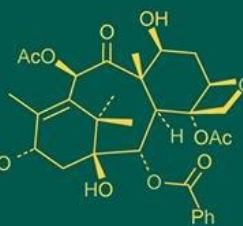
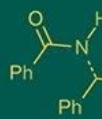


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Roshan Ara

Department of Genetics and
Plant Breeding, Indira Gandhi
Krishi Vishwavidyalaya
Raipur, Chhattisgarh, India

PK Chandrakar

Department of Genetics and
Plant Breeding, Indira Gandhi
Krishi Vishwavidyalaya
Raipur, Chhattisgarh, India

Rajeev Shrivastav

Department of Genetics and
Plant Breeding, Indira Gandhi
Krishi Vishwavidyalaya
Raipur, Chhattisgarh, India

Upasana Mohanty

Department of Genetics and
Plant Breeding, Indira Gandhi
Krishi Vishwavidyalaya
Raipur, Chhattisgarh, India

Study of association among the yield and its contributing traits in safflower (*Carthamus tinctorius* L.)

Roshan Ara, PK Chandrakar, Rajeev Shrivastav and Upasana Mohanty

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Abstract

Current research was conducted during rabi 2022-23. In order to study genetic parameter and association among yield and its contributing traits in safflower. Analysis of variance indicates that all characters viz., days to 50% flowering, days to maturity, plant height, no. of primary branches per plant, number of capitulum per plant, 100 seed weight, seed yield per plant, volume weight and oil content. This indicates scope of improvement in genotypes through selection with significant variability. The largest level of genotypic and phenotypic variability were reported for traits like number of primary branches per plant, plant height and 100 seed weight. For variables like number of primary branches per plant, 100 seed weight, biological yield, seed yield per plant, and harvest index, high heritability with high genetic advance as % of mean estimate has been estimated. Association studies indicates that the seed yield per plant is significantly positive correlated with days to 50% flowering (0.364*), number of primary branches per plant (0.241*), number of capitulum per plant (0.340*), biological yield per plant (0.778*), harvest index (0.300*), volume weight (0.335*), while shows negative correlation with oil content (-0.238*). Oil content exhibited significant positive correlation with number of primary branches per plant (0.237*).

Keywords: Correlation, yield contributing traits, safflower, variability

Introduction

Safflower (*Carthamus tinctorius* L.) is a dry land oilseed crop from the *Asteraceae* family, genus *Carthamus*, tribe *Tubiflorae*, sub division *Angiosperm*, division *Phanerogams* (Singh and Nimbkar, 2005) [18]. A diploid (2n= 24) crop. It is most commonly known as 'kusum' in India, derived from the Sanskrit, 'kusumbha' (Chavan, 1961) [4], and as 'honghua' (red flower) in China. Also, known as bastard saffron, fake saffron, thistle saffron, and dyers saffron all are the terms for a less expensive saffron replacement (Weiss, 1983) [20]. Safflower is highly demanded for its seed oil it contains both high linoleic acid, (where 64-79 percent of total fatty acids) and high oleic acid (where 10-81 percent of total fatty acid). (Purkayasth, 2017; Linthoi 2022) [16, 11]. Dried petals of safflower have therapeutic value and are being extensively used in preparation of herbal medicines. Safflower is a rich source of polyunsaturated fatty acid (PUFA) that helps in reducing the cholesterol level in blood (Katkade *et al.*, 2018) [10]. Being an often-cross pollinated crop (4-10% outcrossing), it is dependent on bees and other insects for allogamy. Anemophily however play a negligible role in seed setting. Common forms of developed achene contain 33-60% hulls and 40-60% kernels. The whole seed has an oil content of 20% to 40% or higher. Correlation coefficients, in general, reflect the strength of linear relationships and correlations between independent features. However, as correlation coefficients can only give a primitive explanation of relationships. The components and interactions of the yield have a big impact on safflower breeding. (Purkayasth and Shrivastava, 2020) [15].

Materials and Methods

The current research work took place in research cum instructional farm of IGKV, Raipur (C.G.) during rabi 2022-23. The experimental material for studies comprises 23 genotypes including four checks A-1, ISF-1, ISF-764 and PBNS-12. The research work was set up in randomise complete block design (RCBD) with 3 replications.

Corresponding Author:**Roshan Ara**

Department of Genetics and
Plant Breeding, Indira Gandhi
Krishi Vishwavidyalaya
Raipur, Chhattisgarh, India

Each genotype was raised in a plot of 1.35 m x 5 m in scale. The row to row spacing was 45 cm and plot to plot spacing 20 cm were maintained for each replication. Crop was sown under irrigated condition 1st irrigation was given at the time of sowing and then 2 more irrigation was given at the time of 60 days stage *i.e.*, initiation of branching stage and the start of flowering phase 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 no. of primary branches (13, 18), no. of capitula per plant (13,17), plant height (5.58, 7.79), and 100 seed weight (16.98, 18.63) showed the highest levels of genotypic and phenotypic coefficient of variation. The data suggested that these traits exhibit a high degree of genotypic-specific variability.

For traits like biological yield per plant (21.30, 22.72), seed yield per plant (21.98, 22.94) and oil content (9.83, 9.97), the level of genotypic and phenotypic coefficient of variation appears to be at its lowest. The findings of Mahajan *et al.* (2009) [13]; Sahoo *et al.* (2022) [17] 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) [3]; Shivani *et al.* (2010) [19]; Bhamnagar *et al.* (2014) [2]; Muhammad *et al.* (2020) [12] for traits number of primary branches per plant, 100 seed weight(g), biological yield per plant, seed yield per plant and harvest index (%). 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 volume weight (g/100 ml), days to 50% flowering and days to maturity, indicated non-additive genetic effect governing the traits.

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.

The seed yield per plant showed significant positive correlation with days to 50% flowering (0.364*), number of primary branches per plant (0.241*), number of capitulum per plant (0.340*), biological yield per plant (0.778*), harvest index (0.300*) and volume weight(0.335*), but showed significant negative correlation with oil content(-0.238*).

The oil content exhibited significant positive correlation with number of primary branches per plant (0.237*), whereas negative correlation with 100 seed weight(-0.681**), seed yield per plant (-0.238*), harvest index(-0.405**), and volume weight (-0.255). This indicated that seed yield can be improved through selection based on days to 50% flowering, number of primary branches per plant, number of capitulum per plant, biological yield per plant, harvest index and volume weight. And for improvement in oil content traits like 100 seed weight, seed yield per plant, harvest index and volume weight should be selected against. The present results confirming the findings of Shivani *et al.* (2010) [19]; Golkar *et al.*, (2012) [8]; Hussain *et al.* (2014) [9]; Dambal and Patil (2016) [5]; Muhammad *et al.* (2020) [12]; Pattar and Patil (2020) [14]; Purkaystha & Srivastava (2020) [15]

Table 1: Genetic parameter of yield and its contributing traits in safflower (*rabi* 2022-23)

S. No	Traits	Mean	Range		PCV (%)	GCV (%)	Heritability (% BS)	Genetic advance	Genetic advance as % of mean
			Min	Max					
1.	Days to 50% flowering	94.80	90.00	100.00	3.66	2.01	30.15	2.16	2.28
2.	Days to maturity	144.33	135.00	150.00	4.10	2.26	30.37	3.71	2.56
3.	Plant height (cm)	96.77	82.33	105.00	7.79	5.58	51.24	7.96	8.23
4.	No. of pr. branches/plant	8.34	5.00	11.00	17.88	13.40	81.57	2.51	30.05
5.	No. of capitula per plant	26.32	15.00	35.00	17.20	13.40	60.73	5.66	21.52
6.	100 seed weight (g)	4.66	3.40	6.10	18.63	16.98	83.09	1.49	31.89
7.	Biological yield (g)	92.32	63.87	139.33	22.72	21.30	87.86	37.97	41.13
8.	Seed yield per plant (g)	24.99	16.22	38.11	22.94	21.98	91.79	10.84	43.38
9.	Harvest index (%)	27.52	21.32	37.95	16.48	14.23	74.54	6.97	25.31
10.	Volume weight (g/100 ml)	54.77	49.46	59.30	4.95	2.71	29.869	1.67	3.05
11.	Oil content (%)	34.47	29.12	40.98	9.971	9.834	97.255	6.886	19.978

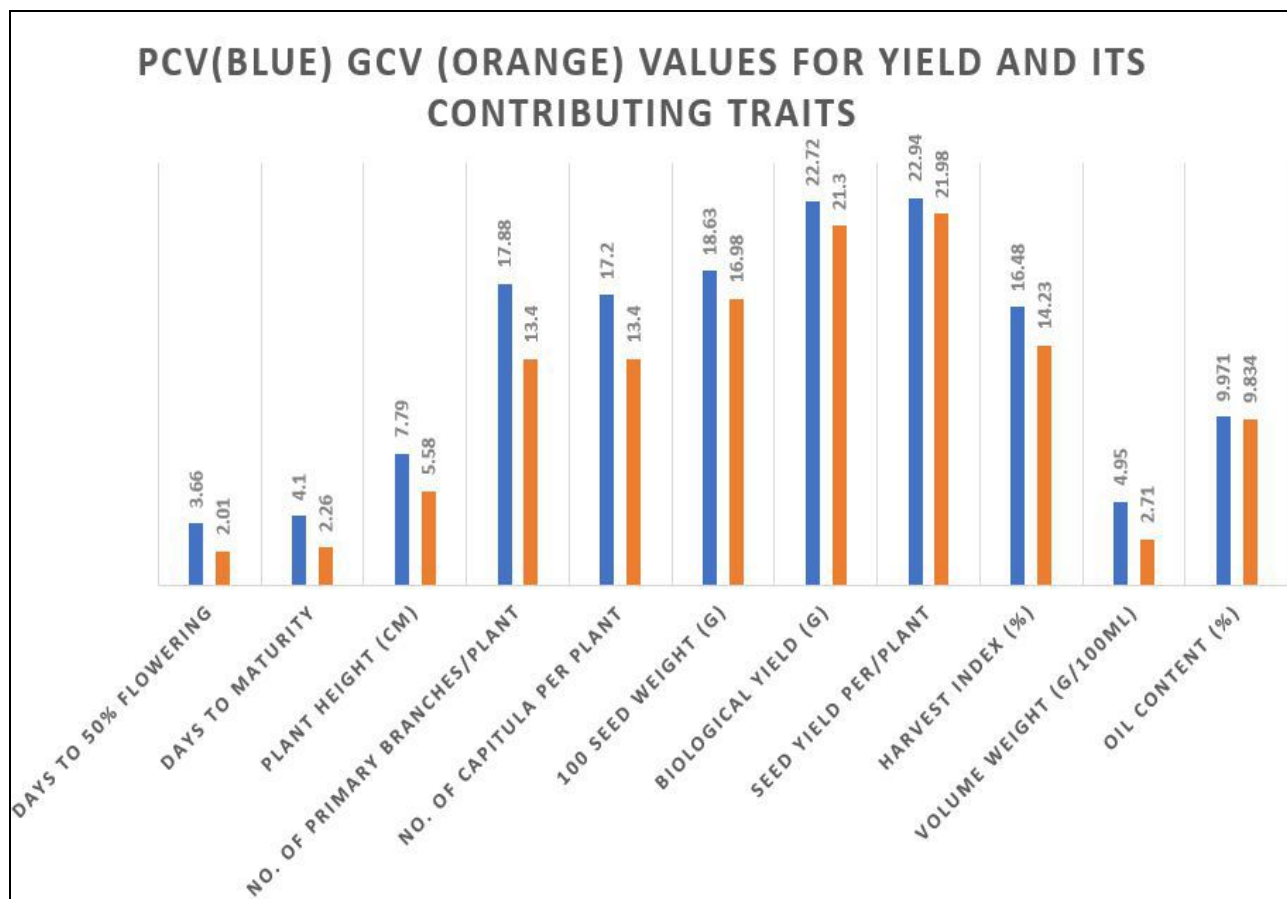


Fig 1: PCV (blue) and GCV (orange) values for yield and its contributing traits

Table 2: Correlation analysis for yield contributing traits in safflower

		Days to maturity	Plant height (cm)	No. of primary branches	No. of capitula/plant	100 seed weight (g)	Biological weight (g)	SeSZed yield/plant (g)	Harvest index (%)	Volume weight (g/100 ml)	Oil (%)
Days to 50% flowering	G	0.603*	-0.1452	0.0170	0.0745	-0.0936	0.266*	0.348*	0.0813	-0.0443	-0.1210
	P	0.606**	-0.145	0.023	0.089	-0.084	0.296*	0.364*	0.108	-0.097	-0.115
Days to maturity	G		-0.0869	-0.0248	0.0958	-0.0025	0.274*	0.233	-0.004	0.016	-0.213
	P		-0.086	-0.023	0.100	0.0008	0.281*	0.235	0.002	0.002	-0.212
Plant height(cm)	G			-0.195	-0.171	0.248*	0.139	0.153	0.022	0.399*	0.011
	P			-0.203	-0.181	0.250*	0.138	0.150	0.020	0.411**	0.009
No. primary branches	G				0.692**	-0.120	0.412**	0.246*	-0.279*	-0.262*	0.240*
	P				0.688**	-0.118	0.413**	0.241*	-0.284*	-0.266*	0.237*
No. of capitula/ plant	G					-0.037	0.397**	0.345*	-0.133	-0.120	0.051
	P					-0.036	0.397**	0.340*	-0.139	-0.116	0.046
100 seed weight (g)	G						0.084	0.200	0.167	0.343*	-0.679**
	P						0.081	0.202	0.263	0.361*	-0.681**
Biological yield (g)	G							0.776*	-0.302*	0.242*	0.018
	P							0.778*	-0.313*	0.265*	0.015
Seed yield/plant (g)	G								0.299*	0.325*	-0.234
	P								0.300*	0.335*	-0.238
Harvest index (%)	G									0.114	-0.399**
	P									0.137	-0.405**
Volume weight (g/100 ml)	G										-0.256*
	P										0.255

Conclusions

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

Traits like number of primary branches, 100 seed weight, biological yield, seed yield per plan and oil percentage had high heritability indicating stable inheritance of these traits from generations without much influence of environment.

While days to 50% flowering, days to maturity and plant height had minimum heritability *i.e.*, much influenced by environment.

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

References

1. Ashri A, Knowles PF. Cytogenetics of safflower (*Carthamus* L.) species and their hybrids. *Agronomy Journal*. 1960;52:11-17.
2. Bhamnagar M, Raji RM, Seloki RA, Shirkoob K. Assessment of broad sense heritability and genetic advance in safflower. *International Journal of Biosciences*. 2014;4(8):131-135.
3. Camas N, Esendal E. Estimates of broad-sense heritability for seed yield and yield components of safflower (*Carthamus tinctorius* L.). *Hereditas*. 2006;143:55-57.
4. Chavan VM. Niger and safflower. Indian Central Oilseeds Committee Publication. Hyderabad, India. 1961:57-150.
5. Dambal IG, Patil RS. Character association and path analysis in safflower germplasm (*Carthamus tinctorius* L.). *Research Journal of Agricultural Sciences*. 2016;7(1):155-157.
6. Dajue L, Mundel HH. Safflower (*Carthamus tinctorius* L.) promoting the conservation and use of underutilized and neglected crops. Germany and International Plant Genetics Resources Institute, Rome; 1996.
7. Ekin Z. Resurgence of safflower (*Carthamus tinctorius* L.) utilization: A global view. *Journal of Agronomy*. 2005:83-87.
8. Golkar P, Arzani A, Rezaei A. Genetic analysis of agronomic traits in safflower (*Carthamus tinctorius* L.). *Notulae Botanicae Horti Agrobotanici Cluj-Napoca*. 2012;40(1):276-281.
9. Hussain T, Tariq MA, Ahmad I, Saghir M, Batool M, Safdar M, Sher M, Tariq M. Character association analysis in safflower (*Carthamus tinctorius* L.). *Journal of Biology, Agriculture and Healthcare*. 2014;4(6):63-65.
10. Katkade MB, Syed HM, Andhale RR, Sontakke MD. Fatty acid profile and quality assessment of safflower (*Carthamus tinctorius*) oil. *Journal of Pharmacognosy and Phytochemistry*. 2018;7(2):3581-3585.
11. Linthoi. Inheritance study of some qualitative traits and generation mean analysis for seed yield and oil content in safflower (*Carthamus tinctorius* L.) [Ph.D. thesis]. Raipur: IGKV; 2022.
12. Muhammad RW, Ali HMW, Hamza A, Ahmad MQ, Qayyum A, Malik W, Noor E. Estimation of different genetic parameters in various safflower (*Carthamus tinctorius* L.) genotypes under field condition. *Pakistan Journal of Agricultural Research*. 2020;33(4):849-857.
13. Mahajan PV, Deshmukh SN, Ratnaparkhi RD. Evaluation of progenies selected from random mating population of safflower using GMS lines. *Journal of Oilseeds Research*. 2009;26(2):156-158.
14. Pattar VK, Patil R. Correlation and path analysis in safflower (*Carthamus tinctorius* L.) genotypes. *Journal of Pharmacognosy and Phytochemistry*. 2020;9(4):1717-1719.
15. Purkayastha S, Srivastava R. Study on correlation and path analysis in F₂ population in safflower. *Journal of Pharmacognosy and Phytochemistry*. 2020;9(1):1652-1655.
16. Purkayastha S. Inheritance and QTL study in safflower (*Carthamus tinctorius* L.) [M.Sc. dissertation]. Raipur: IGKV; 2017.
17. Sahoo BC, Shrivastava R, Odhar H. Determination of optimum plant characters in safflower (*Carthamus tinctorius* L.) under rice-based late sown condition. *Electronic Journal of Plant Breeding*. 2022;13(1):225-229.
18. Singh V, Nimbkar N. Genetic Resource Chromosome Engineering, and Crop Improvement: Oil Crops. New York: CRC Press; 2007. p. 168-194.
19. Shivani D, Sreelakshmi Ch, Kumar CV. Genetic studies for yield and component characters in germplasm lines of safflower (*Carthamus tinctorius* L.). *Madras Agricultural Journal*. 2010;97(10-12):337-339.
20. Weiss EA. Oilseed crops: Safflower. London: Longman Group Limited; 1983. p. 216-281.