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Correlation studies in M_5 generation of safflower [*Carthamus tinctorius* (L.)]

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Abstract

The current research was performed at the experimental farm of All India Co-ordinated Research Project on Safflower, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani. (M.S.) during *Rabi*, 2023-24. In M_5 generation, forty selected progenies from M_4 generation along with four standard checks, namely PBNS-12, PBNS-86, ISF-1, and Sharda were assessed in randomised block design. Correlation studies revealed that, the seed yield per plant was significantly and positively correlated with days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of capitula per plant and oil content at both genotypic and phenotypic level whereas negatively and non-significantly with volume weight at both genotypic and phenotypic level.

Keywords: Safflower, M_5 generation, genotypic correlation, phenotypic correlation

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Introduction

Safflower, a multipurpose crop, has been grown for centuries in India for the orange-red dye (Carthamin) extracted from its brilliantly coloured flowers and is cultivated mainly for its seed, which gives edible oil. Traditionally, this crop was grown for its flowers, fabric dyes, food colouring and for medicinal purposes (Weiss, 2000) [14]. It belongs to the family Compositeae or Asteraceae. In the wild genus *Carthamus* is reported to have 25 species (Yuan *et al*., 1989) [15]. Amongst the species of *Carthamus*, only safflower (*Carthamus tinctorius* L.) is grown worldwide containing 24 pairs of chromosomes.

Safflower is an important oilseed crop as it contains 78% of PUFA (Linoleic Acid) which is useful for heart patients as it reduces blood cholesterol levels. Linoleic acid can keep cell membranes soft, strengthen the elasticity and vitality. It also contains 16-20% mono saturated fatty acid (Oleic Acid) and only 8% saturated fatty acid, 2-3% stearic acid, 6-8% palmitic acid (Hamdan *et al*., 2011) [4]. Safflower is an annual herbaceous thistle like plant having many branches. It is 2 to 6 feet tall, and has numerous long, sharp spines on its leaves. Its flower head, or capitulum, is yellow or orange (rarely white to red), and seeds of safflower are white, shiny, and smooth. Safflower is primarily self-pollinating crop; however, insect pollinators may increase out crossing rates and seed production. Safflower is considered to have 10% cross pollination; however, this number is highly variable and can be increased by honey bees, bumblebees, beetles, and other insects.

The primary goal of plant breeding was to create varieties with desirable characteristics such as higher yield, disease resistance, drought resistance, early maturity, and better oil quality. Grain yield is a complex quantitative trait depending from the interaction between different yield components and environmental effects. It was very important to choose the appropriate selection criteria to improve grain yield (Samonte *et al*., 1998) [10]. Correlation has been used by plant breeders to identify characters that are useful as selection criteria to improve crop yield.

Correlation is a metric used to assess the mutual relationship between two variables. It acts as a gauge of how linearly and closely related two variables and studying correlations can help plant breeders better understand how the growth of one character will influence the concurrent growth of other characters. Character association research can be used to establish selection criteria for yield in parental lines so that the plants with the desired combination of characters can be successfully isolated (Kante *et al*., 2022) [5]. Phenotypic correlation is the relationship between phenotypic values, and it can change as a result of environmental factors. The genomic correlation is the breeding value correlation. Therefore, understanding the relationships between various characters is crucial for creating a sound breeding programme (Shrotri *et al*., 2021) [11].

Materials and Methods

The present investigation correlation studies in Safflower mutants was conducted at All India Co-ordinated Research Project on Safflower, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani, Maharashtra, India. In M_5 generation, forty selected progenies from M_4 generation along with four standard checks, namely PBNS-12, PBNS-86, ISF-1, and Sharda were assessed in randomised block design during *Rabi* season of 2023-24. The harvested seeds of M_4 plants were sown at 45 cm x 20 cm spacing on plant-to-row basis. The prescribed cultural and plant protection techniques have been compiled to raise healthy M_5 generation. Five randomly chosen plants of sole genotype was utilized to document the observations for eleven diverse quantitative traits *viz*., days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of capitula per plant, number of seeds per capitulum, 100-seed weight (g), hull content (%), volume weight (g/lit), oil content (%) and seed yield per plant (g). The data were subjected to simple correlation analysis as per Singh and Choudhary (1977) [12].

Result and Discussion

Correlation among seed yield and yield attributes help in identifying a suitable genotype with desired characteristics. This study aimed at selecting such desirable genotypes. The success of selection depends on the choice of selection criteria for improvement of seed yield. Correlation coefficient analysis could indicate significant relationship among the evaluated traits. The genotypic correlation coefficient and phenotypic correlation coefficient of eleven traits are presented in table 1and table 2 respectively.

The seed yield per plant recorded significant and positive association with days to 50% flowering (0.143), days to maturity (0.211), plant height (0.789), the number of primary branches per plant (0.259), number of capitula per plant (0.255) and oil content (0.156). The character volume weight (-0.036) showed negative and non-significant association. The character which had non-significant but positive association with number of seeds per capitulum (0.012), 100-seed weight (0.061) and hull content (0.032) at genotypic level.

The phenotypic correlation of the character seed yield per plant recorded significant and positive association with days to 50% flowering (0.131), days to maturity (0.173), plant height (0.227), number of primary branches per plant (0.251), number of capitula per plant (0.242) and oil content (0.110). The characters which showed non-significant but positive association with 100-seed weight (0.057), number of seeds per capitulum (0.029). The characters which showed non-significant but negative association with hull content (-0.002) and volume weight (-0.017).

Similar results were reported by Hajghani *et al*. (2009) [3], Roopa and Ravikumar (2010) [9], Golparvar (2011) [2], Lattief (2012) [6], Pavithra *et al*. (2016) [7], Sirel and Aytac (2016) [13], Arzu *et al*. (2018) [1] and Raju *et al*. (2019) [8].

This study also indicates that a high yield in general correlate with low oil content. However, a genotype with both high yield and high oil content could be more useful for strengthening breeding programme.

Table 1: Genotypic correlation coefficient matrix for seed yield per plant (g) and other parameters Safflower mutants

Sr. No.	Characters	Days to 50% flowering	Days to maturity	Plant height	Number of primary branches/plant	Number of capitula/plant	Number of Seeds/capitulum	100 seed weight	Hull content	Volume weight	Oil content	Seed yield /plant
1	Days to 50% flowering	1.000	0.961**	1.426**	0.080	-0.394**	-0.068	0.423**	- 0.076	0.458**	-0.064	0.143
2	Days to maturity		1.000	1.419**	0.035	-0.360**	-0.079	0.448**	- 0.090	0.561**	-0.113*	0.211
3	Plant height (cm)			1.000	-2.010	-0.852**	0.535**	1.525**	- 0.395	1.613**	0.487	0.789**
4	Number of primary branches/plant				1.000	0.348**	-0.084	0.139	0.055	-0.380**	0.240**	0.259
5	Number of capitula/plant					1.000	-0.218*	-0.150	0.318**	-0.175*	-0.047	0.255**
6	Number of seeds/capitulum						1.000	-0.064	0.100*	-0.101	0.088	0.012
7	100-seed weight (g)							1.000	0.074	0.339	0.069	0.061
8	Hull content (%)								1.000	0.140*	0.154*	0.032
9	Volume weight (g/lit)									1.000	0.031	-0.036
10	Oil content (%)										1.000	-0.156*
11	Seed yield/plant (g)											1.000

* Significance at 5% level ** Significance at 1% level.

Table 2: Phenotypic correlation coefficient matrix for seed yield per plant (g) and other parameters in Safflower mutants

Sr. No.	Characters	Days to 50% flowering	Days to maturity	Plant height	Number of primary branches/plant	Number of capitula/plant	Number of seeds/capitulum	100 seed weight	Hull content	Volume weight	Oil content	Seed yield/ plant
1.	Days to 50% flowering	1.000	0.948**	0.396**	0.101	-0.209	0.016	0.281**	- 0.062	0.340**	0.016	0.131
2.	Days to maturity		1.000	0.360**	0.089	-0.170	0.003	0.283**	- 0.097	0.396**	-0.029	0.173
3.	Plant height (cm)			1.000	0.027	-0.031	0.190	0.270 *	- 0.027	0.321**	0.108	0.227*
4.	Number of primary branches/plant				1.000	0.338**	-0.020	0.119	0.029	-0.267*	0.177	0.251*
5.	Number of capitula/plant					1.000	-0.191	-0.136	0.105	-0.148	- 0.049	0.242*
6.	Number of seeds/capitulum						1.000	-0.038**	0.072	-0.103	0.064	0.029
7.	100-seed weight (g)							1.000	0.083	0.290**	0.079	0.057
8.	Hull content (%)								1.000	0.104	0.154	-0.002
9.	Volume weight (g/lit)									1.000	0.022	-0.017
10.	Oil content (%)										1.000	0.110
11.	Seed yield/plant (g)											1.000

*Significance at 5% level **Significance at 1% level.

Conclusion

The present investigation revealed that, the seed yield per plant was significantly and positively correlated with days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of capitula per plant and oil content at both genotypic and phenotypic level. These yield components could be used in any future Safflower breeding programme for yield improvement. Hence, higher yield could be obtained by exerting selection pressure over any of these traits.

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