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Study of Genetic variability in Safflower (Carthamus tinctorius L.)

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ABSTRACT: The present experiment was conducted at the Research cum Instructional farm of Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, during *rabi* 2021-22 in order to study the genetic parameters and correlation among yield contributing traits in safflower. Eighteen safflower genotypes including 3 checks *viz.*, A-1, PBNS 12 and IGKV kusum were evaluated. The largest levels of genotypic and phenotypic variability were reported for traits like biological yield per plant, seed yield per plant, number of capitula per plant, harvest index, and 100 seed weight. For variables like plant height, seed weight per hundred seeds, biological yield, and seed yield per plant, high heritability with high genetic advance estimate has been estimated. Association studies indicated that seed yield per plant is positively correlated with number of primary branches per plant (0.117), number of capitulum per plant (0.108), 100 seed weight (0.216), harvest index (0.462**) and oil content (0.371**) while shows negative association with days to 50% flowering (-0.257), days to maturity (-0.006) and plant height (-0.532**). Oil content exhibited significant positive correlation with biological yield / plant (0.649**).

Keywords: Safflower, PCV, GCV, heritability, genetic advance, correlation, oil content, seed yield.

INTRODUCTION

Safflower (Carthamus tinctorius L.) is one of the most ancient of cultivated oilseed crop. It is an annual rabi crop from the Asteraceae family, genus Carthamus, tribe Tubiflorae, division sub Angiosperm, division Phaenerogams (Singh and Nimbkar 2007). The most popular names for it are "honghua" (red blossom) in China and "kusum" (derived from the Sanskrit "kusumbha"; Chavan, 1961). Also, known by the name of bastard saffron, safflower is used as a cheap substitute of saffron. It is a branched, thistle-like herbaceous plant, with short spines on the leaves (Dajue and Mundel 1996). The fruit is a cypsela, often referred to as an achene. The deep tap root system (2-3 m) of safflower helps it thrive in semi-arid conditions or in water deficit areas. The cultivated form of safflower has a chromosome number of 2n=24. Among the wild relatives of safflower, only two species (Carthamus oxyacanthus Bieb. and Carthamus palaestinus Eig.) are easily crossable with cultivated species (Ashri and Knowles, 1960). Safflower is a crop of multipurpose importance. The red, yellow and orange

coloured dye extracted from the dried florets is used as a food colouring agent and in textile dyeing. Particularly in Asian nations like Turkey, China, andIndia, spice made from dried flower petals is utilised in food preparation (Ekin, 2005). Safflower is a rich source of polyunsaturated fatty acid (PUFA) that helps in reducing the cholesterol level in blood. Linoleic acid (76.2%) and Oleic acid (13.75%) were found to the dominant among PUFAs (Katkade *et al.*, 2018). It is also known that oleic acid, a monounsaturated fatty acid, lowers blood levels of low-density lipoprotein (LDL; bad cholesterol), without changing high-density lipoprotein (HDL; good cholesterol) (Purkayasth, 2017; Linthoi 2022).

MATERIAL AND METHOD

The research work took place during *rabi* 2021-22 at IGKV, Raipur. The experimental materials for current studies comprise eighteen genotypes (including 3 checks) of safflower. The research work was set up in Randomized Block Design (RBD) with three replications. Each genotype was raised in a plot of $1.35 \text{ m} \times 5 \text{ m}$ in scale. The row to row spacing was

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45 cm and the plant to plant spacing was kept at 20 cm for each replication. Crop was sown on 22 November of 2021 under irrigated conditions, one comes up, i.e., after seed sowing and two more irrigations are supplied at the time of branching and the start of flowering phases of crop development. Normal recommended doses of fertilizers, i.e., 40N: 40P: 20K, were used.

RESULTS AND DISCUSSIONS

The GCV and PCV were estimated in Parameters like biological yield per plant (22.8, 35.69), seed yield per plant (17.87 and 41.46), number of capitulum/plant (17.51, 23.93), harvest index (15.07, 22.4), and 100 seed weight (16.74 and 18.41) showed the highest levels of genotypic and phenotypic coefficient of variation. The data suggest that these traits exhibit a high degree of genotype-specific variability.

For traits like days to 50% flowering (5.07, 5.42), days to maturity (4.34, 4.71), and oil content (9.32, 9.68), the level of genotypic and phenotypic coefficient of variation appears to be at its lowest. The findings of Bidgoli *et al.* (2006); Mahajan *et al.* (2009); Sahoo *et al.* (2022) are being supported by the current findings.

High heritability in addition with high GA as % of mean for the traits expected in next generation indicate the preponderance of additive gene action for the expression of these traits which is fixable in subsequent generation. These results find the support of earlier studies by Camas and Esendal (2006); Shivani *et al.* (2010); Bhamnakar *et al.* (2014); Muhammad *et al.* (2020) for the traits 100 seed weight (g) and plant height (cm). The author suggested that these parameters were under additive

gene effect. This also indicated that these parameters could be manipulated according to requirement and worthwhile achievement could be achieved through selection.

Low heritability coupled with low genetic advance was observed in harvest index (%) and seed yield per plant (g) indicated non-additive genetic effects governing this trait.

To select effective breeding strategies, such as parent selection, it is important to have an understanding of the relationship between yield and the qualities that contribute to it. The genotypic correlation coefficient provides a tight level of association that can be useful among the features to the entire enhanced plants, whilst the phenotypic correlation coefficients help to determine the selection index.

As opposed to a strong negative correlation with days to 50% flowering (-0.257), days to maturity (-0.006), plant height (-0.532**), and the number of seeds per capitulum (-0.09), seed yield per plant is positively correlated with the number of primary branches per plant (0.117), number of capitula per plant (0.108), 100 seed weight (0.216), harvest index (0.462**), and oil content (0.371**). This indicated that seed yield, oil content can be improved through selections based on primary branches per plant, number of capitulum per plant, 100 seed weight, harvest index and oil content. Characters like days to maturity, plant height should be selected against.

The present results confirming the findings of Shivani *et al.* (2010); Golkar *et al.*, (2012); Hussain *et al.* (2014); Dambal and Patil (2016); Muhammad *et al.* (2020); Pattar and Patil (2020); Purkaystha & Srivastava (2020).

Sr. No.	Traits Mean		Range Min Max		GCV (%)	PCV (%)	Heritability (%BS)	Genetic advance	Genetic advance as % of mean	
1.	Days to 50 % flowering	99.87	88.00	111.00	5.07	5.42	87.84	9.79	9.803	
2.	Days to maturity	140.13	121.00	149.00	4.34	4.71	84.94	11.55	8.24	
3.	Plant Height (cm)	84.92	57.60	107.00	11.14	11.82	88.79	18.36	21.62	
4.	Number of branches/ plants	7.26	4.40	9.60	11.89	15.95	55.62	1.32	18.27	
5.	Number of capitulum/plant	26.85	11.20	43.60	17.51	23.93	53.46	7.08	26.36	
6.	Number of seeds/capitulum	36.18	28.00	51.00	11.32	14.39	61.89	6.64	18.34	
7.	100 seed weight (g)	4.62	3.10	6.60	16.74	18.41	82.68	1.44	31.35	
8.	Biological yield / plant (g)	56.67	16.20	117.20	22.88	35.69	41.10	17.13	30.22	
9.	Harvest index (%)	27.03	13.50	45.40	15.07	22.14	46.38	5.72	21.15	
10.	Oil Content (%)	33.29	28.20	39.80	9.32	9.68	92.56	6.15	18.47	
11.	Seed yield / plant (g)	15.52	3.00	35.0	17.87	41.46	43.13	5.72	36.84	

Table 1: Genetic parameter of yield and its contributing traits in safflower (*rabi* 2021-22).

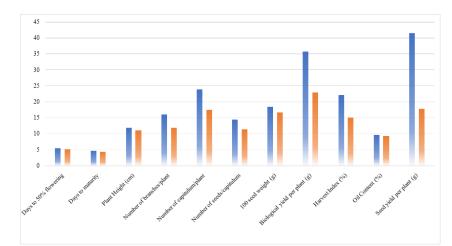


Fig. 1. PCV (blue) and GCV (orange) values for yield and its contributing traits.

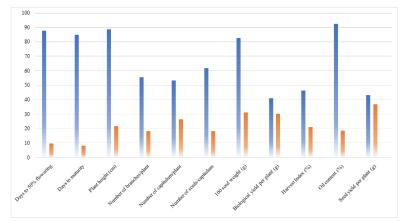


Fig. 2. Heritability (blue) and Genetic Advance (orange) as % of mean for yield and its contributing traits

Table 2: Correlation analysis for yield contributing traits in Safflower.

		Days to 50 % flowering	Days to maturity	Plant Height(cm)	Number of primary branches /plants	Number of capitulum/plant	Number of seeds /capitulum	100 seed weight (g)	Biological yield /plant (g)	Harvest Index (%)	Oil content (%)
Days to maturity	G	0.860**									
	Р	0.827**									
Plant height	G	0.592**	0.289								
(cm)	Р	0.556**	0.271*								
Number of primary	G	0.469**	0.536*	0.242							
branches/ plant	Р	0.379**	0.425**	0.248							
Number of capitulum/plant	G	0.341	0.581*	-0.004	0.430						
cupituluii, piulit	Р	0.230	0.432**	0.075	0.487**						
Number of seeds/	G	0.046	-0.126	0.181	0.003	-0.597**					
capitulum	Р	0.051	0.044	0.145	0.059	-0.275*					
100 seed	G	-0.611**	-0.546*	-0.141	-0.498*	-0.306	-0.643**				
weight(g)	Р	-0.548**	0.452**	-0.188	-0.379**	-0.205	-0.395**				
Biological yield	G	-0.132	0.097	-0.731**	0.444	0.244	0.036	-0.155			
/plant (g)	Р	-0.011	0.167	-0.345**	0.289*	0.188	0.022	-0.062			
Harvest Index	G	-0.608**	-0.366	-0.542*	-0.734**	-0.524*	-0.377	0.906**	0.075		
(%)	Р	-0.384**	-0.195	-0.368**	-0.267	-0.150	-0.273*	0.496**	-0.011		
Oil content (%)	G	0.087	0.199	-0.091	0.137	-0.271	0.579*	-0.114	0.649**	0.302	
	Р	0.076	0.165	-0.082	0.088	-0.227	0.419**	-0.132	0.395**	0.161	
Seed yield	G	-0.495**	-0.164	-0.98**	-0.056	-0.595	-0.225	0.346	0.823**	0.653**	0.619**
/plant(g)	Р	-0.257	-0.006	-0.532**	0.117	0.107	-0.090	0.216	0.835**	0.462**	0.371**

CONCLUSIONS

The values of PCV were higher than the values of GCV indicated the various amount of influence of environment in different traits existed which also confirmed by the percentage of heritability.

Traits like oil content, plant height, days to 50% flowering, days to maturity and 100 seed weight had high heritability indicating stable inheritance of these traits from generations without much influence of environment. While harvest index and seed yield/plant had minimum heritability i.e., much influenced by environment. The lowest heritability was noticed for biological yield/plant.

Association studies indicated that seed yield/plant is positively correlated with number of primary branches/plant, number of capitulum/plant ,100 seed weight, harvest index and oil content while shows negative association with days to 50% flowering, days to maturity and plant height.

FUTURE SCOPE

The characters that show high heritability can be selected by the breeder for improving the seed and oil yield of the crop as they are less affected by environment. The characters that exhibit positive correlation can be selected for while characters exhibiting negative correlation with seed and oil yield can be selected against.

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