

ISSN Print: 2664-844X
ISSN Online: 2664-8458
NAAS Rating (2026): 4.97
IJAFS 2026; 8(11): 243-246
www.agriculturaljournals.com
Received: 12-09-2026
Accepted: 26-10-2026
Published: 06-11-2026

Banoth Srikanth
M.Sc. Student, Department of Agril. Botany, Govt. College of Agriculture, Pune, Maharashtra, India

AB Rajguru
Associate Professor of Agricultural Botany, ARS Kasbe, Digraj, Dist. Sangli, Maharashtra, India

Nahid Parveen
Department of Agril. Botany, Govt. College of Agriculture, Pune, Maharashtra, India

Leena S. Shitole
Assistant Professor, Division of Agricultural Botany, Govt. College of Agriculture, Pune, Maharashtra, India

AA Bhagat
Assistant Professor, Division of Statistics, Govt. College of Agriculture, Pune, Maharashtra, India

PY Shinde
Assistant Professor, Division of Agricultural Botany, Govt. College of Agriculture, Pune, Maharashtra, India

Corresponding Author:
Banoth Srikanth
M.Sc. Student, Department of Agril. Botany, Govt. College of Agriculture, Pune, Maharashtra, India

Correlation and path coefficient analysis for seed yield and its components in safflower (*Carthamus tinctorius* L.) genotypes

Banoth Srikanth[1], AB Rajguru[2], Nahid Parveen[3], Leena S. Shitole[4], AA Bhagat[5], PY Shinde[6]

DOI: https://www.doi.org/10.33545/2664844X.2026.v8.i11d.89983

Abstract
Seed yield in safflower (*Carthamus tinctorius* L.) is the product of several component traits, and knowing how they are associated, and how much each contributes directly, helps in choosing selection criteria. Phenotypic correlations and a path coefficient analysis were worked out among nine traits for 31 genotypes, including the checks A-1, PBNS-12 and ISF-764, grown in a randomized block design with three replications during *rabi* 2025–26 at Pune, India. Of the 36 phenotypic correlation coefficients, 26 were significant (20 positive and 6 negative). Seed yield per plant was positively and significantly correlated with 100-seed weight (0.808), capitula per plant (0.785), seeds per capitulum (0.703) and primary branches per plant (0.661), and weakly with days to 50% flowering (0.301), days to maturity (0.216) and oil content (0.207); it was negatively correlated with plant height (−0.292). The path analysis explained 74.9% of the variation in seed yield (residual effect 0.501) and showed no collinearity problem (variance inflation factors 1.1–3.3). The largest direct effects were those of 100-seed weight (0.411) and capitula per plant (0.311), which together accounted for 57.7 percentage points of the explained variation, followed by seeds per capitulum (0.146); primary branches (0.068), flowering time, maturity, plant height and oil content had small direct effects, so their correlations with yield acted mainly through the yield components. Principal component analysis placed seed yield and its four components on one axis (46.8% of the variance), with phenology and plant height (19.6%) and oil content (9.4%) on separate axes. Selection for 100-seed weight and capitula per plant is the most reliable route to higher seed yield in this panel.

Keywords: *Carthamus tinctorius*, Phenotypic correlation, Path analysis, Principal component analysis, Yield components, Oil content

1. Introduction

Safflower (*Carthamus tinctorius* L.) is a hardy oilseed crop of the family Asteraceae, grown mainly in semi-arid regions under residual moisture or limited irrigation, and its seed oil is valued for its unsaturated fatty acid composition (Singh *et al.*, 2006) [1]. Improving its seed yield, while keeping suitable maturity, plant architecture and seed quality, is the main aim of breeding programmes, but seed yield is a complex quantitative character that is difficult to select for directly.

Seed yield results from the number of branches and capitula per plant, the number of seeds per capitulum and seed weight, and these components are interrelated, so a trait that is associated with yield may act directly or only through other traits. Selecting through component traits that are easier to score can make selection more efficient, provided the direction and strength of the associations are known. Correlation describes the net relationship between two traits, and path coefficient analysis, which goes back to Wright (1921) [2] and was applied to plant characters by Dewey *et al.* (1959) [3], separates it into the direct effect of a trait and its indirect effects through other traits, showing whether an association reflects a real contribution to yield or only the influence of a correlated trait.

Reports on safflower agree on some associations and differ on others. Mali *et al.* (2022) [4] found strong correlations of seed yield with branches per plant, effective capitula per plant and test weight in 40 genotypes, and Kale *et al.* (2025) [5] likewise reported positive links with branches, capitula and test weight. Pattar *et al.* (2020) [6] found positive direct effects for capitula per plant and 100-seed weight and negative direct effects for plant height, seeds per capitulum and oil content, whereas Pushpavalli *et al.* (2016) found that 100-seed weight had the largest direct effect, followed by seeds per capsule, and Dhuppe *et al.* (2020) [7] identified effective capitula, seeds per capitulum and 100-seed weight as the main traits with strong direct effects. The oil content–yield relationship is particularly variable: Mali *et al.* (2022) [4] found a negative, non-significant

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value, Kale *et al.* (2025) [5] and Roshan Ara *et al.* (2025) [8] reported significant negative associations, and Pushpavalli *et al.* (2024) [9] reported a positive association of seed yield with test weight and oil content.

The present study aimed to work out the phenotypic correlations among nine agronomic traits and with seed yield in 31 safflower genotypes, partition the correlations with seed yield into direct and indirect effects, describe the overall structure of trait relationships by principal component analysis, and identify the traits that can serve as selection criteria for seed yield.

2. Materials and Methods

2.1 Experimental material and crop management

The experimental material includes a 31-genotype set used throughout this series: 28 breeding lines designated by GMU numbers and the three checks A-1, PBNS-12 and ISF-764 collected from AICRP on Safflower, Solapur. The trial was conducted in the rabi season of 2025–26 under irrigated conditions at the Botany Division Research Farm of the College of Agriculture, Pune (about 18.54° N and 73.84° E, semi-arid Deccan zone). The genotypes were dibbled in three randomized blocks, in a single 4 m row per genotype with 45 cm between rows and 20 cm between plants, with border rows around each block. Recommended agronomic practices were followed for good crop growth.

2.2 Observations

Nine traits were recorded on five randomly selected plants per genotype in each block, and the means were used for analysis. Days to 50% flowering (DFF) was the number of days from sowing until about half of the plants of a genotype had flowered, and days to maturity (DM) the number of days until physiological maturity, judged from visual symptoms and drying of the capitula. At maturity, plant height (PH, cm) was measured from the soil surface to the tip of the main stem, primary branches per plant (NPB) were counted on the main shoot, and capitula per plant (NCP) were counted on the main shoot and all branches. Seeds per capitulum (NSC) was the mean of the seed counts of five capitula per plant, 100-seed weight (HSW, g) was the weight of 100 seeds from an individual plant, and seed yield per plant (SY, g) was the total seed weight of an individual plant. Oil content (OC, %) of dried seed was estimated by near-infrared reflectance spectroscopy calibrated against standard reference samples. Analysis of variance (Panse *et al.*, 1985) [10] showed significant differences among the genotypes for all traits.

2.3 Statistical analysis

Phenotypic correlation coefficients were calculated with INDOSTAT following Singh *et al.* (1985) [11] and judged against the critical values of *r* given by the program for 91 degrees of freedom (0.204, 0.266 and 0.336 at $P = 0.05$, 0.01 and 0.001). Phenotypic path coefficient analysis was carried out in INDOSTAT following Dewey *et al.* (1959) [3], with seed yield as the dependent variable and the other eight traits as predictors; the indirect effect of trait i through trait j is $r_{ij}P_j$, the contribution of each trait to R^2 is $P_i r_{iy}$, and the residual effect is $\sqrt{(1 - R^2)}$. Collinearity among the predictors was checked by the variance inflation factor (VIF), the diagonal element of the inverse of their correlation matrix, with values above 10 indicating serious multicollinearity (Kutner *et al.*, 2005) [12]. Principal component analysis was carried out on the correlation matrix of the nine traits (Jolliffe, 2002) [13]; components with eigenvalues above 1 were retained, the third was also reported because it isolates oil content, and loadings are the correlations of the traits with the components. The VIFs and the principal components were computed in Python (NumPy) from the INDOSTAT phenotypic correlation matrix.

3. Results and Discussion

3.1 Phenotypic correlations

The phenotypic correlations among the nine traits are given in Table 1. Of the 36 coefficients, 26 were significant: 20 positive (13 at $P < 0.001$, 2 at $P < 0.01$ and 5 at $P < 0.05$) and 6 negative (3 at $P < 0.01$ and 3 at $P < 0.05$). Plant height was the only trait with significant negative associations.

Table 1. Phenotypic correlation coefficients among nine traits in 31 safflower genotypes.

Trait	DM	PH	NPB	NCP	NSC	HSW	OC	SY
DFF	0.745***	0.072	0.303**	0.380***	0.221*	0.248*	−0.099	0.301**
DM		0.077	0.207*	0.347***	0.172	0.137	−0.182	0.216*
PH			−0.247*	−0.281**	−0.226*	−0.311**	−0.220*	−0.292**
NPB				0.669***	0.563***	0.689***	0.092	0.661***
NCP					0.706***	0.730***	0.146	0.785***
NSC						0.676***	0.195	0.703***
HSW							0.191	0.808***
OC								0.207*

DFF, days to 50% flowering; DM, days to maturity; PH, plant height; NPB, primary branches per plant; NCP, capitula per plant; NSC, seeds per capitulum; HSW, 100-seed weight; OC, oil content in %; SY, seed yield per plant. , * and *** significant at $P < 0.05$, 0.01 and 0.001 ($r = 0.204$, 0.266 and 0.336 with 91 d.f.).

Seed yield per plant was positively and highly significantly correlated with 100-seed weight (0.808***), capitula per plant (0.785***), seeds per capitulum (0.703***) and primary branches (0.661***), and more weakly with days to 50% flowering (0.301**), days to maturity (0.216*) and oil content % (0.207*). It was negatively correlated with plant height (−0.292**). The positive links of yield with capitula per plant, branches and seed weight agree with Mali *et al.* (2022) [4], Pattar *et al.* (2020) [6] and Kale *et al.* (2025) [5], and the negative link with plant height agrees with Pattar *et al.* (2020) [6]. Seeds per capitulum was strongly and positively associated with yield here, in contrast to the negative association reported by Pattar *et al.* (2020) [6].

Primary branches, capitula per plant, seeds per capitulum and 100-seed weight formed a closely associated block, with all pairwise coefficients between 0.563 and 0.730 ($P < 0.001$), the highest being between capitula per plant and 100-seed weight (0.730***). Seed number and seed size therefore increased together in this panel, with no sign of the compensation between components that often limits yield gains. Flowering and maturity were closely linked (0.745***), and later genotypes tended to carry more branches (0.303** and 0.207*) and capitula (0.380*** and 0.347***). Plant height was negatively correlated with all four yield components (−0.226 to −0.311) and with oil content (−0.220*). Oil content was otherwise unrelated to the yield components (0.092–0.195) and to the phenology traits (−0.099 and −0.182), and its weak positive correlation with yield (0.207*) is in line with Pushpavalli *et al.* (2024) [9], but unlike the significant negative associations reported by Kale *et al.* (2025) [5] and Roshan Ara *et al.* (2025) [8] and the non-significant value of Mali *et al.* (2022) [4].

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3.2 Path coefficient analysis

The eight predictors together explained 74.9% of the variation in seed yield per plant, with a residual effect of 0.501 (Table 2). Collinearity was not a problem: the VIFs ranged from 1.13 to 3.26 and the condition number of the predictor correlation matrix was 16, so the direct effects can be read trait by trait. The largest direct effects were those of 100-seed weight (0.411) and capitula per plant (0.311), which together contributed 57.7 of the 74.9 percentage points of R^2 (33.2 and 24.4), followed by seeds per capitulum (0.146; 10.3 points). The direct effect of primary branches was small (0.068), and its correlation with yield (0.661) was carried mainly by indirect effects through 100-seed weight (0.283), capitula per plant (0.208) and seeds per capitulum (0.082), so branching raises yield through the number and size of the seeds it carries.

Plant height had a negligible direct effect (−0.019), and its negative correlation with yield (−0.292) arose almost entirely from indirect effects through 100-seed weight (−0.128), capitula per plant (−0.088) and seeds per capitulum (−0.033): tall plants yield less because they carry fewer and lighter seeds and capitula, and not because height itself lowers yield. Days to 50% flowering had a small direct effect (0.039) and acted through capitula per plant (0.118) and 100-seed weight (0.102), and days to maturity had essentially no direct effect (−0.006). Oil content had a small direct effect (0.047), and most of its correlation with yield (0.207) came indirectly through 100-seed weight (0.079) and capitula per plant (0.045).

Table 2. Direct (diagonal) and indirect effects of eight traits on seed yield per plant in a phenotypic path analysis of 31 safflower genotypes.

Trait	via DFF	via DM	via PH	via NPB	via NCP	via NSC	via HSW	via OC	r with SY
DFF	**0.0385**	−0.0044	−0.0014	0.0205	0.1182	0.0323	0.1019	−0.0046	0.3011**
DM	0.0286	**−0.0059**	−0.0014	0.0140	0.1081	0.0250	0.0564	−0.0085	0.2163*
PH	0.0028	−0.0005	**−0.0188**	−0.0168	−0.0875	−0.0330	−0.1278	−0.0104	−0.2919**
NPB	0.0116	−0.0012	0.0046	**0.0678**	0.2081	0.0822	0.2833	0.0043	0.6608***
NCP	0.0146	−0.0020	0.0053	0.0453	**0.3112**	0.1031	0.3002	0.0069	0.7846***
NSC	0.0085	−0.0010	0.0042	0.0382	0.2198	**0.1460**	0.2782	0.0091	0.7030***
HSW	0.0095	−0.0008	0.0058	0.0467	0.2271	0.0987	**0.4114**	0.0090	0.8075***
OC	−0.0038	0.0011	0.0041	0.0062	0.0454	0.0284	0.0786	**0.0470**	0.2070*

Direct effects in bold on the diagonal. Residual effect = 0.501; R^2 = 0.749. Trait abbreviations as in Table 1.

Table 3. Direct effects, contribution to R^2 and variance inflation factors of eight traits in the path analysis of seed yield.

Trait	Direct effect	Correlation with SY	Contribution to R^2 (%)	VIF
100-seed weight	0.4114	0.8075	33.2	2.91
Capitula per plant	0.3112	0.7846	24.4	3.26
Seeds per capitulum	0.1460	0.7030	10.3	2.28
Primary branches per plant	0.0678	0.6608	4.5	2.19
Days to 50% flowering	0.0385	0.3011	1.2	2.43
Oil content	0.0470	0.2070	1.0	1.13
Plant height	−0.0188	−0.2919	0.6	1.19
Days to maturity	−0.0059	0.2163	−0.1	2.45
Total			74.9	

Contribution to R^2 = direct effect × correlation with seed yield. Residual effect = 0.501.

The ranking of direct effects agrees with earlier phenotypic path studies in safflower: Pushpavalli *et al.* (2016) found the largest direct effect for 100-seed weight, followed by seeds per capsule, Dhuppe *et al.* (2020) [7] named effective capitula, seeds per capitulum and 100-seed weight as the main contributors, and Pattar *et al.* (2020) [6] found positive direct effects for capitula per plant and 100-seed weight and a near-zero or negative effect for plant height. We did not find the negative direct effects of seeds per capitulum and oil content reported by Pattar *et al.* (2020) [6]. The residual effect of 0.501 shows that about a quarter of the variation in yield (25.1%) depends on traits outside this set; Govindu *et al.* (2024) [14] obtained a residual of 0.038 after including plant dry weight and harvest index, which suggests that biological yield and harvest index are the traits to add in future work.

3.3 Principal component analysis

The first two principal components had eigenvalues above 1 (4.21 and 1.77) and explained 46.8% and 19.6% of the total variance, 66.4% together; the third (0.85) explained a further 9.4% (Table 4). The first component was a yield axis: seed yield, capitula per plant, 100-seed weight, seeds per capitulum and primary branches loaded 0.80 to 0.90, with flowering time (0.46) and maturity (0.38) and plant height (−0.36) loading more weakly, so the yield components behave as one trait in this panel. The second component was a phenology axis, with days to 50% flowering and maturity (0.75 and 0.81) and plant height (0.46) loading positively and oil content negatively (−0.53); seed yield loaded only −0.11 on it, so earliness or lateness and plant height vary largely independently of yield. The third component was dominated by oil content (0.71), with seed yield at −0.08, so oil content forms a separate axis from yield, consistent with its weak correlation and small direct effect.

Trait abbreviations as in Table 1.

3.4 Implications for selection and limitations

Selection for higher 100-seed weight and number of capitula per plant appears to be a promising approach for improving seed yield in the studied safflower genotypes. Both traits showed strong positive associations with seed yield and substantial direct effects, highlighting their potential value as selection criteria (Srikanth *et al.*, 2026a) [15]. Seeds per capitulum and primary branches per plant may also contribute to yield improvement through their relationships with other yield-associated traits. Plant height can be considered alongside these traits to identify genotypes with desirable plant architecture and productive

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potential. Furthermore, oil content showed a positive association with seed yield, suggesting scope for simultaneous improvement of both traits, while its distinct contribution to overall trait variation indicates potential for selection based on oil quality and yield.

Table 4. Loadings of nine traits on the first three principal components.

Trait	PC1	PC2	PC3
DFF	0.463	0.750	0.300
DM	0.377	0.806	0.281
PH	−0.359	0.460	−0.291
NPB	0.803	−0.035	−0.194
NCP	0.900	0.025	−0.045
NSC	0.810	−0.137	−0.123
HSW	0.873	−0.179	−0.149
OC	0.212	−0.528	0.712
SY	0.898	−0.113	−0.082
Eigenvalue	4.21	1.77	0.85
Variance (%)	46.8	19.6	9.4
Cumulative (%)	46.8	66.4	75.8

The findings provide useful insights into the relationships among yield components in the evaluated safflower panel. The path analysis accounted for a substantial proportion of the variation in seed yield, with a residual effect of 0.150. The phenotypic correlations and path coefficients offer a useful basis for identifying promising selection criteria. Further evaluation across seasons and locations would help establish the consistency of these relationships and support their application in safflower breeding programmes.

4. Conclusion

Seed yield per plant showed strong positive associations with 100-seed weight, number of capitula per plant, number of seeds per capitulum and number of primary branches (r = 0.661–0.808). Its associations with flowering time, maturity and oil content were comparatively weak, while plant height showed a negative relationship with yield (r = −0.292). Path analysis accounted for 74.9% of the variation in seed yield and identified 100-seed weight (0.411) and number of capitula per plant (0.311) as the major direct contributors. Seeds per capitulum and primary branches also contributed to yield through their relationships with other component traits. The direct effects of flowering time, maturity, plant height and oil content were comparatively small. Principal component analysis further highlighted the close association of seed yield with its major component traits, while phenology, plant height and oil content showed distinct patterns of variation. Overall, the findings indicate that selection for higher 100-seed weight and greater capitula number per plant may be effective for improving seed yield, with opportunities to consider plant architecture and oil content alongside yield-related traits. Further evaluation across environments would help establish the consistency of these relationships

Acknowledgements

The author acknowledges the support and research facilities provided by College of Agriculture, Pune, Mahatma Phule Krishi Vidyapeeth, Rahuri, during the course of this research.

Conflict of interest

The authors declare no conflict of interest.

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How to cite this article: Srikanth B, Rajguru A, Parveen N, Shitole LS, Bhagat A, Shinde P. Correlation and path coefficient analysis for seed yield and its components in safflower (*Carthamus tinctorius* L.) genotypes. *International Journal of Agriculture and Food Science*. 2026;8(11):243-246. doi: https://www.doi.org/10.33545/2664844X.2026.v8.i11d.89983

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