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Research Article

GENETIC VARIABILITY STUDIES FOR YIELD AND YIELD COMPONENT CHARACTERS IN SAFFLOWER (*CARTHAMUS TINCTORIUS* L.)

MALI B B*, WADIKAR P B, KHANDEBHARAD P R

Department of Agricultural Botany, College of Agriculture, Latur, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani, Maharashtra, India. Email: bharatmali.breeder@gmail.com

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ABSTRACT

The field experiment was conducted with 40 genotypes of safflower at the Experimental Farm of College of Agriculture, Latur, during Rabi 2020–2021, with the purpose of exploring genetic diversity, heritability, and genetic progress for yield and yield contributing features in safflower. The presence of wide genetic variability in the experimental materials was demonstrated by an analysis of variance involving 40 safflower genotypes for ten quantitative characters, which revealed significant differences for all of the traits under study. Seed yield per plant, number of branches per plant, number of seeds per capitulum, test weight, and number of effective capitulum per plant all had a significant genotypic coefficient of variation and phenotypic coefficient of variation magnitudes. The character seed yield per plant, hull content, plant height, and test weight were similarly linked to the greatest broad sense heritability scores. The number of seeds per capitulum, number of effective capsules per plant, number of branches per plant, oil content, and days to 50% flowering were also associated with high broad sense heritability values. Characters, such as the number of branches per plant, number of effective capitulum per plant, number of seeds per capitulum, test weight, plant height, and seed yield per plant were associated with high heritability values in the broad sense, along with high expected genetic advance, indicating the role of additive genes in governing the inheritance of these traits, which could be improved through simple segregation.

Keywords: Genetic variability, Heritability, Genotypic coefficient of variation, Phenotypic coefficient of variation, Genetic advance, Safflower.

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INTRODUCTION

Safflower is one of the oldest oilseed crops (*Carthamus tinctorius* L.). According to archeological traces dating as far as 2500 BC, it was first farmed in Mesopotamia. Safflower has been grown in India since the beginning of time, and it is known in ancient scriptures as kuswtiba. It is frequently grown in the hot and arid climate of the Middle East, whence it derives its origins and diversity. The Arabic name quartilum or gurtum refers to the color of safflower flower dye, and *Carthamus* is a Latinized synonym for it. Safflower is one of India's most significant Rabi oilseed crops, and it is heat, drought, and salinity resistant. The safflower (*C. tinctorius* L.) is an important tropical oil seed crop.

Safflower belongs to the compositae family, *Asteraceae* subfamily, tubiflorae tribe, and phanerogams division of the angiosperms. The safflower plant is a bushy, herbaceous perennial with many primary, secondary, and tertiary branches, all of which terminate in a spherical structure known as the capitulum. There are 36 species in the *Carthamus* genus, with *C. tinctorius* L. (2n=24) being the only cultivated safflower used for oil extraction and the rest being wild species. Plants range in height from 30 to 150 cm, with globular flower heads (capitula) with bright yellow, orange, or red flowers. Safflower oil offers excellent cooking qualities, with an average of 75% linoleic acid and tocopherols, which have an antioxidant effect and a high Vitamin E concentration. India produces the most safflower in the world (43.67 MT) and has the most acreage (5.17 lakh hectares); however, the average production in 2019–2020 is just 843 kg/ha. Maharashtra and Karnataka are the two most important safflower-growing states, with 72 and 23% of area and 63 and 35% of production, respectively. (Ministry of Agriculture and Farmers Welfare, Government of India).

MATERIALS AND METHODS

During Rabi 2020–2021, forty genotypes of safflower were investigated at the College of Agriculture, Lature, under of V.N.M.K.V., Parbhani. Each genotype was cultivated in a single row of 4 m × 3 m in length with a spacing of 50 cm between rows and 20 cm between plants within a row by using a randomized block design with two replications. To raise a good crop, a recommended package of operations was followed. Five plants were identified and labeled at random from each row and replication for recording observations, and the mean of the five plants was employed for statistical analysis. The data were recorded for days to 50% flowering, days to maturity, plant height at maturity (cm), number of branches per plant, number of effective capitula per plant, number of seeds per capitulum, 100-seed weight (g), seed yield per plant (g), hull content (%), oil content (%). Analysis of variance was performed to test the significance of differences between the genotypes for all the characters. The analysis of variance was done as suggested by Panse and Sukhatme (1985). Broad sense heritability was estimated for various characters as per the formulae suggested by Lush (1949). The genetic advance was calculated in percent as per the formula suggested by Johnson et al., (1995).

RESULTS AND DISCUSSION

The analysis of variance for a set of 40 safflower genotypes for ten quantitative characters revealed highly significant differences among genotypes for the characters studied, including days to 50% flowering, day to maturity, plant height, number of branches per plant, number of capsules per plant, number of seed per capsule, test weight, hull content, and oil content. For all ten characters studied, the mean sum of the square was non-significant due to replication. The general analysis of variance was carried out for each character to find out the amount of variation for various characters given in (Table 1). Phenotypic variance (V_p) values were more than the genotypic variance (V_g) for all the characters. High genotypic and phenotypic variances were observed for the characters' plant height and seed yield per plant. The present findings are in close agreement with those of Lakshyadeep *et al.* (2005) and Inchanal *et al.* (2010), Sreelakshmi (2015) and Monpara and Khairnar (2016).

Table 1: Analysis of variance for yield and yield contributing characters in safflower

Source of variation	d. f.	Plant height (cm)	Days to maturity	Days to 50% Flowering	No. of capsules/ plant	No. of seeds/ capsule	Hull content (%)	100-seed wt.(g)	Harvest index (%)	Oil content (%)	Seed yield/ plant
		1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**
Replication	1	1.012	19.012	2.485	1.201	3.164	7.875	0.001	0.037	6.745	4.905
Treatment	39	15.154**	30.577*	191.652**	3.423**	30.127**	31.404**	1.121**	5.215**	22.127**	163.907**
Error	39	2.577	9.474	18.64	0.461	3.726	3.881	0.012	0.789	1.581	11.284

* and ** indicates significance at 5 and 1% levels, respectively

Table 2: Parameters of genetic variability for yield and yield contributing characters in safflower

S.No.	Characters	Range	General mean	Genotypic variance	Phenotypic variance	GCV (%)	PCV (%)	h2 (broad sense)	Genetic advance	Genetic advance (%)
1	Days to 50% flowering	76–89.50	82.713	6.37	9.02	3.03	3.598	70.935	4.351	5.257
2	Days to maturity	113–128	121.738	11.03	18.927	2.671	3.68	52.69	4.857	3.994
3	Plant height (cm)	82.90–125.50	107.921	86.88	105.920	8.624	9.507	82.272	17.379	16.113
4	Number of branches per plant	7.50–13.60	10.559	1.49	1.956	11.519	13.191	76.261	2.189	20.723
5	Number of capsules per plant	20.70–35.60	29.225	13.2	16.92	12.432	14.077	77.987	6.61	22.616
6	Number of seeds per capsule	18.55–35.85	26.654	13.830	17.320	13.938	15.781	78.005	6.749	25.358
7	Test weight (g)	3.28–5.89	4.992	0.552	0.560	14.94	15.096	97.938	1.518	30.457
8	Oil content (%)	25.02–31.43	28.002	2.281	2.57	5.297	6.169	73.729	2.631	9.37
9	Hull content (%)	32.33–46.60	41.446	10.14	11.05	7.755	8.33	86.666	6.147	14.872
10	Seed yield per plant (g)	26.75–62.21	39.324	76.87	88.19	22.222	23.809	87.118	16.796	42.728

GCV: Genotypic coefficient of variation, PCV: Phenotypic coefficient of variation, h^2: Heritability

Moderate genotypic and phenotypic variances were observed for character days to maturity, number of capsules per plant, number of seeds per capsule, and hull content. Inchanal *et al.* (2010) reported the lowest and moderate genotypic and phenotypic variance values for the number of primary branches, 100 seed weight, hull content (%) and days to 50% flowering. The lowest genotypic and phenotypic variances were observed for character test weight, oil content, number of branches per plant, and days to 50% flowering. Lakha *et al.* (1992) studied similar findings for 100 seed weight and number of branches per plant. As genotypic and phenotypic variances are low for these characters, they can be improved by developing a segregating population using diverse parents and selecting good transgressive segregants.

In the present investigation, high estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for seed yield per plant, number of seeds per capitulum, test weight, number of effective capitulum per plant and number of branches per plant. For the remaining characters plant height, hull content, oil content, days to maturity, and days to 50% flowering the values of GCV and PCV are lower.

Higher values of PCV than genotypic coefficient variation were also reported by More et al. (2006), Lakshyadeep et al. (2005), and Rathod et al. (2021) and Sandeep et al. (2018) reported highest estimates of GCV and PCV for number of seeds per capitulum and seed yield per plant. The low genotypic and PCVs were observed for days to maturity, days to 50% flowering, oil content, hull content, and plant height. Similar results were reported by Pavithra et al. (2016) for days to maturity, days to 50% flowering, and hull content. The characters that have less influence on the environment may be improved by simple selection methods such as mass selection or by pure line selection.

The heritability estimates along with expected genetic advance are more useful in predicting yield under phenotypic selection than heritability estimates alone. The broad sense heritability estimates are always of higher magnitude than narrow sense heritability estimates. Therefore, it should be regarded as crude estimates of gene action, operating for a particular character, and the inference drawn to be viewed accordingly.

In the present investigation, the range of the broad sense heritability was from 52.69% for days to maturity to 97.93% for test weight. Very high broad sense heritability values were also associated with the character seed yield per plant (87.11) and hull content (86.66), plant height (82.27), and test weight (97.94). High broad sense heritability values were also associated with the character number of seeds per capitulum (78.00), number of effective capsules per plant (77.98), number of branches per plant (76.6), oil content (73.72) and days to 50% flowering (70.93) were reported, Dhage *et al.* (2020), Lakshyadeep *et al.* (2005), and Ichanal *et al.* (2010). Moderate heritability was observed for days to maturity (52.69). Low heritability for yield and yield components suggested that non-additive gene action and the selection for such characters then becomes difficult as they are influenced by the environment. However, in broad sense heritability estimates, the contribution of dominance and epistasis also included and are prone to changes from location to location and interaction with the environment. The low and moderate heritability estimates for yield contributing characters were also reported by Kavani *et al.* (2000), More *et al.* (2006), and Nair *et al.* (2006).

The high genetic advance was observed for the characters' seed yield per plant (42.72), number of seeds per capitulum (25.35), test weight (30.45), number of effective capitulum per plant (22.61), and number of branches per plant (20.72). The characteristics, such as plant height (16.11) and hull content (14.82) were recorded as moderate genetic advance. The low genetic advance was observed for the characters' days to 50% flowering (5.25), days to maturity (3.99), and oil content (9.37).

As a result of the preceding discussion, it is clear that the characters seed yield per plant, number of seeds per capitulum, test weight, number of effective capitulum per plant, number of branches per plant, and plant height had high heritability combined with the high expected genetic advance, indicating the presence of additive gene action and phenotypic selection effectiveness. Thus, while exploiting genetic variability a due weightage should be given to these characters were also reported by Rathod *et al.* (2021), Vijaya et al. (2004) and Camas and Esenda *et al.* (2006).

CONCLUSION

The treatment differences in the analysis of variance were found statistically significant for all of the characters. The magnitude of genotypic and PCV also indicated the presence of a good amount of variability in the experimental materials. In the present study, high estimates of genotypic and PCV were observed for various characters. High heritability values in a broad sense coupled with high expected genetic advance were associated with the characters, such as the number of branches per plant, number of effective capitulum per plant, number of seeds per capitulum, test weight, plant height, and seed yield per plant. High heritability coupled with a high genetic advance expressed as percent of the mean offers the most effective condition for selection.

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