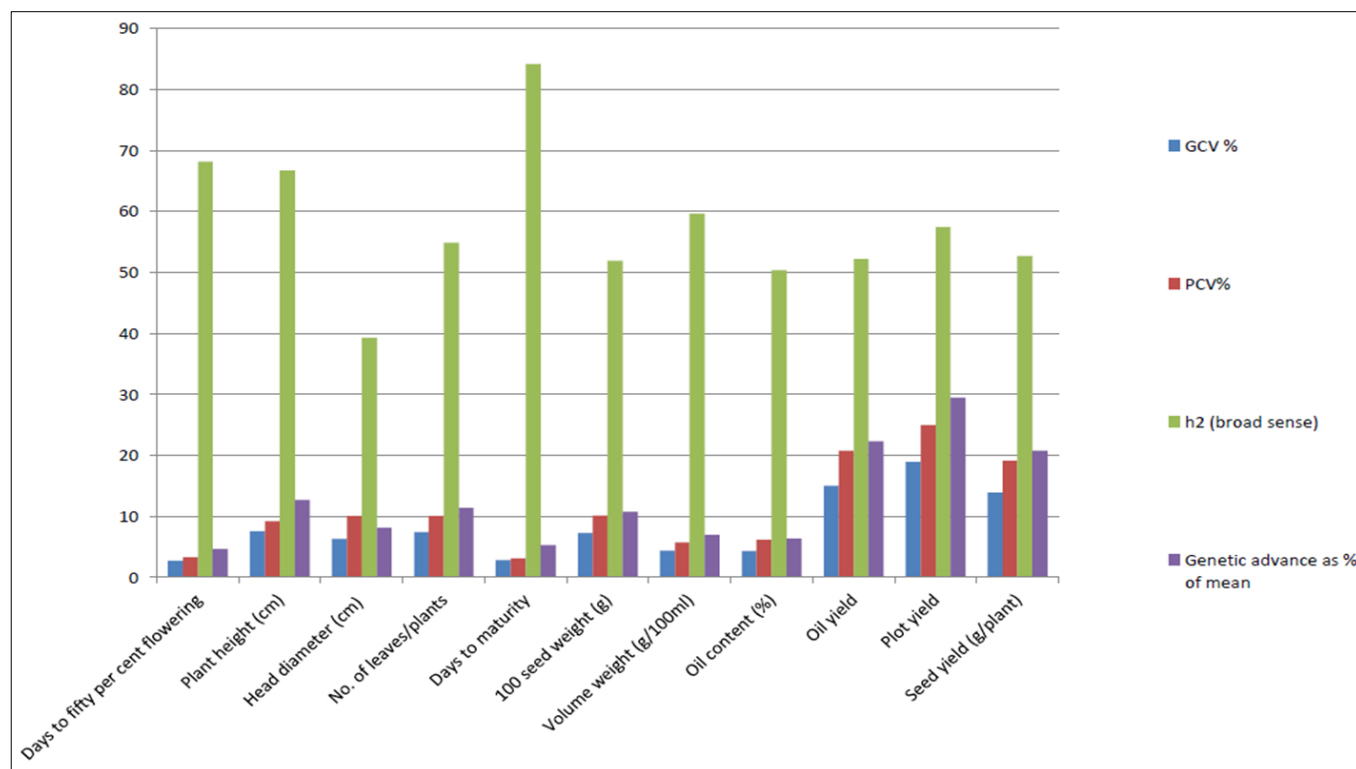
Fig 2: Graphical representation of GCV, PCV, h2 % (bs) and GA as % of mean for 11 quantitative characters

Correlation among other component traits

Correlation analysis among the 11 quantitative traits (Table 6 & 7) revealed generally similar trends at both genotypic and phenotypic levels, with genotypic correlations being consistently higher, indicating stronger inherent genetic relationships. Days to 50% flowering showed significant positive correlations with number of leaves per plant and days to maturity at both levels, but negative and non-significant correlations with 100-volume weight, oil content, oil yield, plot yield and seed yield. Plant height exhibited strong positive and significant associations with head diameter, number of leaves per plant, 100-seed weight, oil yield, plot yield and seed yield, while showing a significant negative correlation with oil content. Head diameter was significantly and positively correlated with 100-seed weight and seed yield, and also positively associated with oil yield. Number of leaves per plant displayed significant positive correlations with days to maturity, 100-seed weight, oil yield, plot yield and seed yield at the genotypic level; similar but slightly weaker trends were observed phenotypically. Days to maturity showed negative correlations with most traits at both levels, except oil yield, with which it had a negative but significant association only at the genotypic level. Hundred-seed weight exhibited significant negative correlations with oil content at both levels. Hundred-volume weight showed significant positive genotypic correlations with oil yield, oil content and seed yield, though all phenotypic correlations were positive but non-significant. Overall, these relationships indicate that traits such as plant height, head diameter and number of leaves per plant are key contributors to yield components in sunflower.

Correlation analysis provides crucial insight into the interrelationships among traits and their collective influence on yield, thereby guiding indirect selection in sunflower improvement programmes. In the present study, a higher number of significant correlations at the genotypic level

than at the phenotypic level indicates that the observed associations were primarily governed by genetic factors, whereas environmental influences tended to weaken phenotypic correlations. Such patterns where genotypic correlations exceed phenotypic correlations have been consistently reported in sunflower (Kandel *et al.*, 2022; Yadav *et al.*, 2023; Bhattarai & Pant, 2024) [27, 15, 3], confirming the reliability of genetic correlations for guiding selection.

Seed yield per plant exhibited strong and significant positive correlations with plant height, head diameter, number of leaves per plant, oil yield, and plot yield at both phenotypic and genotypic levels. These results indicate that vigorous vegetative growth and larger reproductive structures contribute directly to higher seed productivity. Similar findings were reported by Tiwari *et al.* (2022) [24], who noted that plant height and head diameter were major determinants of seed yield in sunflower. Likewise, Verma *et al.* (2023) [25] observed that leaf number and head diameter were strongly correlated with yield, supporting the idea that photosynthetic capacity and sink size are key contributors to productivity. The significant positive phenotypic association between 100-seed weight and seed yield aligns with observations by Mankar *et al.* (2021) [17], who emphasized the importance of seed size in determining overall yield potential. The absence of significant correlations between seed yield and both days to flowering and maturity suggests that earliness is not a strong determinant of yield in the studied material an interpretation consistent with Reddy and Shankar (2023) [20], who found weak or non-significant associations between phenological traits and yield.

Oil yield showed significant and positive correlations with plant height and number of leaves per plant at both levels, reflecting the role of vegetative vigor in enhancing assimilate supply for oil biosynthesis. Additionally, its significant positive genotypic association with 100-volume weight indicates that denser, heavier seed lots may

contribute to higher oil productivity. This aligns with results from Das *et al*. (2022) [4] and Rani *et al*. (2022) [19], who also reported positive relationships between seed physical characteristics and oil output. Oil content, on the other hand, displayed significant negative correlations with plant height, number of leaves per plant, head diameter, and 100-seed weight. This suggests a potential trade-off between morphological robustness and oil concentration possibly due to differential allocation of assimilates between structural biomass, seed size, and lipid deposition. Similar inverse relationships between oil content and plant size traits were reported by Azeem *et al*. (2021) [2] and Patel and Chandel (2024) [18], who argued that breeding for high oil percentage might require careful balancing of seed and plant growth characteristics.

Table 6: Phenotypic correlation coefficient (r_p) among 11 characters in 25 sunflower genotypes

Characters	PH (cm)	HD (cm)	NLP	DM	100-SW (g)	VW (g/100 ml)	OC (%)	OY (kg/ha)	PY (q/ha)	SYP (g/plant)
DFF	0.247	-0.069	0.396**	0.875**	0.130	0.074	-0.223	-0.063	0.005	-0.075
PH (cm)		0.500**	0.751**	0.166	0.460**	0.218	-0.287*	0.283*	0.358*	0.465**
HD (cm)			0.217	-0.136	0.427**	0.247	-0.118	0.271	0.308*	0.403**
NLP				0.321*	0.290*	0.141	-0.291*	0.361*	0.442**	0.468**
DM					0.155	0.085	-0.186	-0.164	0.117	-0.146
100-SW (g)						0.178	-0.377**	0.059	0.149	0.308*
VW (g/100 ml)							0.142	0.213	0.177	0.223
OC (%)								0.250	0.004	0.081
OY (kg/ha)									0.966**	0.794**
PY (q/ha)										0.789**

* = Significant at 5%, ****** = Significant at 1% & Values below the diagonal are omitted for clarity, as the correlation matrix is symmetrical.

Table 7: Genotypic correlation coefficient ($r_{(g)}$) among 11 characters in 25 sunflower genotypes

Characters	PH (cm)	HD (cm)	NLP	DM	100-SW (g)	VW (g/100 ml)	OC (%)	OY (kg/ha)	PY (q/ha)	SYP (g/plant)
DFF	0.390**	0.127	0.631**	0.914**	0.333*	-0.092	-0.266	0.054	0.124	-0.067
PH (cm)		0.778**	0.959**	0.249	0.695**	0.089	-0.477**	0.371**	0.467**	0.650**
HD (cm)			0.696**	0.024	0.664**	0.430**	-0.607**	0.072	0.207	0.532**
NLP				0.426**	0.523**	0.109	-0.463**	0.650**	0.739**	0.749**
DM					0.222	-0.093	-0.193	-0.219	-0.148	-0.229
100-SW (g)						0.187	-0.642**	-0.346*	-0.181	0.101
VW (g/100 ml)							0.298*	0.301*	0.213	0.412**
OC (%)								-0.020	-0.300*	-0.030
OY (kg/ha)									0.962**	0.805**
PY (q/ha)										0.770*

* = Significant at 5%, ****** = Significant at 1% & Matrix above diagonal is shown; the lower triangle is omitted due to symmetry

Days to 50% flowering exhibited strong positive correlations with number of leaves per plant and days to maturity at both levels, indicating that later-flowering genotypes tend to have more vegetative growth and longer life cycles. This trend is similar to findings by Singh *et al*. (2021) [22], who linked extended vegetative duration with delayed maturity in sunflower hybrids. Plant height showed strong and significant positive correlations with head diameter, leaf number, 100-seed weight, plot yield, and seed yield at both levels, confirming its role as an indicator of overall plant vigor. These results correspond with those of Kandel *et al*. (2022) [15], who also observed that taller plants tend to produce larger heads and higher yields. Head diameter was positively associated with 100-seed weight, oil yield, and seed yield, reinforcing its importance as a determinant of sink capacity an observation supported by Verma *et al*. (2023) [25] and Jat and Sharma (2023) [12]. Number of leaves per plant showed strong positive correlations with yield components at the genotypic level, reinforcing the importance of canopy development. Days to maturity showed mostly negative correlations with key traits, suggesting that late-maturing genotypes may not offer yield advantages an interpretation consistent with Bhattarai and Pant (2024) [3]. Volume weight exhibited positive genotypic correlations with oil yield, oil content and seed yield, consistent with findings reported by Das *et al*. (2022) [4], who noted that seed density is a useful indicator of both seed quality and oil potential.

The correlation patterns observed suggest that plant height, head diameter, number of leaves per plant, and 100-seed weight are key components influencing seed and oil productivity in sunflower. Since these traits show strong genetic associations with yield, they can serve as reliable indirect selection criteria. Negative associations between oil content and growth traits imply that simultaneous improvement of oil percentage and plant size may require careful selection strategies or index-based selection. The combined interpretation of phenotypic and genotypic correlations demonstrates that yield improvement efforts should prioritize traits with strong, positive, and genetically driven associations with seed and oil yield.

Conclusion

The present investigation on pre-release sunflower hybrids demonstrated substantial genetic variability across all eleven morphological and yield-attributing traits, confirming strong potential for genetic improvement. Higher phenotypic variance compared to genotypic variance for most characters indicated environmental influence, though the relatively small differences between PCV and GCV for several traits suggested predominant genetic control. Traits such as plant height, head diameter, oil yield, plot yield and seed yield per plant exhibited high variability, highlighting

their potential contribution to yield enhancement. High heritability combined with high genetic advance for seed yield per plant revealed the predominance of additive gene action, making this trait highly amenable to direct selection. Plant height also showed high heritability and moderate genetic advance, suggesting its utility as an indirect selection criterion. Correlation analysis indicated strong positive associations of seed yield with plant height, head diameter, number of leaves per plant, oil yield and plot yield at both genotypic and phenotypic levels. The study also identified several promising hybrids IOSH-1321, IOSH-1327, IOSH-1329, IOSH-1331, IOSH-1335, IOSH-1336 and IOSH-1346 for high plot yield, and IOSH-1326, IOSH-1329, IOSH-1331, IOSH-1335, IOSH-1336 and IOSH-1346 for superior oil yield indicating their potential for advancement in breeding programmes. Overall, the findings underscore the importance of selecting traits such as plant height, head diameter, days to maturity, 100-seed weight and 100-volume weight to enhance seed and oil productivity. The study provides valuable guidance for future sunflower improvement strategies aimed at developing high-yielding, high-oil hybrids suited to diverse growing environments.

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