

Original Research Article

<https://doi.org/10.20546/ijcmas.2018.712.423>**Genetic Variability, Heritability and Genetic Advance Studies
in Safflower (*Carthamus tinctorius* L.)****C. Manikya Minnie, S. Sandeep* and K. Sujatha***Agricultural Research Station, Tandur, Professor Jayashankar Telangana State Agriculture University, Rajendranagar, Hyderabad (Telangana) – 501141, India***Corresponding author***A B S T R A C T****Keywords**

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The study was carried out at Agricultural Research Station, Tandur (PJTSAU) during *Rabi*, 2017-18 to determine genetic variability, heritability and genetic advance estimates in thirty genotypes of safflower. Analysis of variance involving a set of thirty genotypes of safflower for seven quantitative characters viz., days to 50% flowering, days to maturity, plant height, number of effective capitula/plant, number of seeds/capitulum, test weight (g) and seed yield (kg/ha) revealed highly significant mean sum of squares for all the characters indicating greater diversity among the genotypes. The genotypic coefficients of variation (GCV) for all the characters studied were lesser than the phenotypic coefficients of variation (PCV) indicating the effect of the environment. High GCV and PCV values were observed for seed yield, number of seeds per capitulum, number of effective capitula per plant and test weight. All the characters showed high estimates of heritability except plant height. High heritability coupled with high genetic advance as per cent of mean was observed for seed yield, number of seeds per capitulum, number of effective capitula per plant and test weight indicating the role of additive genes in governing the inheritance of these traits which could be improved through simple selection.

Introduction

Safflower (*Carthamus tinctorius* L.) is most commonly known as ‘kusum’ (India, Pakistan), derived from the Sanskrit, ‘kusumbha’ (Chavan, 1961), and as ‘honghua’ (red flower) in China. Its use as a less costly substitute for saffron is indicated by the names false saffron, bastard saffron, thistle saffron and dyer’s saffron (Weiss, 1983). It is one of the oldest domesticated oilseed crops grown

mostly in the Middle East regions which is said to be its centre of origin and diversity. It belongs to family Asteraceae or Compositae, genus- *Carthamus*, tribe- *Tubiflorae*, sub division - Angiosperm of division Phanerogams and is the only cultivated type of Safflower that contains $2n=24$ chromosomes. It has been traditionally grown in different countries such as India, Mexico, China, Australia, Turkey and Iran (Singh, 2007). In India, it is cultivated in an area of 127.52

thousand hectares with production of 53,000 tonnes and the productivity of 416kg/ha. Highest acreage is noticed in Maharashtra (57000 ha) followed by Karnataka (54000 ha), Madhya Pradesh (10000ha) and Telangana (4000ha) (Indiastat, 2016-17). The crop is mainly cultivated for its seed, which is used primarily for edible oil. Traditionally, it is grown for its flowers used for coloring and flavoring foods, extracting dyes and in medicines. However due to an increase in demand for vegetable oil in human diet, its production as an oilseed crop has received a great deal of importance.

It is highly demanded due to its high linoleic and oleic acid proportions when compared to other vegetable oils. Dried petals of safflower have therapeutic value and are being extensively used in preparation of herbal medicines. Genetic variability is of greatest interest to the plant breeder as it plays a vital role in framing successful breeding programme. Heritability of a metric character is a parameter of particular significant to the breeder as it measures the degree of resemblance between the parents and the off-springs and its magnitude indicates the heritability with which a genotype can be identified by its phenotypic expression, while genetic advance aids in exercising the necessary selection pressure. Study of variability, heritability and genetic advance in the germplasm will help to ascertain the real potential value of the genotypes. Since the material used in the present study has got novelty for various characters a study has been conducted to assess the variability present in the germplasm.

Materials and Methods

Thirty safflower genotypes were evaluated in Randomized Block Design during *Rabi*, 2017-18 at Agricultural Research Station, Tandur. The entries were sown in 5m long three row

plots with a spacing of 45cm between the rows and 20cm between the plants. Recommended agronomic practices were followed to raise a good crop. Data was recorded for seven characters viz., days to 50% flowering, days to maturity, plant height, number of effective capitula/plant, number of seeds/capitulum, test weight (g) and seed yield (kg/ha) in each genotype across all the three replications.

Analysis of variance was computed based on Randomized Block Design for each of the character separately as per standard statistical procedure given by (Panse and Sukhatme, 1978). Heritability (h^2) in the broad sense was calculated according to the formula given by (Allard, 1960) for all characters. Phenotypic and genotypic coefficients of variation (PCV and GCV) were computed according to (Burton, 1952). For statistical analysis, Windostat Version 9.1 software package was used.

Results and Discussion

Analysis of variance for the experiment involving a set of 30 genotypes of safflower for seven quantitative characters revealed highly significant mean sum of squares for all the characters indicating greater diversity among the genotypes. The results of Analysis of Variance were presented in Table 1. The results pertaining to genetic parameters viz., phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad sense heritability (h^2_{bs}) and genetic advance as percent of mean (GAM) for all the seven characters are furnished in Table 2 and Figure 1. The Highest magnitude of both PCV and GCV were observed for seed yield (39.82%, 38.22%) followed by Number of seeds per capitulum (31.54%, 28.51%), Number of effective capitula per plant (27.54%, 23.48%) and Test weight (22.52%, 21.02%) suggesting that these characters were under the influence of genetic control.

Similar reports were earlier given by (Thombre and Joshi, 1977; Ramesh *et al.*, 1980; Patil *et al.*, 1991; Pandya and Patil, 1994; Pandya *et al.*, 1996 and Patil and Deshmukh, 1998). The characters plant height (13.72, 9.08%) recorded moderate magnitude PCV and low GCV, respectively. The traits days to maturity (6.79%, 6.46%) and days to 50% flowering (4.75%, 4.76) showed lower magnitudes of both PCV and GCV, respectively. Heritability estimates were high for all the traits under study except for plant height which recorded moderate estimate of

heritability. This suggested the greater effectiveness of selection and improvement to be expected for these characters in future breeding programme as the genetic variance is mostly due to the additive gene action. The results are in consonance with the reports given by (Mathur *et al.*, 1976; Thombre and Joshi, 1977; Pandya and Patil, 1994 and Yadav *et al.*, 1987.). Higher genetic advance was recorded for seed yield (75.59%) followed by Number of seeds per capitulum (53.11%), Number of effective capitula per plant (40.64%) and Test weight (40.41%).

Table.1 Analysis of variance for seven characters in safflower (*Carthamus tinctorius* L.)

S.No.	Character	Mean Sum Of Squares		
		Replications (D.F. = 2)	Treatments (D.F. = 29)	Error (D.F. = 58)
1.	Days To 50% Flowering	2.21	100.57**	3.45
2.	Days To Maturity	4.01	102.26**	4.50
3.	Plant Height (cm)	17.30	235.79**	70.55
4.	Number of Effective Capitula /Plant	1.23	88.16**	10.74
5.	Number of Seeds/Capitulum	8.33	150.42**	10.41
6.	Test Weight (g)	0.13	4.59**	0.21
7.	Seed Yield (kg/ha)	92894.47	1630359.5**	45073.35

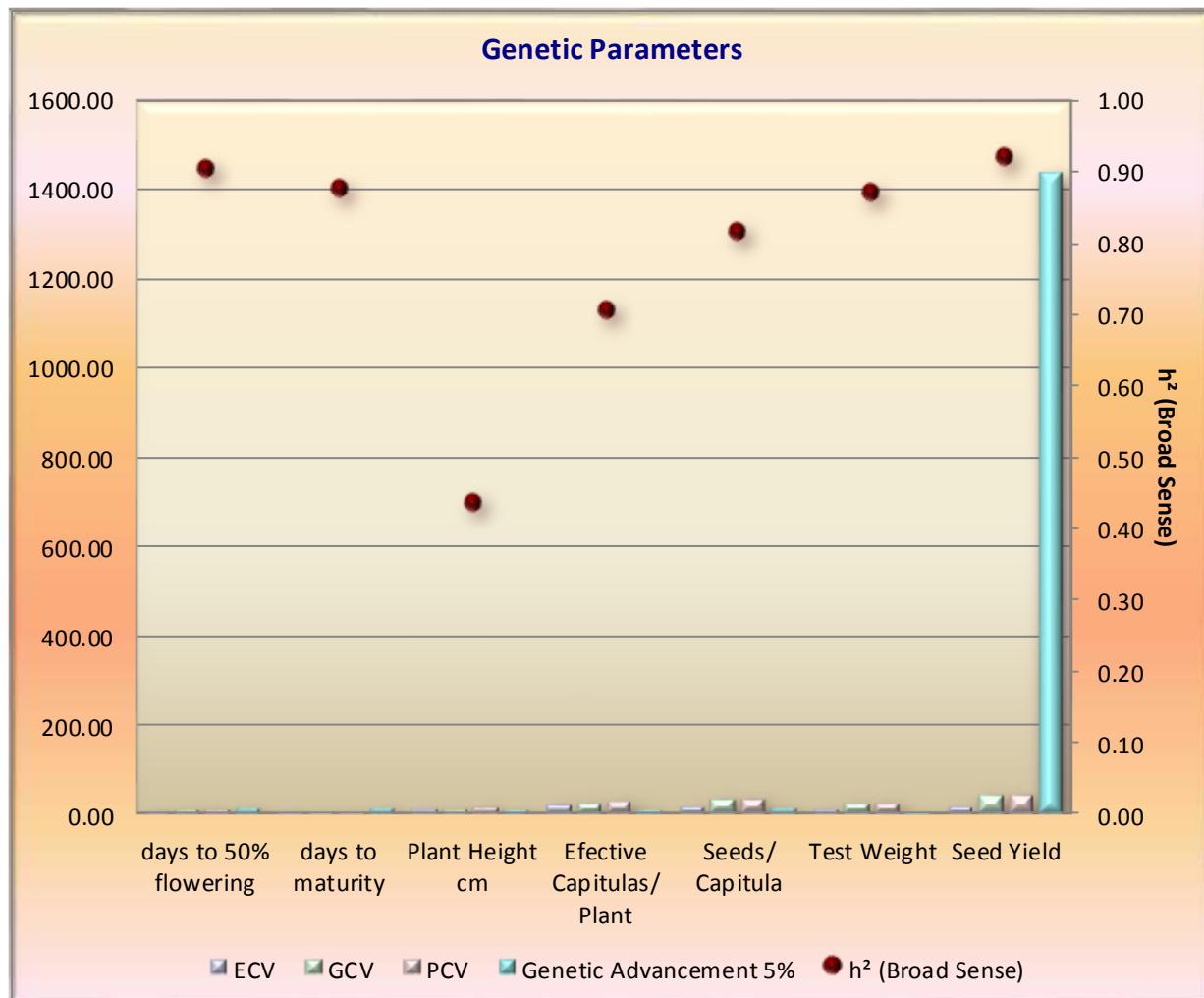
*Significant at 5 per cent level and ** Significant at 1 per cent level

Table.2 Estimation of genetic parameters for seven characters in safflower (*Carthamus tinctorius* L.)

S.No.	Characters	PCV (%)	GCV (%)	Heritability (h^2_{bs}) (%)	GAM	Genetic advancement (5%)
1.	Days To 50% Flowering	6.79	6.46	90.00	11.14	12.65
2.	Days To Maturity	4.75	4.46	88.00	11.02	8.60
3.	Plant Height (cm)	13.72	9.08	44.00	10.12	12.39
4.	Number of Effective Capitula /Plant	27.94	23.48	71.00	8.79	40.64
5.	Number of Seeds/Capitulum	31.54	28.51	82.00	12.72	53.11
6	Test Weight (g)	22.52	21.02	87.00	2.32	40.41
7.	Seed Yield (kg/ha)	39.82	38.22	92.00	1437.43	75.59

PCV= Phenotypic coefficient of variation, GCV= Genotypic coefficient of variation, ECV= Environmental coefficient of variation and GAM= Genetic Advance as percent of mean at 5% level.

Fig.1 Graph showing distribution of genetic parameters for yield and yield related traits



Similar results for high genetic advance of these traits were earlier reported by (Mathur *et al.*, 1976; Chanesappa *et al.*, 1980; Yadav *et al.*, 1987; Singh *et al.*, 1993 and Patil and Deshmukh, 1998.). High heritability coupled with high genetic advance was observed for seed yield, number of seeds per capitulum, number of effective capitula per plant and test weight. Similar results for high heritability coupled with high genetic advance for these traits were earlier reported by (Thombore and Joshi, 1977; Patil *et al.*, 1987 and Ghongade *et al.*, 1993). It indicates the role of additive gene action in controlling the traits; hence pedigree method of breeding will be a rewarding one to improve the traits under investigation.

In conclusion, high estimates of PCV and GCV were recorded for seed yield, number of seeds per capitulum, number of effective capitula per plant and test weight which provides considerable variability and offers scope for genetic improvement through selection.

Further high heritability coupled with high genetic advance were observed for seed yield per plot, seeds per capita, effective capitula per plant and test weight indicate the role of additive gene action in controlling the traits, hence pedigree method of breeding will be a rewarding one to improve the traits under investigation.

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