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## Genetic variability, heritability and genetic advance estimates for morphological and quantitative traits in M<sub>4</sub> 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, Vasanttrao Naik Marathwada Krishi Vidyapeeth, Parbhani. (M.S.), during *Rabi*, 2022-23. In M<sub>4</sub> generation, the trial material comprised of forty selected progenies from M<sub>3</sub> and two standard checks, which was assessed using an Augmented Block Design. The analysis of variance, was conducted for the M<sub>4</sub> 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) result indicated statistical significance for each of the examined traits. This implies that there is enough variability present among the genotypes and their respective component traits. Most 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. For such traits, selection would be effective to bring about genetic improvement in desired way.

**Keywords:** Safflower, M<sub>4</sub> generation, variability, heritability, genetic advance, augmented block design

### Introduction

Safflower (*Carthamus tinctorius* L.) is an annual herbaceous thistle like oilseed crop that is highly adaptable to hot and dry climates. In the Indian-subcontinent, it is called as '*Kusum*' in Hindi, arise from Sanskrit word '*Kusumbha*' and '*kardai*' in Marathi (Chavan, 1961) [4]. While in China, it spell as '*honghua*' means red flower. There are total 25 species in genus *Carthamus* among which *Carthamus tinctorius* L. is only under cultivation. It is thought to have evolved from the wild and closely related species *Carthamus oxyacantha* and *Carthamus lanatus* (Gupta and Das, 1997) [29].

Safflower was cultivated in the Middle East for its dried flowers and as a dye plant. Its orange-red-colored petals are a significant source in the production of carthamin dye. But seed is the main reason behind its cultivation, which is utilised to make edible oil over worldwide. The seed oil content ranges between 28 to 36%, which is rich source of linoleic acid and 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). About 90% of all fatty acids are made up of these. Standard safflower oil has 6 to 8 percent palmitic acid, 2 to 3 percent stearic acid, 16 to 20 percent oleic acid, and 71 to 75 percent linoleic acid (Velasco and Fernandez, 2001) [28].

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). The potential states of safflower production in India are Karnataka (54%), Maharashtra (34%), Gujarat and partially in Telangana, Madhya Pradesh, Chhattisgarh, Odisha and Bihar.

In India, Area under safflower cultivation decreased year after year, because the genotypes suffering from problems as long maturity period (140-145 days), low seed yield and low seed oil content.

Therefore, the need to develop early, high seed yield with high oil content variety of safflower to overcome these problems and to increase the area under safflower cultivation. Crop enhancement is dependent on the level of genetic variability and the degree to which the desirable traits are heritable. Genetic variability for economic traits is prior requirement for any successful breeding plan 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 dried and uniform seeds of selected progenies (mutants) of variety "PBNS-12 (Parbhani Kusum)" were procured from All India Co-ordinated Research Project on Safflower, Vasant Rao Naik Marathwada Krishi Vidyapeeth, Parbhani, Maharashtra, India. In M<sub>4</sub> generation, forty selected progenies from M<sub>3</sub> generation along with four standard checks, namely PBNS-12, PBNS-86, ISF-1, and Sharda were assessed in augmented block design during *Rabi* season of 2022-23. The laboratory work for estimation of oil content was performed at ICAR-IOR, Hyderabad.

The harvested seeds of M<sub>3</sub> 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<sub>4</sub> generation. Five randomly chosen plants of sole genotype was utilized to document the observations for nine diverse morphological and quantitative traits *viz.*, days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of effective capitula per plant, number of seeds per capitulum, 100 seed weight (g), seed yield per plant (g) and oil content (%).

The standard approach of Panse and Sukhatme's (1985) [16] was utilized in computing the analysis of variance (ANOVA) to ascertain the significance of differences between the treatments for each trait. The mean values of all the treatments for the various genotype traits were calculated by dividing the total value of the observations by the number of observations. Using the mean square from the variance table (Lush, 1940) [13], the genotypic and phenotypic variance was computed and the genotypic and phenotypic coefficient of variation was assessed using Cockerham's (1963) [6] approach. In a broad sense, heritability is the ratio of genotypic variance to the total amount of observable variance within a population. Heritability (h<sup>2</sup>) in the broadest sense, was determined utilizing the equation provided by (Burton and Devane, 1953) [3]. The genetic progress for every character at 5% selection intensity measured using the Johnson *et al.* (1955) [9] formula.

### Results and Discussion

The presence of genetic diversity in plants for a specific trait is efficient for success of plant breeding initiatives. Analysis of variance (Table 1) unveiled that mean sum of squares due to genotypes was found to be highly significant at 1% and 5% level of significance for each of the nine quantitative characters indicating that existence of adequate amount of variability among genotypes and there is sufficient space for improvement via effective selection.

### Mean Performance of the promising genotypes

The average performance of genotypes for nine metric traits in M<sub>4</sub> generation were represented in Table 2. The traits

showing high degree of variation have greater scope for development via selection. The highest oil per cent observed in the genotype R<sub>1</sub>-T<sub>1</sub>-13-19 (34.18%) followed by R<sub>1</sub>-T<sub>7</sub>-9-10 (34.10%) and R<sub>1</sub>-T<sub>13</sub>-1-4 (33.57%). While, genotypes R<sub>1</sub>-T<sub>8</sub>-11-14 (52.42 g) followed by R<sub>1</sub>-T<sub>11</sub>-7-11 (52.38 g) and R<sub>1</sub>-T<sub>8</sub>-7-10 (51.42 g) exhibited highest seed yield (g) in M<sub>4</sub> generation.

### Genotypic and phenotypic coefficient of variation, Heritability and Genetic advance

For nine quantitative traits in the M<sub>4</sub> generation, the range of variation and the estimates of genetic parameters include GCV, PCV, heritability in broad sense and genetic advance (GA) as% of mean were carried out and results were displayed in Table 3 accordingly. The significant genetic variation in range of morphological traits observed through coefficient of variation (CV). The measure of coefficient of variation is pivotal tool in the comparison of variation in a set of data with distinct units. Moreover, a high CV revealed varied dispersion.

The PCV in M<sub>4</sub> progenies for days to 50% flowering was found to be low with the value of 3.11% and it was recorded a low GCV of 2.99%. This trait also expressed high heritability value of 92.68% and low value (5.94%) 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 findings are in consensus with the reports of Sikarwar *et al.*, (2017) [24] in Yellow Sarson, Rajanna *et al.*, (2020) [19] in Linseed, Dogra *et al.*, (2020) [7] in Linseed, Khattab *et al.*, (2018) [11] and Minnie *et al.*, (2020) [15] in Safflower.

Days to maturity in the M<sub>4</sub> progenies registered a low PCV of 1.91% and a low GCV of 1.84%. This trait also expressed high heritability value of 92.32% and low value of 3.64% of GA as % of mean. In current 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 similar with the reports of Shivani *et al.*, (2011) [22] in Safflower Khattab *et al.*, (2018) [11] in Safflower, Minnie *et al.*, (2020) [15] in Safflower, Thakur *et al.*, (2020) [26] in Linseed, Meena *et al.*, (2020) [14] in Linseed and Belete *et al.*, (2012) [2] in Ethiopian mustard.

In M<sub>4</sub> progenies plant height registered low PCV value of 6.35% and low GCV value of 6.33%. This trait also expressed high heritability value of 99.19% and followed by GA as % of mean of 13.00% (Table 3). These results are in broad agreement with the reports of Rai *et al.*, (2014) [18] in Linseed, Sikarwar *et al.*, (2017) [24] in Yellow Sarson and Belete *et al.*, (2012) [2] in Ethiopian mustard.

For number of primary branches per plant in the M<sub>4</sub> progenies registered a moderate PCV of 16.87% and a moderate GCV of 16.77%. This trait also expressed high heritability value of 98.87% followed by high GA as % of mean of 34.41%. These findings are consistent with the reports of Thakur *et al.*, (2020) [26] in Linseed, Sikarwar *et al.*, (2017) [24] in Yellow Sarson, Chavan and Chopade (1981) [5] in Sesame and Leelavati and Mogali (2018) [12] in Linseed.

The PCV in M<sub>4</sub> progenies for number of capsules per plant was found to be moderate with the value of 19.03% and it was recorded a moderate GCV of 19.02%. This trait also expressed high heritability value of 99.97% and high value

of 39.24% of GA as % of mean. These outcomes are in accordance with the reports of Kalaiyarasi *et al.*, (2019) <sup>[10]</sup> in Sesame, Leelavati and Mogali (2018) <sup>[12]</sup> in Linseed, Rajanna *et al.*, (2020) <sup>[19]</sup> in Linseed, Meena *et al.*, (2020) <sup>[14]</sup> in Linseed, Umamaheswari *et al.*, (2019) <sup>[27]</sup> in Sesame, and Khattab *et al.*, (2018) <sup>[11]</sup> in Safflower

The M<sub>4</sub> progenies registered a low PCV of 7.12% and a low GCV of 6.79% for number of seeds per capsule. This trait also expressed high heritability value of 90.95% followed by moderate GA as % of mean of 13.36%. These results are in accordance with the reports of Rathod *et al.*, (2021) <sup>[20]</sup> in Safflower, Minnie *et al.*, (2020) <sup>[15]</sup> in Safflower, Kalaiyarasi *et al.*, (2019) <sup>[10]</sup> in Sesame, Leelavati and Mogali (2018) <sup>[12]</sup> in Linseed and Rajanna *et al.*, (2020) <sup>[7]</sup> in Linseed.

The 100 seed weight in the M<sub>4</sub> progenies registered a low PCV of 8.88% and a low GCV of 8.39%. This trait also expressed high heritability value of 89.35% followed by moderate GA as % of mean of 16.36%. These results are in accordance with the reports of Phanindra *et al.*, (2018) <sup>[17]</sup> in Sunflower, Pushpavalli and Kumar (2017) <sup>[30]</sup> in Safflower, Khattab *et al.*, (2018) <sup>[11]</sup> in Safflower, Minnie *et al.*, (2020) <sup>[15]</sup> in Safflower, Leelavati and Mogali (2018) <sup>[12]</sup> in Linseed and Rajanna *et al.* (2020) <sup>[19]</sup> in Linseed.

The M<sub>4</sub> progenies registered a low PCV of 3.91% and a low GCV of 3.90% for days to first flowering. This trait also expressed high heritability value of 99.58% followed by low GA as% of mean of 8.04%. These results are in broad agreement with the reports of Phanindra *et al.*, (2018) <sup>[17]</sup> in Sunflower, Meena *et al.*, (2020) <sup>[14]</sup> in Linseed and Rathod

*et al.*, (2021) <sup>[7]</sup> 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) <sup>[8]</sup> in Sunflower, Siddiqui *et al.*, (2009) <sup>[23]</sup> in Rapeseed and Singh *et al.*, (2020) <sup>[25]</sup> in Sesame.

The PCV in M<sub>4</sub> progenies for seed yield per plant was found to be moderate with the value of 17.08% and it was recorded a moderate GCV of 17.06%. This trait also expressed high heritability value of 99.80% and high value of 35.16% 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) <sup>[19]</sup> in Linseed, Leelavati and Mogali (2018) <sup>[12]</sup> in Linseed, Khattab *et al.*, (2018) <sup>[11]</sup>, Minnie *et al.*, (2020) <sup>[15]</sup> in Safflower and Sanghani *et al.*, (2016) <sup>[21]</sup> in Sesame.

In the present investigation of M<sub>4</sub> generation, a high heritability coupled with high GA as per cent of mean and 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. While for days to 50% flowering, days to maturity and oil content exhibited low PCV and GCV for all the mutants. This clearly denoted the pre-dominance of additive gene effect for these traits which may be favorably exploited for further improvement of these characters by selection.

**Table 1:** Analysis of variance for nine morphological and quantitative characters in M<sub>4</sub> 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	1	15.19*	24.08**	82.16**	12.00**	269.80**	5.47*	1.61**	6.29**	61.65**
2	Genotypes	43	9.76*	11.96*	90.11**	2.72**	91.34**	18.37**	0.60**	1.35**	62.95**
3	Error	3	0.5	0.5	0.3	0.03	0.02	0.29	0.02	0.01	0.09

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

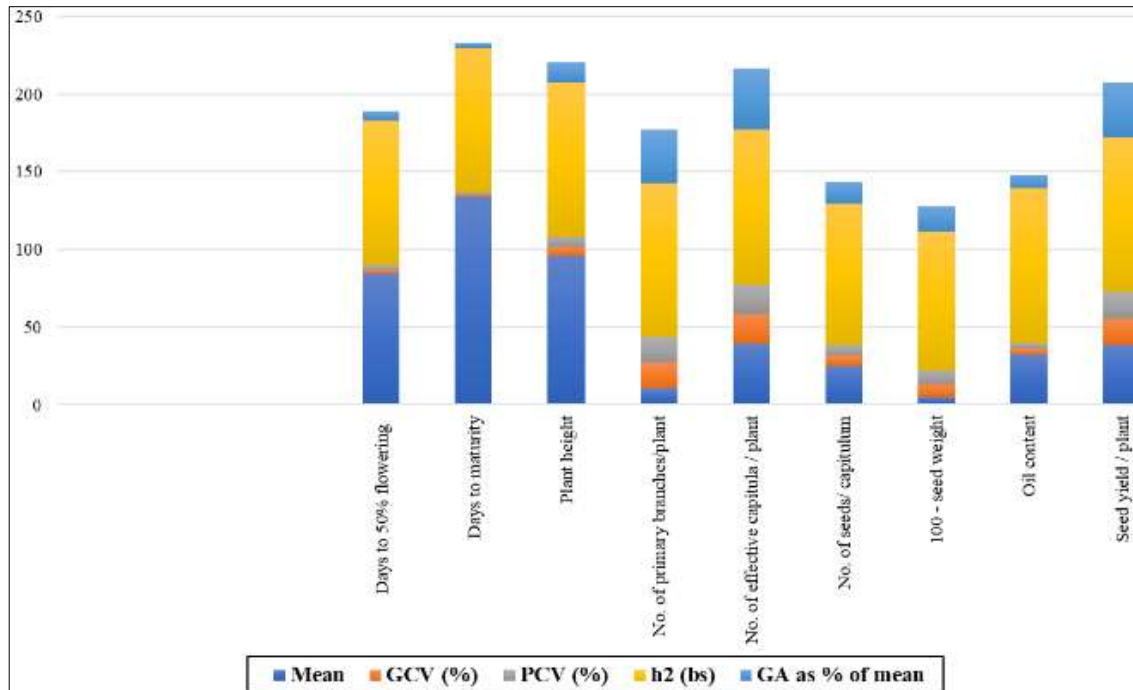
**Table 2:** Mean, range and character wise promising genotypes for various traits in M<sub>4</sub> generation

Sr. No.	Characters	Range	Mean	Promising genotypes
1	Days to 50% flowering	76-91	84.07	R <sub>3</sub> -T <sub>2</sub> -4-10, R <sub>2</sub> -T <sub>2</sub> -14-20
2	Days to maturity	126-140	133.59	R <sub>2</sub> -T <sub>2</sub> -14-20, PBNS-86, ISF-1, R <sub>3</sub> -T <sub>2</sub> -4-10
3	Plant height (cm)	86.63-106.58	95.42	ISF-1, R <sub>2</sub> -T <sub>3</sub> -11-15, R <sub>2</sub> -T <sub>11</sub> -8-13, R <sub>1</sub> -T <sub>13</sub> -1-3
4	Number of primary branches /plants	7.45-13.45	10.18	R <sub>3</sub> -T <sub>4</sub> -5-15, R <sub>2</sub> -T <sub>3</sub> -2-2, R <sub>1</sub> -T <sub>8</sub> -11-14
5	No. of effective capitula /plant	23.78-52.03	39.43	R <sub>1</sub> -T <sub>3</sub> -11-14, R <sub>1</sub> -T <sub>11</sub> -7-11, R <sub>2</sub> -T <sub>3</sub> -2-2
6	No. of seeds per capitulum	20.27-28.87	24.93	R <sub>1</sub> -T <sub>11</sub> -4-5, R <sub>1</sub> -T <sub>1</sub> -4-12, R <sub>1</sub> -T <sub>4</sub> -12-14
7	100 seed weight (g)	3.65-5.35	4.88	R <sub>2</sub> -T <sub>8</sub> -2-4, R <sub>1</sub> -T <sub>1</sub> -4-12, R <sub>1</sub> -T <sub>9</sub> -10-13
8	Oil content (%)	29.15-34.18	32.04	R <sub>1</sub> -T <sub>1</sub> -13-19, R <sub>1</sub> -T <sub>7</sub> -9-10, R <sub>1</sub> -T <sub>13</sub> -1-4
9	Seed yield /plant (g)	27.03-52.42	38.35	R <sub>1</sub> -T <sub>8</sub> -11-14, R <sub>1</sub> -T <sub>11</sub> -7-11, R <sub>1</sub> -T <sub>8</sub> -7-10

**Table 3:** Genetic variability parameters for nine morphological and quantitative characters in M<sub>4</sub> Generation of Safflower mutants

Sr. No.	Characters	Range	Mean	$\sigma^2(g)$ Genotypic variance	$\sigma^2(p)$ Phenotypic variance	GCV (%)	PCV (%)	h <sup>2</sup> b.s. (%)	GA	GA as % of mean
1	Days to 50% flowering	76-91	84.07	6.33	6.83	2.99	3.11	92.68	5.00	5.94
2	Days to maturity	126-140	133.59	6.01	6.51	1.84	1.91	92.32	4.86	3.64
3	Plant height	86.63-106.58	95.42	36.47	36.76	6.33	6.35	99.19	12.41	13.00
4	No. of primary branches/plant	7.45-13.45	10.18	2.92	2.95	16.77	16.87	98.87	3.50	34.41
5	No. of effective capitula/plant	23.78-52.03	39.43	56.27	56.29	19.02	19.03	99.97	15.47	39.24
6	No. of seeds/ capitulum	20.27-28.87	24.93	2.86	3.15	6.79	7.12	90.95	3.33	13.36
7	100 - seed weight	3.65-5.35	4.88	0.17	0.19	8.39	8.88	89.35	0.80	16.36
8	Oil content	29.15-34.18	32.04	1.56	1.57	3.90	3.91	99.58	2.57	8.04
9	Seed yield / plant	27.03-52.42	38.35	42.80	42.89	17.06	17.08	99.80	13.48	35.16

GCV = Genotypic coefficient of variation BS = Broad sense PCV = Phenotypic coefficient of variation



**Fig 1:** Genetic variability parameters for nine morphological and quantitative characters in M<sub>4</sub> Generation

### Conclusion

According to the analysis of variance, observable differences were found for each attributes under studied. There was ample 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 implies that genetic factors especially 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 pivotal role in determining trait expression.

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