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Genetic variability, heritability and genetic advance studies in safflower (*Carthamus tinctorius* L.)

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Abstract

The field experiment was carried out at All India Co-ordinated Research Project on Safflower, Vasant Rao Naik Marathwada Krishi Vidyapeeth, Parbhani during Rabi-2019-20 to evaluate the genetic variability, heritability and genetic advance estimates in sixty two genotypes along with two local checks PBNS-12 and A-1 of safflower. Analysis of Variance involving 64 genotypes of safflower for eleven quantitative characters viz., days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of effective capitula/plant, number of seeds per capitulum, 100-seed weight (g), seed yield per plant (g), hull content (%) and oil content (%) revealed highly significant mean sum of squares for all the characters indicating greater diversity among the genotypes. Phenotypic coefficient of variation was higher in magnitude than the genotypic coefficient of variation in respect of all the characters indicating the effect of the environment. Number of secondary branches per plant, seed yield per plant, number of primary branches per plant, number of effective capitula per plant, number of seeds per capitulum shown high phenotypic and genotypic coefficient of variation. Heritability in broad sense were higher for almost all the characters except hull content and oil content. High heritability coupled with high genetic advance as percent of mean was observed for number of secondary branches per plant followed by seed yield per plant, number of seeds per capitula, number of primary branches/plant, number of effective capitula per plant, plant height, 100-seed weight indicating the role of additive genes in governing the inheritance of these traits which could be improved through simple selection.

Keywords: Genetic variability, heritability, genotypic coefficient of variation, phenotypic coefficient of variation, genetic advance

1. Introduction

Safflower (*Carthamus tinctorius* L.) is an oilseed crop belonging to family *Compositae* or *Asteraceae* which is originated in the Middle East and part of Africa, but Mediterranean has the major area of production. Safflower is a diploid ($2n=24$) annual herbaceous crop which grows well in hot and dry climate. Amongst the species of *Carthamus*, only safflower it is also known as 'kusum' in Sanskrit literature also called 'Agnisikha'. *Carthamus* is the Latinized synonym of the Arabic word 'quartum' or 'gurtum' which means the colour of the dye extracted from safflower flowers. 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). Safflower is most commonly known as 'kardai' in Marathi and 'kusum' in Hindi. In China it is known as 'hong hua' (red flower).

Safflower is cultivated mainly in Maharashtra (58%), Karnataka (21%), Gujarat (12%) and to a limited extent in Telangana, Madhya Pradesh, Chhattisgarh, Odisha and Bihar. In India area, production, productivity under safflower during 2017-18 was 0.81 lakh/ha, 0.45 lakh tones and 557 kg/ha respectively. In Maharashtra, area under safflower in 2017-18 was 0.33 lakh/ha, production 0.20 lakh tones and productivity 580 kg/ha.

Traditionally, it was grown for its flowers, used for colouring and flavoring food, fabric painting and for medicinal purposes. It's orange coloured petals are an important source in the manufacture of carthamin dye, a natural colouring agent and also used for making 'saffo-tea'. It is also used as hay or silage. Safflower oil is rich in polyunsaturated fatty acids (linoleic acid 78%) that helps to reduce blood cholesterol (Weiss, 2000). Linoleic acid can keep cell membranes soft, strengthen the elasticity and vitality. The petals have several medicinal properties and are useful in curing several chronic elements.

The germplasm possessing high genetic variability for quantitative traits is the basic material with plant breeder to initiate breeding programme. In order to design appropriate breeding programme, it is important to know how much the phenotypic variation of a trait is heritable.

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Since, the efficiency of a selection programme is mainly dependent on the magnitude of genetic variation and heritability of a trait (Falconer and Mackay, 1996). The coefficient of variation indicates only the extent of variability existing for various characters, but does not give any information regarding heritable proportion of it. Hence, amount of heritability permits greater effectiveness of selection by separating out the environmental influence from the total variability and to indicate accuracy with which a genotype can be identified phenotypically. The genetic advance expressed as percent of mean is the product of genetic coefficient of variation, the square root of heritability ratio and selection intensity. The high heritability estimates enable plant breeder to base the selection programme on phenotypic performance. Johnson *et al.*, (1955) [5] suggested that heritability estimates in conjunction with genetic advance were reliable in predicting the resultant effect from selecting the best individuals.

2. Materials and Methods

Sixty two genotypes along with two local checks of safflower were evaluated during *Rabi*, 2019-20 at All India Co-ordinated Research Project on Safflower, V.N.M.K.V., Parbhani. The Randomized Block Design was used with two replication and each accession was grown in single row of 5 m length with a spacing of 45 cm between rows and 20 cm between plants within a row. Recommended package of practices were followed to raise the good crop. Five plants at random from each row and replication were selected and labeled for recording observations and the mean of five plants was used for statistical analysis. The data were recorded for

days to 50% flowering, days to maturity, plant height at maturity (cm), number of primary branches per plant, number of secondary 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 (1962). 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).

3. Results and Discussion

Analysis of variance for the experiment involving a set of 64 genotypes of safflower for eleven quantitative characters revealed highly significant mean sum of squares for all the characters indicating greater diversity among the genotypes (Table-1). The results pertaining genetic variability 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 eleven characters (Table-2). The highest magnitude of both GCV and PCV were observed for number of secondary branches (51.97%, 52.70%) followed by seed yield per plant (36.15%, 36.93%), number of primary branches per plant (30.47%, 33.26%), number of effective capitula per plant (29.03%, 30.26%), number of seeds per capitulum (28.75%, 29.45%) suggesting that these characters were under the influence of genetic control.

Table 1: Analysis of variance for yield and its contributing traits in Safflower

Sr. No.	Source of variation	D.F.	Mean sum of squares										
			Days to 50% flowering	Days to maturity	Final plant height (cm)	Number of primary branches /plant	Number of Secondary branches /plant	No. of effective capitula per plant	No. of seeds per capitulum	100 – seed weight (g)	Seed yield per plant (g)	Hull content (%)	Oil content (%)
			1	2	3	4	5	6	7	8	9	10	11
1	Replication	1	0.781	19.531	21.945	3.125	0.382	1.531	3.445	0.187	1.201	18.757	9.608
2	Treatments	63	149.146**	96.773**	320.448**	13.590**	115.071**	60.503**	125.888**	1.598*	33.762**	43.235**	28.823**
3	Error	63	11.416	11.118	11.389	1.188	1.620	2.515	3.048	0.089	0.721	11.122	9.842

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

Table 2: Genetic variability parameters for yield and yield contributing characters in Safflower lines

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	58.50 – 94.55	82.17	68.86	80.28	10.09	10.90	85.77	15.83	19.26
2	Days to maturity	109.50 – 139.50	127.29	42.82	53.94	5.14	5.77	79.38	12.01	9.43
3	Plant height at maturity (cm)	34.50 – 86.50	62.36	154.52	165.91	19.93	20.65	93.13	24.71	39.62
4	No. of primary branches/plant	3.50 – 14.50	8.17	6.20	7.39	30.47	33.26	83.89	4.69	57.50
5	No. of secondary branches/plant	5.50 – 33.50	14.49	56.72	58.34	51.97	52.70	97.22	15.29	105.56
6	No. of effective capitula / plant	9.50 – 31.00	18.54	28.99	31.50	29.03	30.26	92.03	10.64	57.37
7	No. of seeds/ capitulum	14.50 – 57.00	27.25	61.42	64.46	28.75	29.45	95.28	15.75	57.81
8	100 - seed weight (g)	3.00 – 6.75	5.20	0.75	0.84	16.70	17.66	89.28	1.69	32.53
9	Seed yield / plant (g)	4.55 – 22.10	11.24	16.52	17.24	36.15	36.93	95.82	8.19	72.90
10	Hull content (%)	37.50 – 57.50	47.42	16.05	27.17	8.44	10.99	59.07	6.34	13.37
11	Oil content (%)	22.39 – 40.61	31.87	9.49	19.33	9.66	13.79	49.09	4.44	13.95

High heritability estimates was found for number of secondary branches per plant (97.22%), followed by seed yield per plant (95.82%), number of seeds per capitulum (95.28%), plant height at maturity (93.13%), 100-seed weight (89.28%), days to 50% flowering (85.77%). Similar reports for highest magnitude of both GCV and PCV were earlier

given by Patil *et al.* (1991), Kavani *et al.*, (2000) [6], Reddy *et al.*, (2004) [11] for seed yield per plant, no. of seeds per capitulum. The moderate genotypic and phenotypic coefficient of variation were observed for days to 50% flowering, 100-seed weight, plant height. The low genotypic and phenotypic coefficient of variation were observed for

days to maturity, hull content, oil content. Higher broad sense variability values were also associated with the character *viz.*, seed yield per plant (95.82), number of seeds per capitulum (95.28%), plant height (93.13%), number of effective capitula (92.03%), 100- seed weight (89.28%), days to 50% flowering (85.77%), number of primary branches (83.89%), days to maturity (79.38%). Dhutmal *et al.*, (2006) ^[4] reported the similar results except for test weight and number of secondary branches. Arslan burhan (2007) ^[11] reported similar findings except for number of secondary branches per plant. 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. This results are in consonance with the reports given by Pandya and Patil (1994) ^[9].

Highest genetic advance as percent of mean observed for number of secondary branches per plant followed by seed yield per plant, number of seeds per capitula, number of primary branches, number of effective capitula per plant, plant height, 100- seed weight. High genetic advance was observed for plant height, Bahmankar *et al.* (2014) ^[2], Mohamed *et al.* (2018) ^[7]. Seed yield per plant had high estimated genetic advance, no. of seeds per capitulum, also same results obtained by Dambal *et al.*, (2015), Valli *et al.* (2016) ^[12], Pushpavalli and Kumar (2017) ^[10] for seed yield per plant. The characters plant height, seed yield per plant, number of seeds per capitulum recorded high heritability coupled with high expected genetic advance, indicating the presence of additive gene action and effectiveness of phenotypic selection. Thus while, exploiting genetic variability a due weightage should be given to these characters.

In conclusion, high estimates of PCV and GCV were recorded for number of secondary branches followed by seed yield per plant, number of primary branches per plant, number of effective capitula per plant, number of seeds per capitulum which provides considerable variability and offers scope for genetic improvement through selection. Further high heritability coupled with high genetic advance were observed for plant height, seed yield per plant, number of seeds per capitulum indicate the role of additive gene action in controlling the traits.

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