

GENETIC VARIABILITY, YIELD PERFORMANCE AND TRAIT
ASSOCIATIONS AMONG SAFFLOWER (*CARTHAMUS TINCTORIUS* L.)
GENOTYPES

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Abstract

Safflower (*Carthamus tinctorius* L.) is an important oilseed crop with considerable potential for edible oil production and adaptation to arid and semi-arid environments. The present study evaluated the genetic variability, yield performance, and trait associations among ten safflower genotypes. The experiment was conducted in a randomized complete block design (RCBD) with three replications at the experimental field of the Oilseeds Research Institute, Tandojam, Pakistan, during the 2025-26 growing season. Data were recorded for days to 75% flowering, days to 90% maturity, plant height, number of capitula plant⁻¹, seed index, seed yield plot⁻¹ (g), seed yield ha⁻¹ (kg), and oil content. Analysis of variance revealed significant differences ($P \leq 0.05$) among genotypes for all studied traits, indicating substantial genetic variability. Genotype N-673 exhibited superior performance with the highest number of capitula plant⁻¹ (22.00), seed index (4.173 g), seed yield ha⁻¹ (880.83 kg), and oil content (34.92%), whereas the genotype PI-258414 was the earliest flowering (115.67 days) and maturing (143.67 days). Correlation coefficient analysis showed that seed index was positively and highly significantly correlated with seed yield ($r = 0.675^{**}$) and oil content ($r = 0.838^{**}$), while number of capitula plant⁻¹ was positively and significantly associated with seed yield ($r = 0.416^{*}$). The results suggested that seed index and number of capitula plant⁻¹ are effective indirect selection criteria for improving seed yield and oil content. Therefore, N-673 is recommended for multi-location evaluation and varietal development, whereas PI-258414 may be used as a valuable parent in breeding programs for early-maturing and climate-resilient safflower cultivars.

INTRODUCTION

Safflower (*Carthamus tinctorius* L.) is one of the oldest cultivated oilseed crops belonging to the family Asteraceae (Cheng et al., 2024). In recent years, safflowers have received increasing attention due to their agronomic resilience, economic value, and potential contribution to sustainable oilseed production under changing climatic conditions (Sabaghnia et al., 2024). Beyond its significance as an oilseed crop, safflower (*Carthamus tinctorius* L.) possesses considerable nutritional, industrial, and medicinal value (Cheng et al., 2024). Its seeds contain approximately 25-40% oil, predominantly composed of unsaturated fatty acids, particularly linoleic and oleic acids, which contribute to improved nutritional quality and human health (Cheng et al., 2024). Safflower has attracted increasing scientific and commercial interest worldwide, highlighting the need to develop high-yielding and superior-quality cultivars through systematic breeding programs (Cheng et al., 2024; FAO, 2024). Genetic variability is an essential criterion for the improvement of quantitative traits such as seed yield and oil content in safflower (Sabaghnia et al., 2024). The availability of sufficient genetic variation enables plant breeders to identify superior genotypes and select desirable parents, thereby increasing the efficiency of breeding programs (Pushpavalli et al., 2024). Evaluation of genetically diverse germplasms under specific agro-climatic conditions is therefore essential for exploiting useful alleles and developing high-yielding, well-adapted cultivars (Sabaghnia et al., 2024). Several recent studies have demonstrated substantial variability among safflower genotypes for important agronomic traits, indicating considerable opportunities for genetic improvement through selection and hybridization (Wani et al., 2023). Seed yield in safflower is a complex quantitative trait that is governed by the combined effects of several interrelated morphological and physiological traits (Wani et al., 2023). Traits such as days to 75% flowering, days to 90% maturity, plant height, number of capitula plant⁻¹, seed index, and oil content directly or indirectly influence final seed

yield (Pushpavalli et al., 2024). Correlation analysis provides valuable information regarding the magnitude and direction of associations among quantitative traits, enabling plant breeders to identify characters that can be used as reliable indirect selection indices for improving seed yield and oil productivity (Sabaghnia et al., 2024). Several recent studies have reported significant associations between yield and its component traits in safflower, suggesting that simultaneous improvement of correlated traits can substantially enhance breeding efficiency and genetic gain (Pushpavalli et al., 2024). However, the performance of genotypes for yield-related traits varies considerably across environments due to genotype × environment interactions (Sabaghnia et al., 2024). Consequently, information generated under one agro-ecological condition cannot always be directly extrapolated to another (Hassani et al., 2024). In Pakistan, particularly under the agro-climatic conditions, the comprehensive information on the genetic variability, yield performance, and trait associations among safflower genotypes remains limited (Saadia et al., 2024). Therefore, the evaluation of diverse safflower germplasm under local environmental conditions is essential for identifying superior genotypes with stable performance and desirable agronomic attributes for future breeding programs (Pushpavalli et al., 2024).

2. Materials and Methods

The current research was carried out during the Rabi season of 2025-26 at the experimental field of the Oilseeds Research Institute (ORI), Tandojam, Sindh, Pakistan, to evaluate the genetic variability, yield performance, and trait associations among safflower (*Carthamus tinctorius* L.) genotypes under the agro-climatic conditions of Tandojam. A total of 10 genotypes (nine advanced lines and one commercial as a check genotype) were used in a Randomized Complete Block Design (RCBD) with three replications. A total of eight traits were recorded, namely: days to 75% flowering, days to 90% maturity, plant height

(cm), number of capitula plant⁻¹, seed index (100-seed weight g), seed yield plot⁻¹ (g), seed yield ha⁻¹ (kg), and oil content (%). Days to 75% flowering and days to 90% maturity were recorded on a plot basis, whereas observations for the remaining traits were recorded from randomly selected competitive plants in each experimental plot. Seed yield ha⁻¹(kg) was calculated from the plot yield and converted to kilograms per hectare. Oil content (%) was determined from seed samples using the Soxhlet solvent extraction method following the standard procedure described by the Association of Official Analytical Chemists (AOAC, 2019). A basal fertilizer dose of 25 kg N acre⁻¹ and 16 kg P₂O₅ acre⁻¹ was applied according to the recommended agronomic practices for safflower cultivation (Muley et al., 2025). All other agricultural practices were carried out in accordance with recommended practices.

Statistical Analysis

The recorded data were subjected to analysis of variance (ANOVA) using the procedures appropriate for a Randomized Complete Block Design (RCBD) using Statistix 8.1 (Analytical Software, Tallahassee, Florida, USA). The significance of differences among genotype means was determined using the Least Significant Difference (LSD) test at the 5% probability level (P

≤ 0.05) following the procedures described by Gomez and Gomez (1984). Pearson's correlation coefficients were computed to determine the relationships between yield and yield-related traits.

Results and Discussion

Analysis of Variance

The analysis of variance (ANOVA) revealed highly significant (P ≤ 0.05) differences among the safflower genotypes for all the studied traits, including days to 75% flowering, days to 90% maturity, plant height, number of capitula plant⁻¹, seed index (100-seed weight g), seed yield plot⁻¹ (g), seed yield ha⁻¹ (kg), and oil content (Table 1). The significant mean squares indicated the presence of genetic variation among the assessed genotypes. The observed variability among genotypes further demonstrated the existence of considerable phenotypic diversity that could be efficiently exploited in future safflower breeding programs. The significant differences among genotypes also confirmed the presence of sufficient genetic diversity for identifying superior genotypes with desirable agronomic performance under the agro-climatic conditions of Tandojam. Similar findings have been reported by several recent studies, where highly significant genotypic differences for yield-related traits were observed in diverse safflower germplasm (Sabaghnia et al., 2024; Pushpavalli et al., 2024; Govindu et al., 2024).

Table 1. Analysis of variance (ANOVA) for agronomic, yield and quality traits of safflower genotypes.

Source of Variation	DF	Days to Flowering (DF)	Days to Maturity (DM)	Plant Height (PH)	Number of Capitula Plant ⁻¹	Seed Index (g)	Seed Yield Plot ⁻¹ (g)	Seed Yield (kg ha ⁻¹)	Oil Content (%)
Replications	2	2.633	1.033	89.200	1.033	0.0035	643.5	794.5	0.493
Varieties	9	26.463**	30.596**	109.496*	11.633**	0.0380**	52023.0**	64221.7**	3.454**
Error	18	5.485	1.441	39.607	3.144	0.0033	4678.7	5773.4	0.203
CV (%)	—	1.93	0.81	4.99	9.98	1.43	11.41	11.41	1.34
Grand Mean	—	121.17	148.77	126.20	17.77	4.002	599.38	665.98	33.68
LSD (5%)	—	1.91	0.98	5.13	1.45	0.05	55.84	62.04	0.37

** = Significant at P ≤ 0.01; * = Significant at P ≤ 0.05; NS = non-significant.

Mean Performance:

Days to Flowering and Days to Maturity

Days to 75% flowering and days to 90% maturity are important earliness traits that determine the

adaptation of safflower genotypes to diverse agro-climatic environments. Early flowering and maturity enable plants to escape terminal heat and drought stress. Therefore, these traits are widely considered important selection criteria in safflower breeding programs (Thoday-Kennedy et al., 2023). The assessed safflower genotypes exhibited significant variation in days to 75% flowering and days to 90% maturity (Table 2). Days to 75% flowering ranged from 115.67 to 125.33 days, whereas days to 90% maturity varied from 143.67 to 153.00 days. Among the evaluated genotypes, PI-258414 flowered earliest (115.67 days) and reached maturity earliest (143.67 days). In contrast, N-147 recorded the longest flowering (125.33 days) and maturity duration (153.00 days). Compared with the check cultivar Thori-78, which flowered at (124.00 days and reached maturity at 151.67 days) exhibited earlier flowering and maturity. The substantial variation observed for flowering and maturity reflects considerable genetic diversity among the evaluated genotypes. Earliness is considered a desirable breeding attribute. Similar genotypic differences for flowering and maturity have been reported in recent safflower studies, confirming that earliness traits are reliable indicators for selecting climate-resilient and well-adapted genotypes (Sabaghnia et al., 2024; Hassani et al., 2024; Bahadori et al., 2025; Zhao et al., 2026).

Plant Height and Number of Capitula Plant⁻¹

Plant height and the number of capitula plant⁻¹ are Important agronomical traits that substantially influence the growth and yield potential of safflower. Plant height reflects vegetative growth, whereas the number of capitula plant⁻¹ is an important yield-contributing trait because each capitulum serves as a potential source of seed production. (Rathod et al., 2021; Minnie et al., 2023). The results for plant height and the number of capitula plant⁻¹ are presented in (Table 2). Plant height ranged from 119.67 to 136.33 cm, while the number of capitula plant⁻¹ varied from 15.67 to 22.00. The tallest plants were recorded in PI-258414 (136.33 cm), followed by PI-253560

(135.00 cm) and N-673 (132.33 cm). In contrast, the genotype PI-251984 produced the shortest plants (119.67 cm). Regarding the number of capitula plant⁻¹ production of (22.00) produced by N-673, followed by PI-304495 (19.33) and PI-248848 (19.00), whereas the lowest number of capitula was (15.67) observed in PI-258414 and PI-253560, respectively. Compared with the check cultivar Thori-78, which produced 125.33 cm plant height and 16.33 number of capitula plant⁻¹. The observed variation in plant height and capitula plant⁻¹ demonstrates the genetic diversity among the tested safflower genotypes. Although plant height contributes to vegetative growth and biomass production, the number of capitula plant⁻¹ is an important yield-contributing trait because each capitulum represents a potential seed-bearing structure. Therefore, the number of capitula plant⁻¹ may serve as a useful selection criterion for improving seed yield in safflower. Similar findings have been reported by Sabaghnia et al. (2024), Pushpavalli et al. (2024), and Zhao et al. (2026).

Seed Index and Seed Yield

The yield parameters (Seed index and seed yield) are economically important traits in safflower because they are directly related to crop productivity and market value. Seed index refers to seed size and weight, whereas seed yield represents the various yield-related components under usual environmental conditions (Sathees et al., 2023; Pillai & Shrivastava, 2023; Govindu et al., 2024). Significant differences were observed among the assessed genotypes for both seed index and yield (Table 2). Seed index ranged from 3.797 to 4.173 g, while seed yield varied between (413.17 to 792.73 g plot⁻¹) and (459.10 and 880.83 kg ha⁻¹). The highest seed index (4.173 g) and seed yield (792.73 g plot⁻¹) and (880.83 kg ha⁻¹) were recorded in genotype N-673, followed by PI-304495, which produced a seed index of 4.133 g and a seed yield of (739.73 g plot⁻¹) and (821.93 kg ha⁻¹). Nonetheless, the check cultivar Thori-78 exhibited the lowest seed index (3.797 g), whereas PI-251984 produced the lowest seed yield (413.17

g plot⁻¹) and (459.10 kg ha⁻¹). Compared with the check cultivar, N-673 highlights its outstanding yield performance under the experimental conditions. The present findings indicate that seed yield is a complex quantitative trait governed by the interaction of several yield-contributing components rather than a single trait. The positive association between seed index and seed yield suggests that selection for higher seed index may contribute to improved seed yield in safflower. Similar results have been reported by Pushpavalli et al. (2024), Sabaghnia et al. (2024), and Zhao et al. (2026).

Oil Content

Oil content is an important quality trait in safflower because of its economic value and its role in the crop's industrial utilization. In addition, high oil content is an important breeding objective in safflower breeding programs aimed at enhancing edible oil production (Bakhshi et al.,

2025; Kurt et al., 2025). The evaluated safflower genotypes exhibited appreciable variation in oil content, ranging from 31.73 to 34.92% (Table 2). The highest oil content was recorded in N-673 (34.92%), followed by PI-304495 (34.64%). Nevertheless, the lowest oil content was observed in the check variety Thori-78 (31.73%). Compared with the check cultivar, the genotype N-673 exhibited a 3.19% increase in oil content, demonstrating its superior seed quality under prevailing environmental conditions. The observed variation in oil content indicates the presence of substantial genetic diversity for this economically important trait. At the same time, superiority for yield and quality traits makes this genotype a promising candidate for future varietal evaluation and utilization in breeding programs. Comparable findings have been reported by Sabaghnia et al. (2024), Pushpavalli et al. (2024), and Zhao et al. (2026).

Table 2. Mean performance of safflower genotypes for phenological, morphological, yield and quality traits.

Genotype	Days to 75 % Flowering	Days to 90% Maturity	Plant Height (cm)	Number of Capitula plant ⁻¹	Seed Index (g)	Seed Yield plot ⁻¹ (g)	Seed Yield (kg ha ⁻¹)	Oil Content (%)
PI- 250 537	121.33	149	124.33	18.33	3.99	443.33	492.6	34.24
PI- 304 495	122.67	150.33	121.33	19.33	4.133	739.73	821.93	34.64
N- 147	125.33	153	123	17.67	3.95	629.17	699.07	32.59
PI- 248 848	123.67	152	122.33	19	4.103	711.4	790.43	34.54
PI- 258 414	115.67	143.67	136.33	15.67	4.04	612.5	680.53	34.19
PI- 253 560	118.67	145.33	135	15.67	3.957	513.33	570.4	34.05
N - 331	120.33	148.33	122.33	16.67	3.947	661.73	735.27	33.38
PI- 251 984	121.67	149.33	119.67	17	3.927	413.17	459.1	32.51
N - 673	118.33	145	132.33	22	4.173	792.73	880.83	34.92
Thori-78 (check)	124	151.67	125.33	16.33	3.797	476.67	529.63	31.73

Correlation Analysis

Correlation analysis is an effective statistical tool for understanding the relationships among agronomic, yield, and quality traits, thereby

facilitating the identification of characters that can be effectively utilized as indirect selection criteria in crop improvement programs (Rajper et al., 2018; Bano et al., 2017 and Zhao et al., 2023). The

results for correlation coefficients among the traits studied are described in (Table 3). The trait days to flowering exhibited a highly significant and positive correlation with days to maturity ($r = 0.789^{**}$). However, days to 75% flowering showed a highly significant but negative association with plant height ($r = -0.753^{**}$) and oil content ($r = -0.391^*$). Similarly, days to 90% maturity showed a highly significant but negative relationship with plant height ($r = -0.612^{**}$) and oil content ($r = -0.460^*$), whereas its relationships with number of capitula plant⁻¹, seed index, seed yield plot⁻¹ and seed yield kg ha⁻¹ were non-significant. Similarly, Capitula plant⁻¹ exhibited a highly significant positive correlation with seed index ($r = 0.595^{**}$), while a positive and significant association was reported with seed yield plot⁻¹ (g), seed yield ha⁻¹ (kg) ($r = 0.416^*$), and oil content ($r = 0.428^*$), respectively. Likewise, the trait seed index showed a highly significant and positive relationship with seed yield plot⁻¹ (g), seed yield ha⁻¹ (kg) ($r = 0.675^{**}$),

and oil content ($r = 0.838^{**}$). Furthermore, seed yield plot⁻¹ (g) indicated a highly significant and positive relationship with seed yield ha⁻¹ (kg) ($r = 0.999^{**}$) and oil content ($r = 0.541^{**}$), whereas the trait seed yield ha⁻¹ (kg) showed a highly positive correlation with oil content ($r = 0.541^{**}$) respectively. The present findings suggest that seed index and capitula plant⁻¹ are the most influential yield components and may serve as reliable indirect selection criteria for improving seed yield and oil content in safflower. The strong positive association between seed index, seed yield, and oil content indicates that improvement of both productivity and quality is viable through appropriate selection approaches. Similar relationships among seed yield, seed index, capitula plant⁻¹, and oil content have been reported by Sabaghnia et al. (2024), Pushpavalli et al. (2024), Hassani et al. (2024), and Zhao et al. (2026).

Table 3. Correlation coefficients among agronomic, yield and quality traits of safflower genotypes.

Traits	DF	DM	PH	Capi	SI	YGP	YKGH
DM	0.789 ^{**}						
PH	-0.753 ^{**}	-0.612 ^{**}					
Capitula	-0.087 ^{NS}	-0.003 ^{NS}	0.153 ^{NS}				
SI	-0.251 ^{NS}	-0.266 ^{NS}	0.220 ^{NS}	0.595 ^{**}			
YGP	-0.029 ^{NS}	-0.053 ^{NS}	0.026 ^{NS}	0.416 [*]	0.675 ^{**}		
YKGH	-0.029 ^{NS}	-0.054 ^{NS}	0.026 ^{NS}	0.416 [*]	0.675 ^{**}	0.999 ^{**}	
OC	-0.391 [*]	-0.460 [*]	0.427 [*]	0.428 [*]	0.838 ^{**}	0.541 ^{**}	0.541 ^{**}

*** = Significant at $P \leq 0.01$ and $P \leq 0.05$; NS = non-significant.

Note: DF= Days to 75% flowering, DM= Days to 90% maturity, PH= Plant height (cm), Capi=

Capitula plant⁻¹, SI= Seed index, YGP= Seed yield plot⁻¹ (g), YKGH= Seed yield ha⁻¹ (kg)

Conclusion

The present study revealed substantial genetic variability among the evaluated safflower genotypes for phenological, morphological, yield, and quality traits. The advanced line N-673 was identified as the most promising genotype, exhibiting superior performance for seed index,

seed yield, number of capitula plant⁻¹, and oil content, whereas the advanced line PI-258414 showed the earliest flowering and maturity. On the other hand, the significant association between the traits

for seed index and seed yield indicated their potential as useful selection criteria. Overall, N-673 may be advanced for multi-location testing and future varietal development, while PI-258414 may serve as a valuable parent/source in breeding programs aimed at developing early maturing safflower cultivars.

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