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Assessment of Heritability and Correlation Analysis of Yield and Oil-Related Traits in Different Safflower (*Carthamus tinctorius* L.) Genotypes

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ABSTRACT

Genetic variability and reliable heritability estimates are prerequisites for effective selection in plant breeding. This study assessed heritability and trait correlations for yield and yield-related characters in ten safflower (*Carthamus tinctorius* L.) genotypes. The experiment was carried out during the Rabi season of 2025–2026 at the Experimental Field, Botanical Garden, Department of Plant Breeding and Genetics, Sindh Agriculture University, Tandojam, Sindh, Pakistan. A Randomized Complete Block Design (RCBD) with three replications was used. Nine yield and yield-related traits were recorded and analyzed. Analysis of variance revealed highly significant ($P \leq 0.01$) differences among the genotypes for all studied traits, indicating the presence of substantial genetic variability and considerable potential for genetic improvement through selection. Based on mean performance, genotypes PI-304093 and PI-306956 exhibited superior performance for most of the evaluated traits, suggesting their potential as valuable genetic resources for developing high-yielding safflower cultivars. Correlation analysis showed that most yield-related traits were positively and significantly associated with one another, indicating the possibility of simultaneous improvement through selection. High broad-sense heritability estimates were observed for days to 90% maturity (96.23%), plant height (97.99%), days to 75% flowering (95.09%), biomass per plant (79.97%), seed yield per plant (78.84%), oil content (67.69%), harvest index (62.25%), and capsules per plant (61.93%). These results indicate that direct phenotypic selection can be effective for most traits, and that harvest index may serve as a useful indirect selection criterion for improving seed yield. Genotypes PI-304093 and PI-306956 are recommended as promising parental material for safflower breeding, while multi-location, multi-season trials are suggested to confirm their stability before use in cultivar development.

Introduction

Pakistan meets less than a third of its edible oil requirement from domestic production, importing the remainder at a cost of billions of rupees annually and placing sustained pressure on foreign exchange reserves (Amjad, 2014; Hussain et al., 2020). Conventional oilseed crops such as cotton (*Gossypium hirsutum* L.), rapeseed (*Brassica napus* L.), and sunflower (*Helianthus annuus* L.). However, their production has not closed the demand gap, creating scope for alternative oilseeds such as safflower (*Carthamus tinctorius* L.), valued for its adaptability and its wide range of industrial and nutritional applications.

Safflower (*Carthamus tinctorius* L.) is a drought-tolerant, deep-rooted, annual oilseed crop belonging to the family Asteraceae. It is believed to have originated in the Mediterranean region and parts of Central Asia and is now cultivated in many countries across North and South America, Australia, Europe, and the Indian subcontinent (Ahmadzadeh, 2013; Golkar et al., 2011). The crop is primarily valued for its premium-quality edible oil, rich in linoleic and oleic acid, and is regarded as one of the healthiest vegetable oils for human consumption (Arslan, 2007); it is also used in paints, cosmetics, pharmaceuticals, and biodiesel (Çamaş & Esendal, 2006). The residual meal obtained after oil extraction is rich in protein and serves as a valuable livestock feed, enhancing the overall economic value of the crop (Bahmankar et al., 2017).

In Pakistan, safflower is well adapted to semi-arid conditions, particularly in Sindh and Balochistan, but remains underutilized because of a narrow genetic base and limited breeding attention (Amjad, 2014; Omid Tabrizi, 2005).

Genetic variability is the foundation of any breeding program, and its assessment in available germplasm is a prerequisite for effective selection (Johnson et al., 1955; Holland et al., 2003). Heritability further partitions this variability into genetic and environmental components, indicating the proportion of phenotypic variance attributable to genetic factors and, therefore, the expected efficiency of phenotypic selection (Falconer, 1989; Lush, 1940). High heritability estimates for plant height, flowering and maturity duration, seed yield, and oil content have been reported in several safflower studies, indicating that these traits respond well to direct selection (Arslan, 2007; Muhammad et al., 2020; Gulati et al., 2023). More recently, Sabaghnia et al. (2024) confirmed substantial genetic diversity for vegetative and agronomic traits in safflower germplasm evaluated under semi-arid conditions, while Pushpa et al. (2023) reported that selection based on branching, capitula number, and seed weight is an effective strategy for improving seed yield.

Correlation analysis complements heritability by quantifying the strength and direction of association between traits, guiding indirect selection when the primary trait is difficult to measure or has low heritability (Singh et al., 2004; Snedecor & Cochran, 1980). In safflower, seed yield has generally been reported to be positively associated with plant height, branch number, capsules per plant, and harvest index (Paikara & Parihar, 2019; Pushpa et al., 2017), although the magnitude and even direction of these relationships vary with genetic background and environment (Carapetian et al., 2019; Golparvar, 2011).

Despite the crop's potential, comprehensive genetic evaluation of safflower germplasm in Pakistan remains limited (Amjad, 2014; Bishnoi et al., 2021), restricting the development of high-yielding, locally adapted cultivars. The present study was therefore conducted to estimate heritability and evaluate correlations among yield and yield-related traits in ten safflower genotypes, with the aim of identifying superior genotypes and informative selection criteria for safflower improvement under the agro-climatic conditions of Sindh, Pakistan.

Materials and Methods

Experimental Site and Design

The experiment was carried out during the Rabi season of 2025–2026 at the Experimental Field, Botanical Garden, Department of Plant Breeding and Genetics, Sindh Agriculture University, Tandojam, Sindh, Pakistan. The experimental material was planted in a Randomized Complete Block Design (RCBD) with three replications. A plant-to-plant spacing of 30 cm and a row-to-row spacing of 75 cm were maintained throughout the experiment. All recommended agronomic practices were uniformly applied to ensure healthy crop growth.

Plant Material

Ten safflower genotypes were evaluated in the present study: PI-260621, PI-240801, PI-304093, PI-405295, PI-248859, PI-392029, PI-250837, PI-340097, PI-253895, and PI-306956. These genotypes are PI-designated exotic germplasm accessions obtained from [AUTHOR: insert the source genebank/institute, e.g., USDA or NARC germplasm collection], selected to represent a broad range of variation for the target yield and oil-related traits; they are experimental accessions rather than released commercial cultivars.

Traits Recorded

Data were recorded on the following nine agronomic and yield-related traits:

Days to 75% flowering, Days to 90% maturity, Plant height (cm), Number of branches per plant, Number of capsules per plant, Seed yield per plant (g), Biomass per plant (g), Harvest index (%), Oil content (%)

Statistical Analysis

The recorded data were subjected to analysis of variance (ANOVA) using Statistix 8.1 statistical software. Mean comparisons among genotypes were performed using the Least Significant Difference (LSD) test at the 5% probability level. Pearson's correlation coefficients among the studied traits were estimated according to the method described by Snedecor and Cochran (1980). Broad-sense heritability (H^2) was estimated following the procedure described by Falconer (1989).

Results

The analysis of variance for seed yield and its associated traits is presented in **Table 1**. Highly significant ($P \leq 0.01$) differences were observed among the ten safflower genotypes for all nine evaluated traits, indicating the presence of substantial genetic variability within the experimental material. The significant variation observed among the genotypes suggests considerable potential for selection and genetic improvement of these traits in future safflower breeding programs.

Table 1. Analysis of variance (ANOVA): Mean squares for yield and yield-related traits in ten safflower (*Carthamus tinctorius* L.) genotypes.

Parameters	Replication (DF 2)	Genotypes (DF 9)	Error (DF 18)
Days to 75% flowering	0.22	10.04**	0.17
Days to 90% maturity	0.36	16.15**	0.20
Plant height (cm)	2.15	233.60**	1.58
Branches plant ⁻¹	0.36	18.86**	3.75
Capsules plant ⁻¹	5.66	129.65**	22.04
Seed yield plant ⁻¹ (g)	6.11	88.66**	7.28
Biomass plant ⁻¹ (g)	16.54	849.57**	65.44
Harvest index (%)	3.31	90.01**	15.13
Oil content (%)	2.21	30.16**	4.14

Note: ** indicates significance at the 0.01 probability level ($P \leq 0.01$).

The mean performance of the ten safflower (*Carthamus tinctorius* L.) genotypes for all evaluated traits is presented in Table 2. Significant variation was observed among the genotypes for all measured parameters, reflecting the presence of considerable genetic diversity.

For days to 75% flowering, genotype PI-340097 recorded the highest value (122.58 days), followed by PI-248859 (122.37 days), whereas PI-240801 exhibited the lowest value (118.27 days). Similarly, for days to 90% maturity, PI-248859 recorded the highest value (157.26 days), followed closely by PI-253895 (157.21 days), while PI-260621 matured earliest, recording the lowest value (151.27 days).

Plant height varied significantly among the genotypes. The tallest plants were produced by PI-340097 (169.63 cm), followed by PI-260621 (165.84 cm), whereas PI-392029 recorded the shortest plants (138.50 cm). For the number of branches per plant, PI-405295 produced the highest number (13.41), followed by PI-248859 (12.66), while PI-340097 produced the fewest branches (5.47).

The highest number of capsules per plant was recorded by PI-304093 (37.59), followed by PI-240801 (35.45), whereas PI-248859 produced the fewest capsules per plant (19.64). Seed yield per plant also differed significantly among the genotypes. Genotype PI-304093 produced the highest seed yield (42.82 g), followed by PI-392029 (37.32 g) and PI-248859 (37.20 g), while PI-250837 recorded the lowest seed yield (26.62 g).

For biomass per plant, PI-306956 recorded the highest value (170.50 g), followed by PI-253895 (167.21 g), whereas PI-260621 produced the lowest biomass (120.18 g). Harvest index was highest in PI-304093 (31.43%), followed by PI-240801 (28.75%),

while PI-253895 recorded the lowest harvest index (16.80%). Similarly, PI-306956 exhibited the highest oil content (32.01%), followed by PI-253895 (31.59%), whereas PI-260621 recorded the lowest oil content (23.04%).

The observed variation in agronomic and yield-related traits among the evaluated genotypes demonstrates the existence of substantial genetic diversity, indicating that these genotypes constitute valuable genetic resources for the selection and development of improved safflower cultivars. Mean comparisons were performed using the Least Significant Difference (LSD) test at the 5% probability level ($P \leq 0.05$). Therefore, differences between genotype means should be considered statistically significant only when they exceed the corresponding LSD value presented in Table 2.

Table 2. Mean performance of safflower (*Carthamus tinctorius* L.) genotypes for yield and yield-related traits

Note: Least Significant Difference (LSD) values were calculated at the 5% probability level using the formula: $LSD (0.05) = t (0.05, 18 \text{ df}) \times \sqrt{(2 \times MSE / r)}$, where *MSE* represents the error mean square obtained from Table 1, and *r* represents the number of replications ($r = 3$). Differences between genotype means exceeding the corresponding LSD value are considered statistically significant.

Varieties	Days to 75% flowering	Days to 90% maturity	Plant height	Branches plant ⁻¹	Capsules plant ⁻¹	Seed yield plant ⁻¹	Biomass plant ⁻¹	Harvest index (%)	Oil content (%)
PI-260621	121.63	151.27	165.84	12.38	21.41	31.55	120.18	26.26	23.04
PI-240801	118.27	154.37	162.74	9.30	35.45	36.68	127.60	28.75	24.36
PI-304093	120.15	156.48	156.91	8.45	37.59	42.82	136.28	31.43	24.73
PI-405295	121.52	151.75	157.64	13.41	32.41	28.90	141.63	20.41	25.48
PI-248859	122.37	157.26	164.29	12.66	19.64	37.20	145.60	25.55	25.92
PI-392029	118.28	155.46	138.50	10.09	31.34	37.32	150.32	24.83	26.29
PI-250837	121.82	156.66	153.68	12.59	21.69	26.62	156.40	17.02	28.15
PI-340097	122.58	156.58	169.63	5.47	34.53	28.25	162.97	17.34	30.41
PI-253895	118.31	157.21	165.27	9.34	34.46	28.08	167.21	16.80	31.59
PI-306956	118.59	152.55	156.77	8.51	27.85	29.21	170.50	17.13	32.01
LSD (0.05)	0.71	0.77	2.16	3.32	8.05	4.63	13.88	6.67	3.49

Correlation coefficients among the studied traits are presented in Table 3. Days to 75% flowering exhibited a significant positive correlation with plant height ($r = 0.3967^{**}$), while positive but non-significant associations were observed with days to 90% maturity ($r = 0.2445^*$) and branches per plant ($r = 0.1238\text{NS}$). However, days to 75% flowering showed a significant negative correlation with capsules per plant ($r = -0.346^*$). Significant negative associations were also recorded with biomass per plant ($r = -0.268^*$) and oil content ($r = -0.301^*$), whereas non-significant negative correlations were observed with seed yield per plant ($r = -0.132\text{NS}$) and harvest index ($r = -0.068\text{NS}$).

Days to 90% maturity exhibited non-significant positive correlations with most of the studied traits, with a significant positive association observed with plant height ($r = 0.242^*$). A non-significant negative correlation was observed between days to 90% maturity and branches per plant ($r = -0.098\text{NS}$).

Plant height showed a non-significant positive correlation with biomass per plant ($r = 0.159\text{NS}$), while significant negative correlations were recorded with branches per plant ($r = -0.358^*$) and harvest index ($r = -0.283^*$).

The number of branches per plant exhibited a significant positive correlation with harvest index ($r = 0.225^*$). In contrast, significant negative correlations were observed with capsules per plant ($r = -0.620^{**}$), biomass per plant ($r = -0.461^{**}$), and oil content ($r = -0.546^*$).

Seed yield per plant showed a highly significant positive correlation with harvest index ($r = 0.949^{**}$), indicating a strong association between these traits. Conversely, seed yield per plant exhibited highly significant negative correlations with biomass per plant ($r = -0.640^{**}$) and oil content ($r = -0.676^{**}$).

Biomass per plant showed a highly significant negative correlation with harvest index ($r = -0.842^{**}$) and a highly significant positive correlation with oil content ($r = 0.962^{**}$). Furthermore, harvest index exhibited a highly significant negative correlation with oil content ($r = -0.837^{**}$).

Overall, the correlation analysis revealed strong associations among several yield-related traits, indicating that these traits may serve as useful selection criteria for improving seed yield and associated characteristics in safflower breeding programs.

Table 3. Correlation coefficients (r) among yield and yield-related traits in safflower (*Carthamus tinctorius* L.) genotypes

Components	Days to 90% maturity	Plant height (cm)	Branches plant ⁻¹	Capsules plant ⁻¹	Seed yield plant ⁻¹ (g)	Biomass plant ⁻¹	Harvest index (%)	Oil content (%)
Days to 75% flowering	0.2445*	0.3967**	0.1238NS	-0.346*	-0.132NS	-0.268*	-0.068NS	-0.301*
Days to 90% maturity		0.242*	-0.098NS	0.032NS	0.102NS	0.063NS	0.036NS	0.013NS
Plant height (cm)			-0.358*	0.166NS	-0.355*	0.159NS	-0.283*	0.324*
Branches plant ⁻¹				-0.620**	0.098NS	-0.461**	0.225*	-0.546*
Capsules plant ⁻¹					0.077NS	0.070NS	0.047NS	0.162NS
Seed yield plant ⁻¹ (g)						-0.640**	0.949**	-0.676**
Biomass plant ⁻¹							-0.842**	0.962**
Harvest index (%)								-0.837**

Note: * and ** indicate significant correlation coefficients at the 0.05 and 0.01 probability levels, respectively; NS indicates a non-significant correlation.

Heritability estimates in the broad sense for yield and yield-associated traits are presented in Table 4. High heritability estimates were observed for plant height ($h^2 = 97.99\%$), days to 90% maturity ($h^2 = 96.23\%$), days to 75% flowering ($h^2 = 95.09\%$), biomass per plant ($h^2 = 79.97\%$), seed yield per plant ($h^2 = 78.84\%$), oil content ($h^2 = 67.69\%$), harvest index ($h^2 = 62.25\%$), and capsules per plant ($h^2 = 61.93\%$). In contrast, branches per plant exhibited moderate heritability ($h^2 = 57.27\%$). The higher heritability values observed for most of the studied traits indicate a greater contribution of genetic factors to phenotypic variation, suggesting that these traits can be effectively improved through selection. In all cases, phenotypic variance was higher than genotypic variance, indicating the influence of environmental factors on the expression of these traits.

Table 4. Broad-sense heritability estimates (h^2_{bs} , %) for yield and yield-related traits in safflower (*Carthamus tinctorius* L.) genotypes

Traits	Genotypic variance (σ^2_g)	Environmental variance (σ^2_e)	Phenotypic variance (σ^2_p)	Heritability (h^2 %)
Days to 75% flowering	3.29	0.17	3.46	95.09
Days to 90% maturity	5.31	0.21	5.52	96.23
Plant height (cm)	77.34	1.58	78.92	97.99
Branches plant ⁻¹	5.03	3.76	8.79	57.27
Capsules plant ⁻¹	35.87	22.04	57.91	61.93
Seed yield plant ⁻¹ (g)	27.12	7.28	34.40	78.84
Biomass plant ⁻¹ (g)	261.37	65.44	326.82	79.97
Harvest index (%)	24.96	15.13	40.09	62.25
Oil content (%)	8.67	4.14	12.81	67.69

Note: Broad-sense heritability (h^2_{bs} , %) was estimated using the formula: $h^2_{bs} = (\sigma^2_g / \sigma^2_p) \times 100$, where σ^2_g represents genotypic variance and σ^2_p represents phenotypic variance.

Discussion

The highly significant genotypic differences ($P \leq 0.01$) observed for all nine traits confirm that the ten safflower genotypes carry substantial genetic diversity, most likely reflecting their diverse origins and independent selection histories rather than a shared narrow gene pool; this corroborates the significant genotypic variation reported by Muhammad et al. (2020) and Gulati et al. (2023) in other safflower germplasm sets.

Differences in phenology among genotypes, such as the early-flowering PI-240801 and the late-flowering PI-340097, likely reflect differences in photoperiod sensitivity and thermal-time requirements, traits that are largely under additive genetic control in safflower and are agronomically useful because they allow cultivar deployment across sowing windows and rainfall patterns. Similarly, the wide range in plant height and branching is consistent with the strongly genotype-dependent architecture reported for safflower by Sabaghnia et al. (2024), and this architectural variation directly shapes capsule number and, in turn, seed yield.

The superior seed yield and harvest index of PI-304093, despite its comparatively short stature and few branches, suggests that this genotype partitions assimilates efficiently toward reproductive structures rather than vegetative biomass, a pattern also noted for high-harvest-index safflower lines by Pushpa et al. (2023). In contrast, PI-306956 combined high biomass with high oil content but a lower harvest index, indicating a source-driven rather than a partitioning-driven yield strategy; the trade-off between these strategies is a recurring theme in oilseed breeding and is reflected in this study's strong negative correlation between harvest index and both biomass and oil content.

The positive correlation between flowering time and plant height, together with negative correlations between flowering time and capsules per plant, biomass, and oil content, suggests that early-flowering genotypes in this germplasm set channel resources into capsule and oil production over a shorter vegetative period, whereas late-flowering genotypes invest comparatively more in vegetative growth. This contrasts with the negative flowering–yield relationships reported by Carapetian et al. (2019) but agrees with the positive associations found by Pushpa et al. (2017), indicating that the direction of this relationship is population- and environment-specific rather than fixed.

The strong positive association between seed yield and harvest index ($r = 0.949^{**}$), together with the negative associations of seed yield with biomass and oil content, indicates a physiological trade-off in this germplasm between harvest efficiency and total plant biomass or oil accumulation. Practically, breeders selecting for seed yield in this material should prioritize harvest index over sheer biomass, and should expect some tension between seed-yield gains and oil-content gains unless traits are selected jointly through an index rather than sequentially.

The consistently high broad-sense heritability recorded for phenological and morphological traits (days to flowering, days to maturity, plant height) indicates that these traits are governed largely by additive genetic effects with limited environmental modification in this environment, so early-generation, single-environment selection should be efficient for them. The comparatively lower heritability of branches per plant, despite significant genotypic differences, implies a larger environmental or genotype $\times$ environment component for this trait, so selection for branching may need to be deferred to later generations or supported by multi-environment testing, a pattern also observed by Muhammad et al. (2020).

Conclusion

This study revealed highly significant genetic variability among the ten safflower genotypes for all measured traits, with high broad-sense heritability for most characters except branches per plant, indicating that direct phenotypic selection can be effective for early-generation improvement. The strong positive correlation between seed yield and harvest index, coupled with negative associations with biomass and oil content, suggests harvest index as a practical indirect selection criterion, though breeders should anticipate trade-offs between seed yield and oil accumulation. Genotypes PI-304093 and PI-306956 emerged as the most promising parental material and are recommended for multi-location, multi-season evaluation prior to use in cultivar development.

Author's Contribution

SH and PAS conducted the experiment, collected data, and performed statistical analysis. SH and PAS contributed to data interpretation and manuscript preparation.

Conflict Of Interest

The authors declare that they have no conflict of interest.

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