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Genetic variability, heritability and genetic advance studies for morphological and quantitative traits in M₃ generation of Safflower [*Carthamus tinctorius* (L.)]

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Abstract

The present investigation was carried out during *Rabi*, 2021-22 for M₃ generation of safflower genotypes. The present field study was undertaken at the experimental farm of All India Co-ordinated Research Project on Safflower, Vasanttrao Naik Marathwada Krishi Vidyapeeth, Parbhani. (M.S.). The experimental material for evaluation in M₃ generation included eighty-eight selected progenies along with two standard checks. The evaluation of the M₃ generation took place by using an Augmented block design. The analysis of variance (M.S.S.) was conducted for the M₃ generation considering various traits including days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of capsules per plant, number of seeds per capsule, 100-seed weight (g), oil content (%), and seed yield per plant (g). The results of the analysis of variance revealed statistically significant for all the examined traits. This indicates that there is sufficient variability present among the genotypes and their respective component traits. The majority of the traits like plant height, number of seeds per capsule, 100-seed weight, oil content and yield per plant exhibited high PCV, GCV, heritability, and genetic advance. This suggests that genetic factors primarily influence these traits, and they are highly responsive to environmental conditions.

Keywords: Variability, genetic advance, augmented block design, safflower

Introduction

Safflower (*Carthamus tinctorius* L.) is an oilseed crop generally known as 'kardai' in Marathi and 'kusum' in Hindi. In Sanskrit literature it is additionally called 'Agnisikha'. It belongs to family Compositae or Asteraceae which is originated from Middle East and part of Africa, further three centers of origin are India, Irano-Afghanistan and Ethiopia (Vavilov, 1949) [26]. Safflower is an annual herbaceous crop that is diploid (2n=24) and highly adaptable to hot and dry climates. Presently, in India mainly nine edible oilseed crops (vegetable oil) viz. safflower, groundnut, rapeseed, mustard, sesame, sunflower, niger, linseed and soybean are grown. Out of them, safflower has high potential value due to nutritional and pharmaceuticals properties of seed oil and petals (Li and Mundel, 1996) [11]. Safflower is one of the favored plant to produce plant made medicines, pharmaceuticals for essential protective medicine. The main reason safflower is grown is for its seed, which is used to make edible oil. The seed's oil content ranges from 28 to 36%; the oil is rich in linoleic acid, an unsaturated fatty acid that lowers blood cholesterol. The two main unsaturated fatty acids in safflower oil are oleic acid (18:1) and linoleic acid (18:2). Safflower is generally a self-pollinating crop; however, insect pollinators may increase outcrossing 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. In India, during 2021-22, a total of 0.45 lakh tonnes of safflower was produced from an area of 0.64 lakh ha with average productivity of 694 kg/ha. In Maharashtra, area under safflower during 2021-22 was 0.23 lakh ha with a production 0.18 lakh tonnes and average productivity was 792 kg/ha. (Anonymous 2022) [1]. Crop improvement is dependent on the magnitude of genetic variability and the extent to which the desirable characters are heritable. Genetic variability for economic traits is the pre-requisite for any successful breeding programme and the inherent variability is limited in safflower for achieving desired

improvement. The breeding efforts in safflower would be enhanced if the range of genetic variability could be broadened.

Materials and Methods

The seeds of selected progenies (mutants) of variety "PBNS-12 (Parbhani Kusum)" were obtained from AICRP on safflower, VNMKV, Parbhani. In M₃ eighty-eight selected progenies along with two standard checks, PBNS-12 and PBNS-86 were evaluated. The evaluation of the M₃ generation carried out during the Rabi season of 2021-22, using an Augmented Block Design. The laboratory work for estimation of oil content was performed at ICAR-IIOR, Hyderabad.

For documenting observations, five plants were randomly chosen from each genotype in each replication. The average value of every characteristic was calculated using the measurements made on certain plants. The following characteristics were noted: days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of capsules per plant, number of seeds per capsule, 100-seed weight (g), oil content (%), and seed yield per plant (g). Following Panse and Sukhatme's [14] typical protocol, an ANOVA (Table 1) was computed to determine the significance of differences between the treatments for each trait (1985). By dividing the total value of the observations by the number of observations, the mean values of all the treatments for the different genotype attributes were calculated. The genotypic and phenotypic variance was computed using the mean square from the variance table (Burton, 1952) [3]. approach was utilized to assess the genotypic and phenotypic coefficient of variation. In a broad sense, heritability is the ratio of genotypic variance to the total amount of observable variance within a population. In its broadest sense, heritability (h^2) was computed using the formula provided by Johnson *et al.* (1955) [7]. The genetic progress for every character at 5% selection intensity was computed using the Johnson *et al.* (1955) [7] formula.

Results and Discussion

Genetic variability parameters studied in M₃ generation

The GCV, PCV, heritability (h^2) and genetic advance (GA) as% of mean were worked out for nine quantitative traits in the M₃ generation and results were presented in Table 2 respectively. The PCV in M₃ for days to 50% flowering was found to be low with the value of 2.59% and it was recorded a low GCV of 2.45%. This trait also expressed high heritability of 88.93% and low value (4.76%) of GA as% of mean. A close observation of PCV and GCV revealed that the values recorded for GCV were very close to PCV indicating thereby that maximum variation were caused by mutations for polygenes. These results are in broad agreement with the reports of Sikarwar *et al.*, (2017) [22] in Yellow Sarson, Rajanna *et al.*, (2020) [17] in Linseed, Dogra *et al.*, (2020) [5] in Linseed, Khattab *et al.*, (2018) [9] and Minnie *et al.*, (2020) [13] in Safflower.

Days to maturity in the M₃ progenies registered a low PCV of 1.58% and a low GCV of 1.49%. The trait also expressed high heritability value of 88.26% followed by low GA as% of mean of 2.88%. In present study, high heritability was also reported, along with low genetic advance as a percent of mean, showing the role of non-additive gene action in determining the inheritance of days to maturity. These

results are in broad agreement with the reports of Shivani *et al.*, (2011) [20] in Safflower Khattab *et al.*, (2018) [9] in Safflower, Minnie *et al.*, (2020) [13] in Safflower, Thakur *et al.*, (2020) [24] in Linseed, Meena *et al.*, (2020) [12] in Linseed and Belete *et al.*, (2012) in Ethiopian mustard.

Plant height in M₃ progenies registered a low PCV of 5.92% and a low GCV of 5.88%. This trait also expressed high heritability of 98.48% followed by GA as% of mean of 12.03%. These results are in broad agreement with the reports of Rai *et al.*, (2014) [16] in Linseed, Sikarwar *et al.*, (2017) [22] in Yellow Sarson and Belete *et al.*, (2012) in Ethiopian mustard.

Number of primary branches per plant in M₃ progenies registered a moderate PCV of 12.76% and a moderate GCV of 12.55%. This trait also expressed high heritability value of 96.80% followed by high GA of 25.48%. These results are consistent with the reports of Thakur *et al.*, (2020) [24] in Linseed, Sikarwar *et al.*, (2017) [22] in Yellow Sarson, Chavan and Chopade (1981) [4] in Sesame and Leelavati and Mogali (2018) in Linseed.

The PCV for number of capsules per plant in M₃ progenies was found to be moderate with the value of 16.87% and it was recorded a moderate GCV of 16.80%. This trait also expressed high heritability value of 99.16% and high value (34.52%) of GA as% of mean. These results are in accordance with the reports of Kalaiyarasi *et al.*, (2019) [8] in Sesame, Leelavati and Mogali (2018) [10] in Linseed, Rajanna *et al.*, (2020) [17] in Linseed, Meena *et al.*, (2020) [12] in Linseed, Umamaheswari *et al.*, (2019) [25] in Sesame, and Khattab *et al.*, (2018) [9] in Safflower

The PCV for number of seeds per capsule in M₃ progenies was found to be low with the value of 7.24% and it was recorded a low GCV of 6.23%. This trait also expressed high heritability value of 74.02% and moderate value (11.06%) of GA as% of mean. These results are in accordance with the reports of Rathod *et al.*, (2021) [18] in Safflower, Minnie *et al.*, (2020) [13] in Safflower, Kalaiyarasi *et al.*, (2019) [8] in Sesame, Leelavati and Mogali (2018) [10] in Linseed and Rajanna *et al.*, (2020) [17] in Linseed.

The PCV for 100 seed weight in M₃ progenies was found to be low with the value of 9.24% and it was recorded a low GCV of 8.61%. This trait also expressed high heritability value of 86.83% and moderate value (16.55%) of GA as% of mean. These results are in accordance with the reports of Phanindra *et al.*, (2018) [15] in Sunflower, Pushpavalli and Kumar (2017) in Safflower, Khattab *et al.*, (2018) [9] in Safflower, Minnie *et al.*, (2020) [13] in Safflower, Leelavati and Mogali (2018) [10] in Linseed and Rajanna *et al.* (2020) [17] in Linseed.

The PCV for oil content in M₃ progenies was found to be low with the value of 3.53% and it was recorded a low GCV of 3.46%. This trait also expressed high heritability value of 96.14% and low value (6.99%) of GA as% of mean. These results are in broad agreement with the reports of Phanindra *et al.*, (2018) [15] in Sunflower, Meena *et al.*, (2020) [12] in Linseed and Rathod *et al.*, (2021) [18] in Safflower. The presence of high/moderate/low heritability, as well as low genetic advance as a percent of the mean, suggests that non-additive gene action governs the inheritance of oil content. These results are in broad agreement with the reports of Jagadeesan *et al.*, 163 (2008) [6] in Sunflower, Siddiqui *et al.*, (2009) [21] in Rapeseed and Singh *et al.*, (2020) [23] in Sesame.

The PCV of M₃ progenies for seed yield per plant was found to be moderate with the value of 13.41% and it was recorded a moderate GCV of 13.37%. This trait also expressed high heritability of 99.53% and high value of 27.53% of GA as% of mean. High heritability was detected along with high genetic advance as a percent of mean, showing the importance of additive gene action in determining the inheritance of seed yield per plant. These results are in broad agreement with the reports of Rajanna *et al.*, (2020)^[17] in Linseed, Leelavati and Mogali (2018)^[10] in Linseed, Khattab *et al.*, (2018)^[9], Minnie *et al.*, (2020)^[13] in Safflower and Sanghani *et al.*, (2016)^[19] in Sesame.

In the present study of M₃ generation, among the traits evaluated, a high heritability coupled with high GA as% of mean, highest PCV and GCV was noted for the number of effective capitulum per plant, seed yield per plant and number of primary branches per plants. Days to maturity and days to 50% flowering, days to maturity and oil content exhibited low PCV and GCV in M₃ generation for all the mutants. This clearly denoted that these traits are governed largely by additive gene effect, which may be favorably exploited for further improvement of these characters by selection.

Table 1: Analysis of variance (ANOVA) for various traits in M₃ generation of Safflower mutants.

Sr no.	Source of variation	D.F.	Mean sum of squares								
			Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches/plants	No. of effective capitula/plant	No. of seeds per capitulum	100 seed weight (g)	Oil content (%)	Seed yield/plant (g)
			1	2	3	4	5	6	7	8	9
1	Block	7	7.19**	5.14**	47.34**	2.10**	18.80**	5.08*	0.18**	18.72**	1.36**
2	Treatments	89	7.73**	11.48**	62.06**	1.51**	46.78**	5.29**	0.94**	43.04**	1.17**
3	Error	7	0.54	0.54	0.46	0.04	0.35	0.75	0.02	0.13	0.05

*,** = Significant at 5% and 1% level significance respectively

Table 2: Genetic variability parameters for morphological and quantitative characters in M₃ Generation of Safflower mutants

Sr. No.	Characters	Range	Mean	$\sigma^2(g)$ Genotypic variance	$\sigma^2(p)$ Phenotypic variance	GCV (%)	PCV (%)	h^2 b.s. (%)	GA	GA as % of mean
1	Days to 50% flowering	78-93	84.81	4.30	4.84	2.45	2.59	88.93	4.04	4.76
2	Days to maturity	129-142	135.07	4.03	4.56	1.49	1.58	88.26	3.89	2.88
3	Plant height	79.54-105.84	93.18	29.98	30.44	5.88	5.92	98.48	11.21	12.03
4	No. of primary branches/plant	7.10-12.90	9.22	1.34	1.39	12.55	12.76	96.80	2.35	25.48
5	No. of effective capitula / plant	21.92-51.03	38.17	41.15	41.50	16.80	16.87	99.16	13.18	34.52
6	No. of seeds/ capitulum	18.51-28.11	23.48	2.14	2.89	6.23	7.24	74.02	2.60	11.06
7	100 - seed weight	3.26-5.46	4.47	0.15	0.17	8.61	9.24	86.83	0.74	16.55
8	Oil content	28.82-34.20	31.81	1.21	1.26	3.46	3.53	96.14	2.22	6.99
9	Seed yield / plant	26.41-52.51	38.85	27.00	27.13	13.37	13.41	99.53	10.69	27.53

GCV = Genotypic coefficient of variation

BS = Broad sense

PCV = Phenotypic coefficient of variation

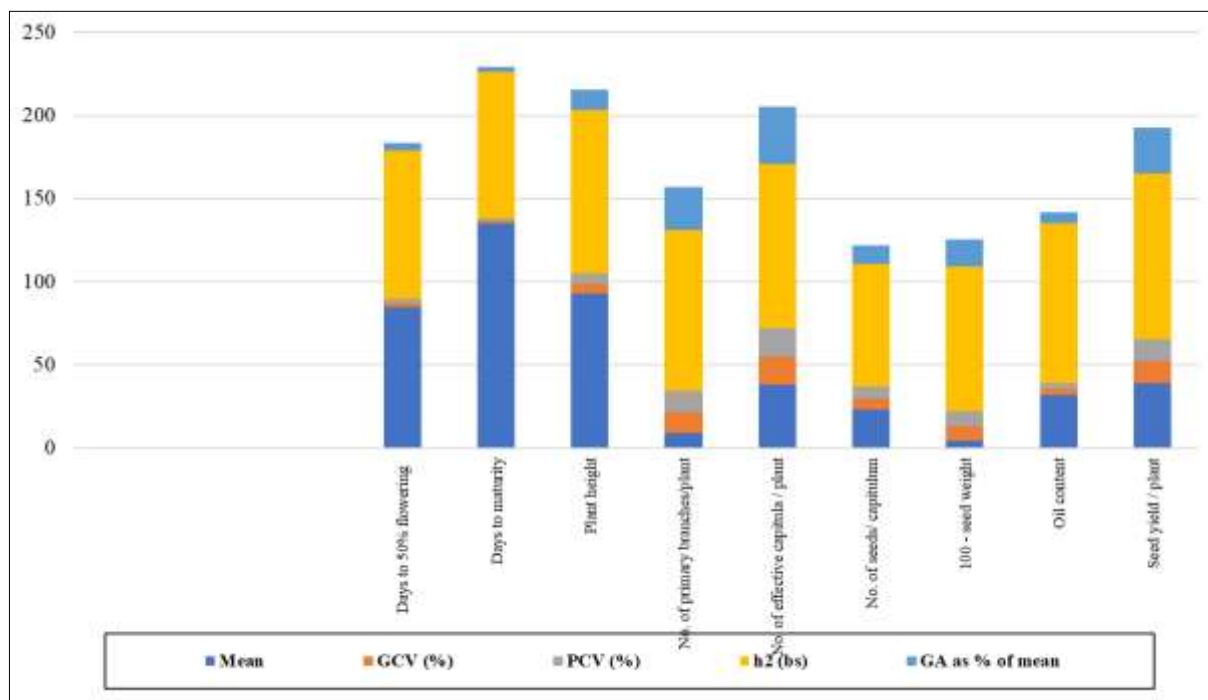


Fig 1: Genetic variability parameters for morphological and quantitative characters in M₃ Generation.

Conclusion

There were notable differences for every character, according to the analysis of variance. There was a good degree of variability in the experiment material, as evidenced by the magnitude of the genotypic and phenotypic coefficient of variation. The majority of the traits like number of effective capitulum per plant, number of primary branches per plants, number of seeds per capsule, and seed yield per plant exhibited high PCV, GCV, heritability, and genetic advance. This suggests that genetic factors primarily influence these traits, and they are highly responsive to environmental conditions. High heritability was consistently observed accompanied by low genetic advance as a percentage of the mean for all the traits. This pattern highlights the significance of non-additive gene action in influencing the inheritance of quantitative traits, indicating that factors other than simple additive genetic effects play a crucial role in determining trait expression.

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