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ASSESSMENT OF GENOTYPIC AND PHENOTYPIC ASSOCIATIONS AMONG SEED YIELD-RELATED TRAITS IN SAFFLOWER (*Carthamus tinctorius* L.)

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ABSTRACT

The present investigation was undertaken to assess the association of seed yield with its contributing characters in safflower (*Carthamus tinctorius* L.). A total of 99 safflower genotypes along with three check varieties (PBNS-12, A-1 and ISF-764) were evaluated during the *Rabi* season of 2025–2026 at the All India Coordinated Research Project on Safflower, Vasantao Naik Marathwada Krishi Vidyapeeth, Parbhani using an augmented design. Observations were recorded for twelve quantitative traits and genotypic and phenotypic correlation coefficients were estimated to determine their relationship with seed yield. The results indicated that seed yield per plant had significant and positive associations with days to 50 per cent flowering, days to maturity, number of primary branches per plant, number of capitula per plant, number of seeds per capitulum, volume weight and biomass per plant at both genotypic and phenotypic levels. In contrast, plant height, 100-seed weight and harvest index exhibited positive but non-significant associations with seed yield while oil content showed a negative association. Thus, traits exhibiting significant positive associations with seed yield may be considered important selection criteria for enhancing seed yield in safflower.

Key words : Safflower, Genotypic correlation, Phenotypic correlation.

Introduction

Safflower (*Carthamus tinctorius* L.) is an important oilseed crop belonging to the family Asteraceae (Compositae). It is an annual, herbaceous and predominantly self-pollinated crop with 24 chromosome pairs and is considered to have originated in the Near East and South-West Asia. Among the species of *Carthamus*, *Carthamus tinctorius* is the cultivated species of major economic importance (Knowles, 1969 and Yuan *et al.*, 1989).

The importance of safflower is mainly attributed to its high-quality edible oil which contains a high proportion

of unsaturated fatty acids particularly linoleic and oleic acids. Besides its use as an edible oil, safflower oil has applications in pharmaceutical, cosmetic and industrial products. The flowers are also valued as a source of natural dye while different parts of the plant have traditionally been used for medicinal purposes (Weiss, 1983; Katkade *et al.*, 2018; Delshad *et al.*, 2018).

Seed yield is a complex quantitative trait influenced by several component characters and environmental conditions. Therefore, understanding the association between seed yield and its contributing traits is essential for effective selection and crop improvement. Correlation analysis provides information on the direction and

magnitude of association between seed yield and its contributing traits and helps in identifying suitable selection criteria for yield improvement in safflower (Pavithra *et al.*, 2016). Genotypic correlation reflects the inherent genetic association among traits whereas phenotypic correlation represents the combined influence of genetic and environmental factors. Thus, correlation analysis provides a useful basis for identifying important yield-contributing traits and formulating effective selection strategies for improving seed yield in safflower.

Materials and Methods

The experiment was undertaken during the *Rabi* season of 2025–2026 at the All India Coordinated Research Project on Safflower, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani, Maharashtra, India. A total of 99 safflower genotypes comprising three checks namely PBNS-12, A-1 and ISF-764 were evaluated following an augmented design. The genotypes were sown in rows at a spacing of 45 cm × 20 cm. Data were recorded from five randomly selected plants of each genotype for twelve quantitative characters including days to 50 per cent flowering, days to maturity, number of primary branches per plant, plant height (cm), number of capitula per plant, number of seeds per capitulum, 100-seed weight (g), volume weight (g/L), biomass per plant (g), harvest index (%), oil content (%) and seed yield per plant (g). For statistical analysis, the genotypic and phenotypic correlation coefficients were calculated from the respective variances and covariances to evaluate the degree of association between different traits. The formulas used for these calculations were proposed by Johnson *et al.* (1955) and are presented below:

Genotypic correlation coefficient (rgxy)

$$(rgxy) = \frac{\text{Cov}(gx.gy)}{\sqrt{\sigma^2_{gx} \cdot \sigma^2_{gy}}}$$

Where,

Cov (gx.gy) = Genotypic covariance between character x and y

σ^2_{gx} and σ^2_{gy} = Genotypic variance of character x and y, respectively

Phenotypic correlation coefficient (rpxy)

$$(rpxy) = \frac{\text{Cov}(px.py)}{\sqrt{\sigma^2_{px} \cdot \sigma^2_{py}}}$$

Where,

Cov (px.py) = Phenotypic covariance between character x and y

σ^2_{px} and σ^2_{py} = Phenotypic variance of character x and y, respectively.

Results and Discussion

Analyzing the association between seed yield and its contributing characters is essential for recognizing traits that can be utilized as effective selection criteria for yield improvement. The primary objective of the present study was to identify characters showing desirable relationships with seed yield and thereby assist in the selection of superior genotypes. The efficiency of selection largely depends on the appropriate identification of traits that contribute favourably to seed yield. In this regard, correlation coefficient analysis provides useful information on the nature and extent of relationships among the characters under investigation.

The genotypic and phenotypic correlation coefficients for the twelve quantitative traits are presented in Tables 1 and 2, respectively. The correlation estimates provide an understanding of the magnitude and direction of association among the characters and help in identifying traits that could serve as dependable indicators for improving seed yield in safflower.

At the genotypic level, seed yield per plant exhibited a positive and significant correlation with days to 50 per cent flowering (0.2228), days to maturity (0.2548), number of primary branches per plant (0.3969), number of capitula per plant (0.5421), number of seeds per capitulum (0.4572), volume weight (0.3564) and biomass (0.9041). These positive relationships indicate that genotypes possessing higher values for these yield-associated traits tended to record greater seed yield. Among these traits, biomass exhibited the strongest genotypic correlation with seed yield followed by number of capitula per plant. Additionally, plant height (0.1626), 100-seed weight (0.1483) and harvest index (0.1122) showed positive but non-significant associations with seed yield suggesting a comparatively weaker relationship. In contrast, oil content (-0.1499) showed a negative association with seed yield indicating a possible inverse relationship between oil content and seed yield at the genotypic level.

The phenotypic correlation supported all of the genotypic findings. Seed yield exhibited positive and significant phenotypic correlations with days to 50 per cent flowering (0.2191), days to maturity (0.2377), number of primary branches per plant (0.2402), number of capitula per plant (0.5339), number of seeds per capitulum (0.4210), volume weight (0.3569) and biomass (0.9042). The close agreement between the genotypic and phenotypic correlations particularly for biomass, number of capitula and number of seeds per capitulum suggests

Table 1 : Genotypic correlation of seed yield and yield contributing traits in Safflower.

Traits	D50%	DM	PH	NPB	NC	NS	100SW	VW	BM	HI	OC	SYPP
D50	1.0000	0.9283**	0.0920	0.0519	0.2286*	0.0775	0.1251	0.0759	0.2065*	0.0171	-0.1028	0.2228*
DM		1.0000	-0.0094	0.0696	0.2697**	0.0001	0.0871	0.1277	0.2695**	-0.0632	-0.0348	0.2548*
PH			1.0000	0.1118	0.1021	0.2900**	-0.0923	0.0608	0.1429	0.0575	0.0271	0.1626
NPB				1.0000	0.0077	0.0506	0.0663	0.1639	0.4174**	0.0179	0.0086	0.3969**
NC					1.0000	0.2595**	0.3642**	0.2361*	0.5493**	-0.0716	-0.0113	0.5421**
NS						1.0000	0.2163*	0.0640	0.4579**	-0.0779	-0.1579	0.4572**
100 SW							1.0000	0.0196	0.0875	0.0200	-0.0931	0.1483
VW								1.0000	0.2812**	0.1034	0.8352**	0.3564**
BM									1.0000	-0.1833	-0.1703	0.9041**
HI										1.0000	0.0129	0.1122
OC											1.0000	-0.1499

*and ** significant at 5 and 1%, respectively

D50%- Days to 50% flowering, **DM**- Days to maturity, **PH**- Plant height (cm), **NPB**-No. of primary branches per plant, **NC**- No. of capitula per plant, **NS**- No. of seed per capitulum, **100SW**- 100 seed weight, **VW**- Volume weight (g/L), **BM**- Biomass (g), **HI**- Harvest index (%), **OC**- Oil content (%), **SYPP**- Seed yield per plant (g).

Table 2 : Phenotypic correlation of seed yield and yield contributing traits in Safflower.

Traits	D50%	DM	PH	NPB	NC	NS	100SW	VW	BM	HI	OC	SYPP
D50	1.0000	0.9072**	0.1021	-0.0339	0.1994*	0.0910	0.1388	0.0733	0.2037*	0.0149	-0.1075	0.2191*
DM		1.0000	-0.0025	0.0406	0.2216*	0.0953	0.1094	0.1166	0.2541*	-0.0689	-0.0392	0.2377*
PH			1.0000	-0.0382	0.0634	0.2436*	-0.1145	0.0544	0.1307	0.0452	0.0142	0.1469
NPB				1.0000	0.1372	0.0980	-0.0923	0.1023	0.2532*	0.0046	0.0418	0.2402*
NC					1.0000	0.2157*	0.3089**	0.2344*	0.5401**	-0.0665	-0.0002	0.5339**
NS						1.0000	0.2264*	0.0536	0.4241**	-0.0812	-0.1493	0.4210**
100 SW							1.0000	0.0188	0.0877	0.0266	-0.0937	0.1473
VW								1.0000	0.2816**	0.1044	0.8346**	0.3569**
BM									1.0000	-0.1814	-0.1691	0.9042**
HI										1.0000	0.0140	0.1142
OC											1.0000	-0.1483

*and ** significant at 5 and 1%, respectively.

D50%- Days to 50% flowering, **DM**- Days to maturity, **PH**- Plant height (cm), **NPB**-No. of primary branches per plant, **NC**- No. of capitula per plant, **NS**- No. of seed per capitulum, **100SW**- 100 seed weight, **VW**- Volume weight (g/L), **BM**- Biomass (g), **HI**- Harvest index (%), **OC**- Oil content (%), **SYPP**- Seed yield per plant (g).

that these relationships were consistently expressed at both levels. On the other hand, plant height (0.1469), 100-seed weight (0.1473) and harvest index (0.1142) maintained positive but non-significant associations in agreement with the genotypic results. Similarly, oil content remained negatively associated with seed yield at the phenotypic level (-0.1483). Thus, the phenotypic results substantiated the genotypic correlation pattern indicating that the observed associations of these traits with seed yield were relatively consistent and may be useful in selection for higher seed yield.

These results are consistent with findings reported by several researchers, including Bahman *et al.* (2010), Sreenivasa *et al.* (2011), Chapade *et al.* (2011), El-Lattief

(2012), Ahmadzadeh *et al.* (2012), Pavithra (2013), Muhammad *et al.* (2014), Pavithra *et al.* (2016), Sýrel and Aytac (2016), Jadhav *et al.* (2018), Paikara and Parihar (2019), Dhage *et al.* (2020), Neelima *et al.* (2021) and Kale *et al.* (2025). Overall, the present study indicates that higher seed yield was generally associated with later flowering and maturity, greater number of primary branches, more capitula per plant, higher number of seeds per capitulum, greater volume weight and increased biomass. Among these traits, biomass and number of capitula per plant showed the strongest positive associations with seed yield, highlighting their potential importance as selection criteria for yield improvement. In contrast, oil content showed a negative association

with seed yield at both levels indicating a possible inverse relationship between yield and oil content. Nevertheless, from a breeding perspective, the most desirable approach would be to identify genotypes that combine high seed yield with high oil content, thereby facilitating the development of superior safflower genotypes with improved productivity as well as oil quality.

Conclusion

The study revealed that seed yield was significantly and positively associated with days to 50 per cent flowering, days to maturity, number of primary branches per plant, number of capitula per plant, number of seeds per capitulum, volume weight and biomass. Among these, biomass and number of capitula per plant showed the strongest associations indicating their potential as effective selection criteria for improving seed yield. Hence, selection for these traits could effectively contribute to increasing seed yield.

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