

International Journal of Advanced Biochemistry Research



ISSN Print: 2617-4693
ISSN Online: 2617-4707
NAAS Rating (2026): 5.29
IJABR 2026; SP-10(9): 437-440
www.biochemjournal.com
Received: 08-06-2026
Accepted: 12-07-2026

Yogeesh BM
Department of Agricultural
Botany (Genetics and Plant
Breeding), Dr. PDKV,
Akola, Maharashtra, India

Ratnaparkhi RD
Associate Professor,
Department of Agricultural
Botany, Dr. PDKV,
Akola, Maharashtra, India

Gahukar SJ
Senior Scientist, Oil Seeds
Research Unit, Dr. PDKV,
Akola, Maharashtra, India

Burghate SK
Assistant Professor,
Department of Agricultural
Botany, Dr. PDKV,
Akola, Maharashtra, India

Mane PN
Assistant Professor,
Department of Entomology,
Dr. PDKV, Akola,
Maharashtra, India

Chidananda T
PG Scholar, Department of
Agricultural Botany (Genetics
and Plant Breeding), Dr.
PDKV, Akola, Maharashtra,
India

Rakesh KR
PG Scholar, Department of
Agricultural Botany (Genetics
and Plant Breeding), College of
Agriculture Dapoli,
Maharashtra, India

Corresponding Author:
Yogeesh BM
Department of Agricultural
Botany (Genetics and Plant
Breeding), Dr. PDKV,
Akola, Maharashtra, India

Assessment of genetic variability, heritability and genetic advance for yield and its components in safflower (*Carthamus tinctorius* L.)

Yogeesh BM, Ratnaparkhi RD, Gahukar SJ, Burghate SK, Mane PN, Chidananda T and Rakesh KR

DOI: <https://www.doi.org/10.33545/26174693.2026.v10.i9Sf.9864>

Abstract

The present study was undertaken to assess the extent of genetic variability and the potential for selection among 38 safflower genotypes for yield and related characters. The genotypes were evaluated in a randomized block design with three replications at OILSEEDS RESEARCH UNIT, Dr. PDKV, AKOLA during RABI 2025 Observations were recorded for days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of capitula per plant, number of seeds per capitulum, diameter of capsule, hundred seed weight, seed yield per plant and oil content. Phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the traits, indicating varying environmental influence on trait expression. Seed yield per plant showed the highest GCV (29.35%) and PCV (31.17%), followed by number of capitula per plant (15.70 and 18.54%) and number of branches per plant (13.39 and 16.81%). Broad-sense heritability ranged from 26.30 to 88.65 percent, with the highest value recorded for seed yield per plant. High heritability was also observed for number of branches per plant, number of capitula per plant, number of seeds per capitulum, diameter of capsule and hundred seed weight. Genetic advance as percent of mean was highest for seed yield per plant (56.92%), followed by number of capitula per plant (27.40%), hundred seed weight (23.65%), diameter of capsule (23.46%) and number of branches per plant (21.99%). The combination of high heritability and high genetic advance as percent of mean for these traits suggests considerable scope for selection. Seed yield per plant, in particular, showed a favourable combination of all the major variability parameters and may therefore receive priority in safflower improvement programmes.

Keywords: Safflower, genetic variability, GCV, PCV, heritability, genetic advance, genetic advance as percent of mean, seed yield

Introduction

Safflower (*Carthamus tinctorius* L.) is an important oilseed crop cultivated for its edible oil and other useful products. Improvement in safflower productivity depends largely on the availability of suitable genetic variation in breeding material. Quantitative characters such as flowering, maturity, plant architecture, yield components and seed yield are influenced by both genetic constitution and environmental conditions. Therefore, estimating the different components of variability is an important step before undertaking effective selection.

Genotypic and phenotypic coefficients of variation provide a measure of the extent of variability present in a population. The genotypic coefficient of variation reflects the genetic component of observed variation, whereas the phenotypic coefficient of variation includes both genetic and environmental effects. Comparing these estimates helps in understanding the extent to which environmental conditions influence the expression of individual characters.

Heritability provides an estimate of the proportion of phenotypic variation attributable to genetic differences among the genotypes. However, heritability alone does not indicate the expected improvement from selection. Genetic advance and genetic advance as percent of mean provide complementary information about the likely response to selection. A combination of high heritability and high genetic advance as percent of mean is particularly useful for identifying characters in which selection may produce substantial improvement.

In the present investigation, 38 safflower genotypes were evaluated to estimate genotypic and phenotypic variability parameters for yield and yield-attributing traits. The study also considered heritability, genetic advance and genetic advance as percent of mean to obtain a broader understanding of the selection potential of the characters.

Materials and Methods

Experimental material and design

The experimental material consisted of 38 safflower genotypes, including NARI 36 as the check. The trial was conducted at OILSEEDS RESEARCH UNIT, Dr. PDKV, AKOLA during RABI 2025. The genotypes were evaluated in a randomized block design with three replications.

Characters recorded

Data were recorded for 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, diameter of capsule (cm), hundred seed weight (g), seed yield per plant (g) and oil content (%).

Estimation of variability parameters

Genotypic variance was estimated from the analysis of variance as $\sigma^2_g = (MSG - MSE)/r$, where MSG is the mean square due to genotypes, MSE is the error mean square and r is the number of replications. Phenotypic variance was obtained as $\sigma^2_p = \sigma^2_g + \sigma^2_e$, where σ^2_e represents environmental variance.

Genotypic coefficient of variation was calculated as $GCV = (\sqrt{\sigma^2_g}/\bar{X}) \times 100$, while phenotypic coefficient of variation was calculated as $PCV = (\sqrt{\sigma^2_p}/\bar{X}) \times 100$. Environmental coefficient of variation was estimated as $ECV = (\sqrt{\sigma^2_e}/\bar{X}) \times 100$.

Broad-sense heritability was estimated following Hanson *et al.* (1956) as $h^2 = (\sigma^2_g/\sigma^2_p) \times 100$. Heritability values were classified as low (0-30%), moderate (30-60%) and high (>60%) following Robinson *et al.* (1951) [8].

Genetic advance was estimated following Johnson *et al.* (1955) [3] using $GA = i h^2 \sigma_p$, where i is the selection differential (2.06 at 5% selection intensity), h^2 is broad-sense heritability and σ_p is the phenotypic standard deviation. Genetic advance as percent of mean was calculated as $GAM = (GA/\bar{X}) \times 100$. GAM values were classified as low (0-10%), moderate (10-20%) and high (>20%) following Johnson *et al.* (1955) [3].

Results and Discussion

Mean performance and variability

The 38 safflower genotypes differed considerably for the characters evaluated. The overall means were 82.05 days for days to 50% flowering, 122.55 days for days to maturity, 87.21 cm for plant height, 17.67 primary branches per plant, 41.16 capitula per plant, 25.64 seeds per capitulum, 2.92 cm for diameter of capsule, 4.91 g for hundred seed weight, 23.65 g for seed yield per plant and 32.29 percent for oil content. The differences among genotypes indicate the presence of exploitable variation for breeding purposes.

Table 2: Statistical summary and descriptive statistics for evaluated traits

Trait	Mean	Min	Max
Days to 50% flowering	82.05	71.99	94.81
Days to maturity	122.55	112.72	135.18
Plant height (cm)	87.21	73.13	98.00
Number of primary branches per plant	17.67	12.25	23.25
Number of capitula per plant	41.16	26.95	58.95
Number of seeds per capitulum	25.64	19.83	35.03
Diameter of capsule (cm)	2.92	2.14	3.64
Hundred seed weight (g)	4.91	3.29	5.95
Oil content (%)	32.29	29.21	35.40
Seed yield per plant (g)	23.65	10.74	44.50

Genotypic and phenotypic coefficients of variation

Phenotypic coefficient of variation (PCV) exceeded genotypic coefficient of variation (GCV) for every character studied, indicating that environmental factors contributed to the phenotypic expression of the traits, although the magnitude of environmental influence varied among characters. A higher PCV than GCV for quantitative traits is commonly reported in safflower and indicates the contribution of environmental variation to the total phenotypic variability (Manikya Minnie *et al.*, 2018; Sudha Rani *et al.*, 2020) [4, 5]. The largest GCV was recorded for seed yield per plant (29.35%), followed by number of capitula per plant (15.70%), number of branches per plant (13.39%), hundred seed weight (13.18%) and diameter of capsule (12.92%). The corresponding PCV values were 31.17, 18.54, 16.81, 15.12 and 14.67 percent, respectively. The relatively high GCV and PCV observed for these traits indicate the presence of considerable variability and suggest greater scope for their improvement through selection. Similar high variability for seed yield, number of capitula per plant and seed weight has been reported in safflower

germplasm (Manikya Minnie *et al.*, 2018; Neelima *et al.*, 2021) [4, 6].

In contrast, oil content recorded the lowest GCV (3.16%) and PCV (6.17%), followed by days to maturity with GCV and PCV values of 3.74 and 7.30 percent, respectively, indicating comparatively limited genetic variability for these characters in the material studied. The relatively small difference between GCV and PCV for seed yield per plant suggests that environmental influence on its expression was comparatively lower than for traits showing a wider difference between the two estimates. Consequently, a substantial proportion of the observed variation in seed yield per plant appears to be attributable to genetic differences among the genotypes. Similar observations of comparatively high GCV and PCV for seed yield and yield components have been reported in safflower.

Heritability, genetic advance and genetic advance as percent of mean

Broad-sense heritability varied from 26.30 to 88.65 percent. Seed yield per plant recorded the highest heritability

(88.65%), followed by diameter of capsule (77.67%), hundred seed weight (75.91%), number of capitula per plant (71.76%), number of primary branches per plant (63.51%) and number of seeds per capitulum (62.76%). Days to 50% flowering showed moderate heritability (47.09%), whereas days to maturity, plant height and oil content had relatively low estimates. Variation in heritability among safflower traits has also been reported in earlier studies, with high heritability observed for several yield and yield-attributing traits.

Genetic advance ranged from 0.69 for diameter of capsule to 13.46 for seed yield per plant. When expressed as a percentage of the mean, the highest genetic advance as percent of mean (GAM) was obtained for seed yield per plant (56.92%). High GAM was also recorded for number of capitula per plant (27.40%), hundred seed weight (23.65%), diameter of capsule (23.46%) and number of primary branches per plant (21.99%). Number of seeds per capitulum had moderate GAM (18.54%), whereas days to 50% flowering, days to maturity, plant height and oil content recorded low GAM values. Similar combinations of high heritability and high genetic advance as percent of mean have been reported for seed yield and several yield components in safflower, suggesting considerable scope for selection of superior genotypes.

The simultaneous occurrence of high heritability and high GAM for seed yield per plant, number of capitula per plant, diameter of capsule, hundred seed weight and number of primary branches per plant indicates substantial genetic variability and greater expected response to selection for these traits. High heritability coupled with high genetic advance is generally considered an indication of the predominance of heritable genetic effects, particularly additive genetic variance, and therefore provides a stronger basis for selection than either heritability or genetic advance considered independently. Among the characters studied, seed yield per plant was particularly promising because it exhibited the highest GCV and PCV together with the

highest heritability and GAM. This combination indicates considerable genetic variability, high transmissibility of the observed variation and substantial expected genetic progress through selection. Similar findings have been reported in safflower, where high heritability coupled with high genetic advance was observed for seed yield and important yield-contributing traits.

Table 3: Genetic variability parameters for yield and yield-related traits in safflower

Character	Mean	GCV (%)	PCV (%)	ECV (%)
Days to 50% flowering	82.05	6.72	9.79	7.12
Days to maturity	122.55	3.74	7.30	6.26
Plant height (cm)	87.21	4.92	9.60	8.24
Number primary of branches/plant	17.67	13.39	16.81	10.15
Number of capitula/plant	41.16	15.70	18.54	9.85
Number of seeds/capitulum	25.64	11.36	14.34	8.75
Diameter of capsule (cm)	2.92	12.92	14.67	6.93
Hundred seed weight (g)	4.91	13.18	15.12	7.42
Oil content (%)	32.29	3.16	6.17	5.29
Seed yield/plant (g)	23.65	29.35	31.17	10.50

Table 4: Heritability, genetic advance and genetic advance as percent of mean

Character	Heritability (%)	GA	GAM (%)
Days to 50% flowering	47.09	7.79	9.49
Days to maturity	26.30	4.84	3.95
Plant height (cm)	26.31	4.54	5.20
Number primary of branches/plant	63.51	3.88	21.99
Number of capitula/plant	71.76	11.28	27.40
Number of seeds/capitulum	62.76	4.75	18.54
Diameter of capsule (cm)	77.67	0.69	23.46
Hundred seed weight (g)	75.91	1.16	23.65
Oil content (%)	26.30	1.08	3.34
Seed yield/plant (g)	88.65	13.46	56.92

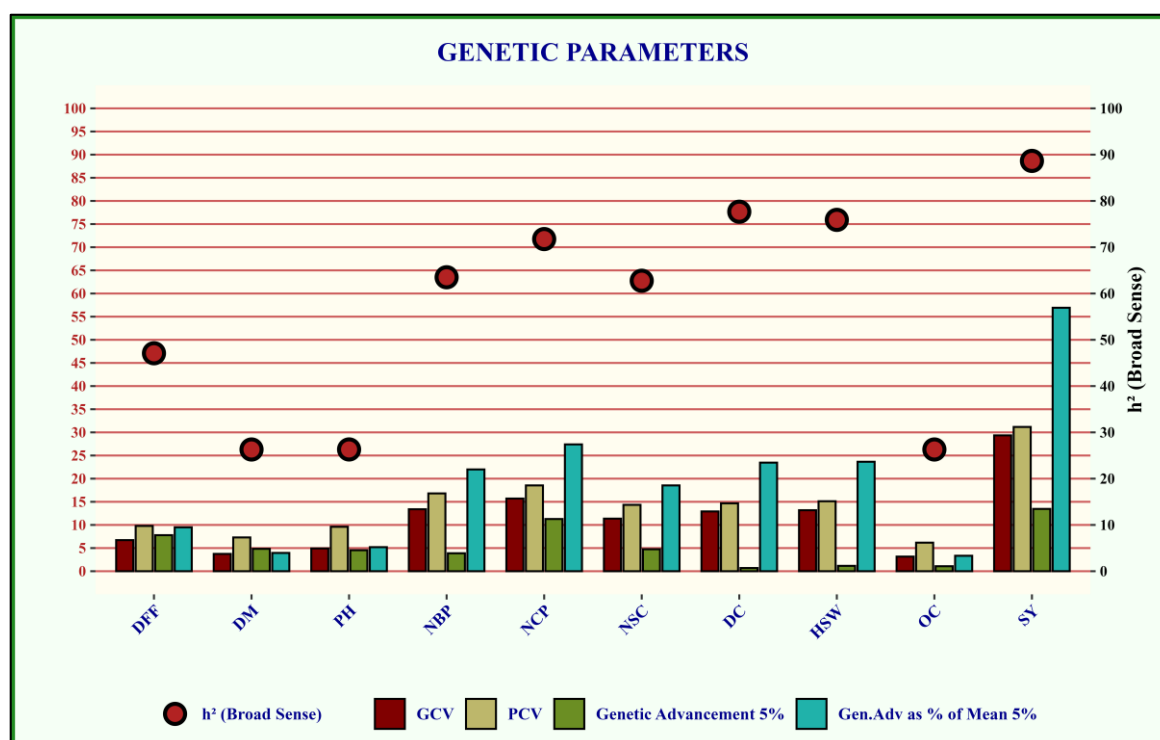


Fig 1: Comprehensive Dual-Axis Genetic Parameters Chart

Conclusion

The evaluation of 38 safflower genotypes demonstrated appreciable genetic variation for yield and associated characters. Phenotypic coefficients of variation were consistently higher than the corresponding genotypic coefficients, confirming some contribution of environmental effects to trait expression. Seed yield per plant showed the most favourable variability profile, with high GCV (29.35%), PCV (31.17%), broad-sense heritability (88.65%) and GAM (56.92%). Number of capitula per plant, hundred seed weight, diameter of capsule and number of primary branches per plant also showed high heritability together with high GAM. These traits therefore appear promising for selection and can be given emphasis in breeding programmes aimed at improving safflower productivity.

References

1. Burton GW. Quantitative inheritance in grasses. Proceedings of the Sixth International Grassland Congress. 1952;1:277-283.
2. Hanson CH, Robinson HF, Comstock RE. Biometrical studies of yield in segregating populations of Korean lespedeza. Agronomy Journal. 1956;48:268-272.
3. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans. Agronomy Journal. 1955;47:314-318.
4. Manikya Minnie C, Sandeep S, Sujatha K. Genetic variability, heritability and genetic advance studies in safflower (*Carthamus tinctorius* L.). International Journal of Current Microbiology and Applied Sciences. 2018;7(12):3714-3718.
5. Manikya Minnie C, Pushpavalli SNCVL, Sujatha K, Sandeep S, Sudhakar C, Rajeshwar Reddy T, *et al.* Genetic analysis for yield and its attributes in safflower (*Carthamus tinctorius* L.). Journal of Oilseeds Research. 2020;37(4):[page numbers not provided].
6. Neelima S, Prabhakar K, Ramanamma KV. Genetic variability, heritability, association and divergence studies in safflower (*Carthamus tinctorius* L.) genotypes. Journal of Oilseeds Research. 2021;38(3):265-269.
7. Rathod PS, Ghuge SB, Wankhade MP. Genetic variability, heritability and genetic advance studies in safflower (*Carthamus tinctorius* L.). The Pharma Innovation Journal. 2021;10(6):765-767.
8. Robinson HF, Comstock RE, Harvey PH. Genotypic and phenotypic correlations in corn and their implications in selection. Agronomy Journal. 1951;43:282-287.