Received: 23 Jan 2023 | Revised: 28 Feb 2023 | Accepted: 28 Feb 2023

Electronic Journal of Plant Breeding

Research Article

Genetic variability and character association studies among seed yield and yield component traitsin safflower (C*arthamus tinctorius* L.) genotypes

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Abstract
A study was carried out to assess the genetic variability and association among yield attributing traits in 60 different safflower genotypes over six environments. The pooled analysis of variance (ANOVA) revealed that all attributes had a considerable degree of variation.The pooled analysis of variability parameters revealed that the phenotypic coefficients of variation (PCV) was higher than the genotypic coefficients of variation (GCV)for all of the characteristics evaluated, indicating that experimental variance contributed to total variation.Petal yield/plant and seed yield/plant had the highest PCV and GCV followed by number of capitula/plant, number of seeds/capitula, height of insertion of first branch, hundred seed weight, number of primary branches/plant, length of longest primary branches, number of secondary branches and height up to main capitula.Number of capitula/plant, seed yield/plant, petal yield/plant, height of insertion of first branch, number of seeds per capitula, hundred seed weight, number of primary branches/plant, length of the longest primary branches, number of secondary branches, height upto main capitula, capitulum diameter and plant height all had high heritability and genetic advance as percent of mean. Seedyield/plant showed positive, significant and directcorrelation with number of capitula/plant, number of seeds/capitulum, height up to the main capitulum, plant height, number of primary branches/plant, capitulum diameter, and hundred seed weight.Number of capitula/planthad the maximum direct effect on grain yield/plant followed by number of seeds/capitulum, hundred seed weight and petal yield/plant. Hence selection of these traits would improve seed and petal yield in safflower breeding program.

Keywords: Genetic variability, heritability, correlation, path analysis, pooled analysis and Safflower

INTRODUCTION

Safflower is one of the world's oldest domesticated crop (Hamdan *et al.,* 2011). It is a multipurpose oilseed crop with multiple applications such as industrial, medical, and food oil production (Upadhyaya *et al.,* 2003). Safflower petals are extensively used for medicinal and culinary purposes in China (Li and Mundel, 1996).Safflower is ranked seventh among India's oilseed crops, which include peanut, rapeseed, mustard, soybean, castor, sunflower, linseed, sesame, and niger. Maharashtra, Karnataka, Andhra Pradesh, Madhya Pradesh, Gujarat, Orissa, and Bihar are major safflower-growing states in India (Navale *et al.,*2014). Safflower is considered to be an underutilized crop when compared to other oilseed crops such as sunflower, rapeseed, and soybean (Ali *et al.,* 2020).

https://doi.org/10.37992/2023.1401.020

Lower oil content, seed yield, insect pest vulnerability and disease susceptibility are key factors influencing safflower production and quality, resulting in underutilization (Zeinali, 1999). However, unattractive characteristics such as low yield, spiny nature, and vulnerability to a variety of biotic stressors have limited its production in a number of countries, including India (Nimbkar, 2008).The safflower petals are discarded as wastage but now a days petals are of great demand because they yield natural dyes *viz.,* yellow (carthmidine) and red (carthamin) dyes. Herbal tea are prepared from petals of safflower which contains medicinal therapeutic values. The highly valued seed oil is abundant in polyunsaturated fatty acids.Hence, a comprehensive program to increase yield of both seed and petal is essential for safflower improvement (Golkar, 2014).

Plant breeders strive to establish cultivars with higher yield and other desired agronomic characteristics.Breeders have the choice of selecting favourable genotypes in early generations or deferring intense selection until later generations.Yield is a complex polygenic trait and the high yield crop program requiresinformation on nature and magnitude of variation in the available material, relationship of yield with other agronomic traits and the amount of environmental influence on the expression of these component traits. Thus direct selection would not be a reliable approach because it was highly influenced by environmental factors. Correlation studies gives information on the nature and level of the relationship between various component traits and seed yield. Path analysis assists in determining the direct effects of traits as well as their indirect effects on other traits. The germplasm is the reservoir for producing successful variation.As a result, the current investigation was carried out in six environments with 60 safflower genotypes.

MATERIALS AND METHODS

A total of 60 safflower genotypes wereobtained from the Indian Institute of Oilseeds Research, Hyderabad (**Table1**). During *rabi* 2020 and 2021, these genotypes were tested in six locations using a randomized block design with three replicates (**Table 2**). The six locations wereAC & RI, Madurai (E1), Thirumangalam, Madurai (E2) and AC & RI, Killikulam (E3) during year 2020-2021 andAC & RI, Madurai (E4), ARS, Vaigaidam (E5) and SRS Melalathur(E6) during the year 2021-2022.The safflower genotypes were sown on ridges and furrows with a spacing of 45cm between the rows and 15 cm between the plants. The recommended agronomic practices were followed to increase the yield.The following fifteen biometrical observations were taken such as days to initial flowering, days to 50% flowering, days to maturity, height of insertion of first branch (From ground level), height upto main capitula (cm), plant height (cm), number of primary branches/plant, number of secondary branches, capitulum diameter, number of capitula per plant, length of the longest primary branches, number of seeds per capitula, hundred seed weight (g), petal yield/plant (g) and seed yield/plant (g).

Table 1. List of genotypes used in the experiments

S. No.	Accessions	Origin	Parentage	Flower colour at bloom	Flower colour at faded stage	Thorn nature
1	GMU-184	IIOR, Hyderabad, India.	-	Yellow	Orange	S
2	GMU-704	IIOR, Hyderabad, India.	-	Yellow	Orange	NS
3	GMU-855	IIOR, Hyderabad, India.	-	Yellow	Orange	S
4	GMU-900	IIOR, Hyderabad, India.	-	White	Grey White	S
5	GMU-1193	IIOR, Hyderabad, India.	-	Yellow	Orange	S
6	GMU-1229	IIOR, Hyderabad, India.	-	Yellow	Orange	S
7	GMU-1303	IIOR, Hyderabad, India.	-	Orange	Deep Red	NS
8	GMU-1437	IIOR, Hyderabad, India.	-	Yellow	Orange	S
9	GMU-1920	IIOR, Hyderabad, India.	-	Yellow	Orange	S
10	GMU-2020	IIOR, Hyderabad, India.	-	Yellow	Orange	S
11	GMU-2347	IIOR, Hyderabad, India.	-	Yellow	Orange	S
12	GMU-2366	IIOR, Hyderabad, India.	-	Yellow	Orange	S
13	GMU-2385	IIOR, Hyderabad, India.	-	Yellow	Orange	S
14	GMU-2551	IIOR, Hyderabad, India.	-	Yellow	Orange	S
15	GMU-2758	IIOR, Hyderabad, India.	-	Yellow	Orange	S
16	GMU-2968	IIOR, Hyderabad, India.	-	Yellow	Orange	S
17	GMU-3098	IIOR, Hyderabad, India.	-	Orange	Deep Red	S
18	GMU-3165	IIOR, Hyderabad, India.	-	Yellow	Orange	S
19	GMU-3185	IIOR, Hyderabad, India.	-	Yellow	Orange	NS
20	GMU-3326	IIOR, Hyderabad, India.	-	Yellow	Orange	NS

https://doi.org/10.37992/2023.1401.020

Table 1. Continued...

S. No.	Accessions	Origin	Parentage	Flower colour at bloom	Flower colour at faded stage	Thorn nature
21	GMU-3438	IIOR, Hyderabad, India.	-	Yellow	Orange	S
22	GMU-3482	IIOR, Hyderabad, India.	-	Yellow	Orange	S
23	GMU-3488	IIOR, Hyderabad, India.	-	Yellow	Orange	S
24	GMU-3708	IIOR, Hyderabad, India.	-	Orange	Deep Red	S
25	GMU-3758	IIOR, Hyderabad, India.	-	Yellow	Orange	S
26	GMU-3781	IIOR, Hyderabad, India.	-	Yellow	Orange	S
27	GMU-3785	IIOR, Hyderabad, India.	-	Pale Yelllow	Pinkish White	S
28	GMU-3865	IIOR, Hyderabad, India.	-	Yellow	Orange	S
29	GMU-3963	IIOR, Hyderabad, India.	-	Yellow	Orange	S
30	GMU-3965	IIOR, Hyderabad, India.	-	Yellow	Orange	S
31	GMU-4009	IIOR, Hyderabad, India.	-	Yellow	Orange	S
32	GMU-4035	IIOR, Hyderabad, India.	-	White	Grey White	S
33	GMU-4093	IIOR, Hyderabad, India.	-	Yellow	Orange	S
34	GMU-4101	IIOR, Hyderabad, India.	-	Pale Yellow	Pinkish White	S
35	GMU-4128	IIOR, Hyderabad, India.	-	Yellow	Orange	S
36	GMU-4814	IIOR, Hyderabad, India.	-	Yellow	Orange	S
37	GMU-5146	IIOR, Hyderabad, India.	-	Yellow	Orange	S
38	GMU-5517	IIOR, Hyderabad, India.	-	Yellow	Orange	NS
39	GMU-5520	IIOR, Hyderabad, India.	-	Yellow	Orange	S
40	GMU-5571	IIOR, Hyderabad, India.	-	Yellow	Orange	S
41	GMU-5712	IIOR, Hyderabad, India.	-	Yellow	Orange	NS
42	GMU-5761	IIOR, Hyderabad, India.	-	Yellow	Orange	S
43	GMU-5815	IIOR, Hyderabad, India.	-	Yellow	Orange	S
44	GMU-5850	IIOR, Hyderabad, India.	-	Yellow	Orange	NS
45	GMU-5933	IIOR, Hyderabad, India.	-	Yellow	Orange	S
46	GMU-5964	IIOR, Hyderabad, India.	-	Orange	Deep Red	S
47	GMU-5965	IIOR, Hyderabad, India.	-	Yellow	Orange	NS
48	GMU-6114	IIOR, Hyderabad, India.	-	Yellow	Orange	NS
49	GMU-6207	IIOR, Hyderabad, India.	-	Yellow	Orange	S
50	GMU-6878	IIOR, Hyderabad, India.	-	Orange	Deep Red	S
51	GMU-6944	IIOR, Hyderabad, India.	-	Orange	Deep Red	NS
52	GMU-7107	IIOR, Hyderabad, India.	-	Orange	Deep Red	S
53	GMU-7243	IIOR, Hyderabad, India.	-	Pale Yellow	Pinkish White	S
54	GMU-7666	IIOR, Hyderabad, India.	-	Orange	Deep Red	NS
55	GMU-7688	IIOR, Hyderabad, India.	-	Orange	Deep Red	NS
56	BHIMA	Dry farming Research Station, Solapur & Mahatma Phule Krishi Vidyapeeth, Rahuri, Maharashtra, India	selection from A-300	Pale Yelllow	Pinkish White	S
57	JSF-1	AICRP (Safflower) Centre, Indore Rajmata Vijayaraje Scindia Krishi Vishwavidyalaya, Gwalior, Madhya Pradesh, India	selection from IC 11839	White	Grey White	S
58	NARI-57	AICRP (Safflower) centre, NARI, Phaltan, Maharashtra, India	Carmax x C-2829-5-2	Orange	Deep Red	S
59	NARI-6	AICRP (Safflower) centre, NARI, Phaltan, Maharashtra, India	Co-1 x JL6	Orange	Deep Red	NS
60	CO-1	TNAU, Coimbatore, Tamil Nadu, India	Pureline selection from CTS 7403	Orange	Deep Red	NS

(Note: IIOR – Indian Institute of Oilseeds Research, AICRP – All India Coordinated Research Project, TNAU – Tamil Nadu Agricultural University, NARI - Nimbkar Agricultural Research Institute, S – Spiny, NS- Non spiny)

Table 2. Description of the six testing locations used for evaluation of safflower genotypes

S. No.	Code	Location Name	Year	Season	Latitude	Longitude
1.	E1	AC & RI, Madurai	2020-2021	*rabi*	9.9232^{0}N	78.1121^{0}E
2.	E2	Thirumangalam, Madurai	2020-2021	*rabi*	9.8193^{0}N	77.9821^{0}E
3.	E3	AC & RI, Killikulam	2020-2021	*rabi*	8.7071^{0}N	77.8609^{0}E
4.	E4	AC & RI, Madurai	2021-2022	*rabi*	9.9232^{0}N	78.1121^{0}E
5.	E5	ARS, Vaigaidam	2021-2022	*rabi*	10.0533^{0}N	77.5897^{0}E
6.	E6	SRS, Melalathur	2021-2022	*rabi*	12.9179^{0}N	79.8755^{0}E

(AC & RI = Agricultural College and Research Institute, ARS = Agricultural Research Station, SRS = Sugarcane Research Station)

The data were recorded on randomly selectedfive plants in each replication, and the mean values were subjected to pooled analysis of variance, genotypic and phenotypic coefficients of variation, heritability, genetic advance as a percentage of mean (GAM), correlation, and path analysis. The statistical analysis was done using the TNAUSTAT software(Manivannan, 2014) for genetic variability, correlation and path analysis and STAR version 2.0.1for pooled ANOVAanalysis developed by International Rice Research Institute, Philippines. Correlation and path analysis were carried out in accordance with Al-Jibouri *et al.* (1958) and Dewey and Lu (1959), respectively.

RESULTS AND DISCUSSION

The pooled analysis of variance over six environments for 15 biometric traits is furnished in **Table 3**. When tested against the Genotype x Environment interaction, the mean squares due to both genotypes and environments were significant for all of the characters investigated. When tested against pooled error, the mean squares due to the Genotype x Environment interaction were also significant for all traits except days to maturity. These finding suggest that there existed substantial variation among the safflower genotypes studied.Neelima *et al.*(2021) reported significant difference in nine yield contributing traits among the 13 safflower genotypes.

The range and genetic variability of 15quantitative characters are furnished in **Table 4.** Wide range of variation was noted in seed yield/plant (0.28-230.32g) followed by number of capitula/plant (2.33-86.67), plant height (27.50-98.93g) and height upto main capitula (11-80.97). These results are on par withNeelima *et al.* (2021) and Mukta *et al.* (2020).

The PCV values were higher than GCV values for all traits, indicating the apparent variation was not only due to genotypes, but also there was influence of environment.The genetic variability parameters for 15 characters are presented in **Table 4, Fig. 1 and 2.**The magnitude of PCV and GCV was high for petal yield/plant (PCV: 76.47and GCV: 75.66) followed by seed yield per plant (PCV: 68.08 and GCV: 67.39). Similar trend was observed for number of capitula/plant, number of seeds/capitula,height of insertion of first branch, hundred seed weight, number of primary branches/plant, length of longest primary branches, number of secondary branches and height upto main capitula. Higher PCV values than GCV values indicated that trait variability was influenced by environmental factors and that selection is successful for these characteristics. Rathod *et al.*(2021), Dhruw *et al.*(2022), Swarup and Singh, (2012) and Rahimi, (2021) reported similar findings. Days to 50% flowering displayed moderate PCV and low GCV(PCV: 10.62 and GCV: 8.00). The same result was documented by Dhruw *et al.* (2022).Low PCV and GCV values were noted for days to initial flowering (PCV: 9.90 and GCV: 8.51) and days to maturity (PCV: 8.11 and GCV: 5.04).The results were in agreement with Swarup and Singh, (2012). Low coefficients of variation for these traits indicated that the variation among the material was low. Hence, search for variation in other material may be required.The coefficients of variation indicate only the extent of variability that exists for different characters and do not indicate heritable portion of a character.Therefore, heritability is estimated, which is a good indicator for character transmission in the off spring (Falconer 1981).

The majority of traits had high heritability and showed dominance of additive gene activity. High heritability was recorded in petal yield/plant (97.09) followed by hundred seed weight (96.95), number of capitula/plant (96.44), height of insertion of first branch (96.30), seed yield/plant (96.23), number of seeds/capitula (94.99), number of primary branches/plant (94.77), length of longest primary branches (94.57), height upto main capitula (93.28), number of secondary branches (89.98), plant height (88.66), capitulum diameter (86.67) and days to initial flowering (60.66) indicating that these traits were less influenced by the environment and selection based on phenotypic observations would be effective. Moderate heritability was observed in days to 50% flowering (55.84). Low heritability was noticed in days to maturity (29.90). The similar results are in contrary to Rathod *et al.* (2021), Swarup and singh, (2012) and Tariq *et al.*(2014). Johnson *et al.* (1955) proposed that heredity in relation to genetic advancement is more accurate than heritability alone in determining the effect of selection. As a result, high

Table 3. Pooled ANOVA for biometrical traits in safflower

S. No.	Character	Mean squares			
		Genotype	Environment	Genotype x Environment	Error (Pooled)
		df=59	df=5	df=295	df=708
1.	Days to initial flowering (DIF)	550.43*	1054.03*	33.83*	20.32
2.	Days to 50% flowering (DFF)	558.15*	1237.71*	33.23*	22.36
3.	Days to maturity (DM)	562.82*	1339.31*	33.62	38.27
4.	Height of insertion of first branch (From ground level) (HIFB)	226.50*	1666.84*	165.41*	2.08
5.	Height upto main capitula (cm) (HMC)	1102.37*	1475.91*	263.34*	8.83
6.	Plant height (cm) (PH)	1285.64*	10196.50*	235.67*	15.38
7.	Number of primary branches/plant (NPB/P)	37.12*	1073.76*	13.73*	0.21
8.	Number of secondary branches/plant (NSB/P)	3.67*	44.75*	0.74*	0.03
9.	Capitulum diameter (CD)	1.09*	25.09*	0.38*	0.01
10.	Number of capitula/plant (NC/P)	623.50*	28525.96*	276.65*	1.77
11.	Length of longest primary branches (LLPB)	1351.39*	10166.17*	57.43*	5.29
12.	Number of seeds/capitula (NS/C)	762.21*	1815.57*	135.45*	2.30
13.	Hundred seed weight (g) (HSW)	22.67*	56.16*	2.64*	0.05
14.	seed yield/plant (g) (SY/P)	1422.76*	33441.61*	725.91*	2.50
15.	Petal yield/plant (g) (PY/P)	171.36*	4892.84*	78.91*	0.76

* Significant at 5% level

Table 4.Genetic variability parameters for 15 quantitative traits in safflower genotypes

Parameters	Range		Mean	PCV (%)	GCV (%)	h^2 (%)	GAM (%)
	Minimum	Maximum					
DIF	38.98	93.75	65.53	9.90	8.51	60.66	9.94
DFF	42.00	96.35	69.03	10.62	8.00	55.84	9.91
DM	72.43	127.15	99.58	8.11	5.04	29.90	6.72
HIFB	0.46	43.78	20.64	37.53	36.85	96.30	74.53
HMC	11.00	80.97	42.67	27.55	26.63	93.28	53.03
PH	27.50	98.93	59.76	20.25	19.08	88.66	37.06
NPB/P	1.00	23.34	6.49	32.75	31.97	94.77	64.29
NSB/P	1.00	4.34	2.35	28.17	26.96	89.98	53.19
CD	0.20	4.00	1.80	25.03	19.90	86.67	46.15
NCPP	2.33	86.67	20.34	48.63	48.03	96.44	97.71
LLPB	11.20	74.00	33.66	29.16	28.35	94.57	56.80
NS/C	4.33	56.78	23.80	37.24	36.59	94.99	74.10
HSW	0.30	9.97	3.77	36.06	35.55	96.95	72.19
PY/P	0.83	41.83	9.34	76.47	75.66	97.09	92.75
SY/P	0.28	230.32	17.77	68.08	67.39	96.23	88.45

heritability coupled with high genetic advance percent of mean would be more stable and effective for selection.High heritability coupled with high genetic advance as percent of mean (GAM) was recorded innumber of capitula/plant, seed yield/plant, petal yield/plant,height of insertion of first branch, number of seeds/capitula, hundred seed weight, number of primary branches/plant, length of the longest primary branches, number of secondary branches, height upto main capitula, capitulum diameter and plant height which indicated that these traits are governed by additive gene action and direct selection could be more effective. High heritability coupled with high GAM was reported in yield by Rathod *et al.* (2021), Swarup and singh, (2012) and Tariq *et al.*(2014).

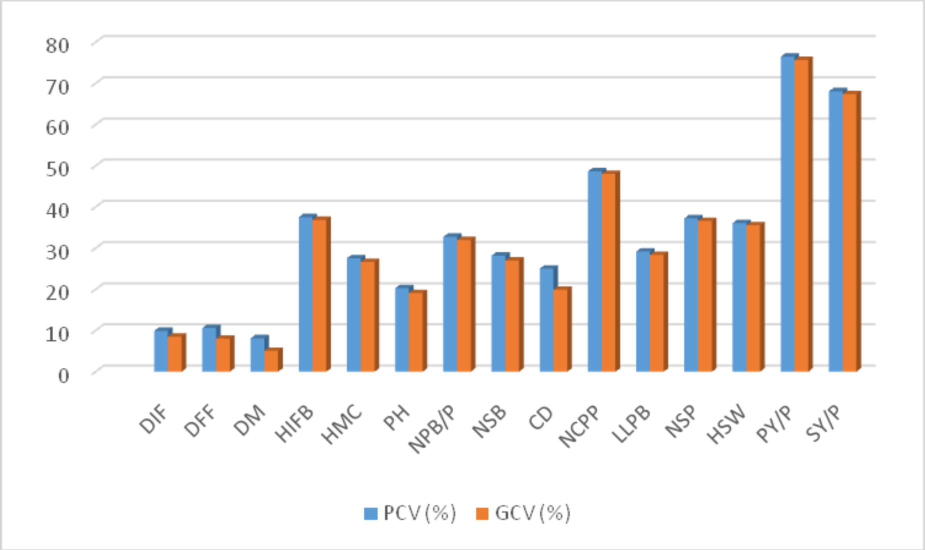

Fig. 1. PCV and GCV for 15 quantitative characters (pooled)

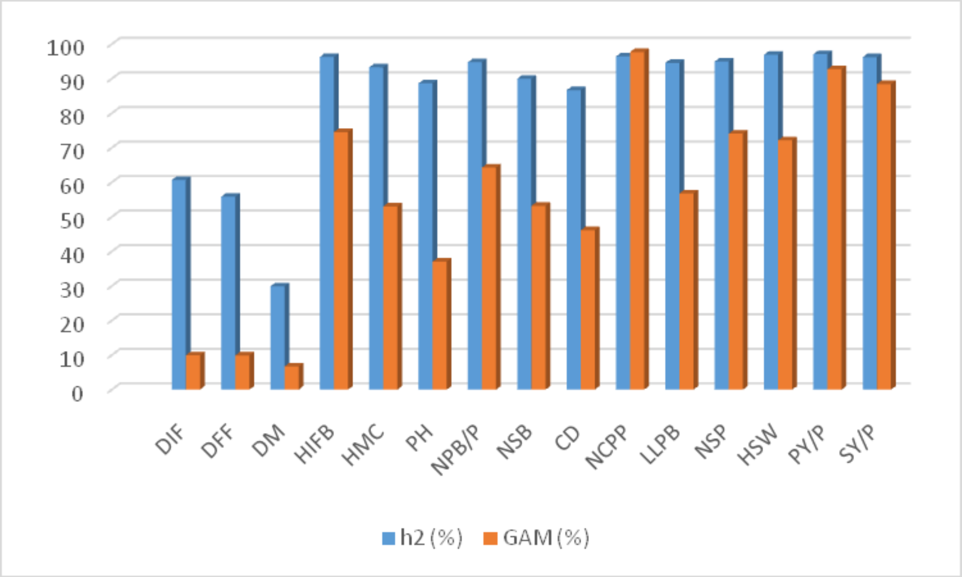

Fig. 2. Heritability and genetic advance as percent of mean (GAM) for 15 quantitative traits (pooled)

High heritability coupled with low GAM was observed fordays to initial flowering indicating the role of favourable environment rather than genotype and therefore, selection may not be rewarding.The same result was reported by Swarup and Singh, (2012). Days to 50% flowering coupled with moderate heritability and low GAM were predominantly governed by non-additive gene action and direct selection may not be possible because most of the variation is attributed to the environmental effects.Similar result wasreported by Pandey and Singh, (2012). Days to maturity showed lowheritability as well as low GAM and it may be governed by non-additive gene action. The same outcome was recorded by Pushpavalli and Kumar, (2017).

Seed yield is a complex character and is dependent on several contributing characters. As a result, character association was investigated in order to examine the link between yield and its components in order to improve the effectiveness of selection.Number of capitula/plant (0.718) and number of seeds/capitula (0.399)exhibited strong correlation with seed yield followed by plant height (0.374), number of primary branches/plant (0.265), capitulum diameter (0.323) and hundred seed weight

(0.258) (**Table 5**).This clearly implied that improvement for seed yield can be achieved if directional selection is practiced for these traits.Similar results were reported by Mali *et al.* (2022) and Bahmankar *et al.*(2014).Positive but non-significant association of seed yield/plant was observed with height of insertion of first branch (0.109), number of secondary branches/plant (0.114), length of longest primary branches/plant (0.235) and petal yield/plant (0.251). The characters days to initial flowering (-0.034), days to 50% flowering (-0.032) and days to maturity (-0.033) were negatively correlated with seed yield/plant which indicates selection for these traits should be made in opposite direction. Similar results were reported by Mokhtassi Bidgoli *et al.* (2006).

Inter correlation among yield components (**Table 5**) revealed that days to initial flowering was significant and positiveindirectcorrelation with days to 50% flowering and days to maturity.Similarly for days to 50% flowering, the days to maturity exhibited significant positive indirect correlation. Height upto main capitula was positively and significantly indirect correlated with plant height, number of primary branches/plant, capitulum diameter, length of the longest primary branches, number of seeds/capitulum and seed yield/plant. The plant height was positively and significantly indirectly correlated with number of primary branches/plant, capitulum diameter, number of capitula/plant, length of the longest primary branches, number of seeds/capitulumand seed yield/plant.Number of primary branches/plant was positively and significantlyindirect correlated with number of capitula/plant, length of the longest primary branchesand seed yield/plant. The capitulum diameter was positively and significantly indirectly correlated with number of seeds/capitulumand seed yield/plant.Number of capitulum/plant and number of seeds/capitulum had positive and significant indirect correlation with petal yield/plant. These results are in contrary to Rathod *et al.* (2021), Mali *et al.* (2022) and Valli *et al.* (2016).

Correlation simply measures the mutual association without any regard to causation, while path coefficientanalysis provides direct and indirect causes of association (**Table 6**).The quantitative traits *viz.,* number of capitula/plant (0.7059), number of seeds/capitulum (0.5917), hundred seed weight (0.5043) and petal yield/plant (0.3498) showed high, positive and direct effect on seed yield/plantindicating that these were the major yield contributing traits in safflower.Days to maturity (0.0056), height upto main capitulam (0.0174), plant height (0.0215) and length of the longest primary branches (0.0723) exhibited negligible, positive and direct effect over the yield. Days to initial flowering (-0.0142), days to 50% flowering (-0.0126), height of insertion of first branch (-0.0602), number of primary branches/plant (-0.0350), number of secondary branches/plant (-0.0394) and capitulum diameter (-0.0142)contributed negligible, negative and direct effect over the yield.

The positive indirect effect of petal yield/plant was observed to be high with number of capitulum/plant (0.3268); moderate with number of seeds/capitulum (0.2213). The positive indirect effect of number of capitula/plant was observed to be moderate withnumber of primary branches/plant (0.2982) and plant height (0.2127); low with number of secondary branches (0.1673), height up to main capitulum (0.1489) and capitulum diameter (0.1054). The number of seeds/capitulm exhibited moderate positive indirect effect with capitulum diameter (0.2155); low positive indirect effect with plant height (0.1707)

Table 5. Genotypic correlationcoefficient among fifteen quantitative traits in safflower genotypes

	DIF	DFF	DM	HIFB	HMC	PH	NPB/P	NSB/P	CD	NC/P	LLPB	NS/C	HSW	PY/P	SPY
DIF	1.000														
DFF	0.696**	1.000													
DM	0.622**	0.642**	1.000												
HIFB	0.124	0.137	0.124	1.000											
HMC	0.043	0.031	0.037	0.238	1.000										
PH	0.159	0.153	0.129	0.239	0.703**	1.000									
NPB/P	-0.077	-0.080	-0.070	-0.017	0.266*	0.362**	1.000								
NSB	-0.087	-0.098	-0.085	0.034	0.019	0.135	0.217	1.000							
CD	0.097	0.109	0.075	0.053	0.306*	0.443**	0.158	-0.048	1.000						
NC/P	-0.063	-0.053	-0.064	0.088	0.225	0.325*	0.284*	0.188	0.184	1.000					
LLPB	0.228	0.238	0.228	0.171	0.288*	0.386**	0.269*	0.176	0.134	0.095	1.000				
NS/C	0.125	0.129	0.114	0.037	0.356**	0.400**	0.132	-0.104	0.521**	0.099	0.149	1.000			
HSW	-0.100	-0.094	-0.095	0.097	0.016	-0.120	0.016	0.085	-0.083	-0.092	0.069	-0.291	1.000		
PY/P	-0.159	-0.152	-0.160	-0.149	0.246	0.247	0.374	0.071	0.197	0.805**	0.127	0.529**	-0.239	1.00	
SPY	-0.034	-0.032	-0.033	0.109	0.327*	0.374**	0.265*	0.114	0.323*	0.718**	0.235	0.399**	0.258*	0.251	1.000

** Significant at 1% level; * Significant at 5% level

Table 6. Path analysis direct (diagonal) and indirect effects of fifteen characters on seed yield/plant in safflower genotypes

	DIF	DFF	DM	HIFB	HMC	PH	NPB/P	NSB	CD	NCP/P	LLPB	NS/C	HSW	PY/P	SY/P
DIF	-0.0142	-0.0174	0.0085	-0.0095	0.0050	0.0039	0.0024	0.0059	-0.0051	-0.0510	0.0220	0.0770	-0.0464	-0.0640	-0.0188
DFF	-0.0176	-0.0126	0.0084	-0.0096	0.0047	0.0037	0.0024	0.0065	-0.0047	-0.0559	0.0213	0.0818	-0.0498	-0.0629	-0.0214
DM	-0.0207	-0.0212	0.0056	-0.0104	0.0044	0.0047	0.0017	0.0069	-0.0076	-0.0532	0.0251	0.0963	-0.0534	-0.0713	-0.0219
HIFB	-0.0009	-0.0024	0.0009	-0.0602	0.0222	0.0034	0.0062	0.0049	-0.0047	-0.0148	0.0045	-0.0278	0.0558	-0.0836	-0.0128
HMC	-0.0007	-0.0026	0.0006	-0.0123	0.0174	0.0180	-0.0125	-0.0037	-0.0049	0.1489	0.0232	0.1463	0.0276	0.1052	0.3454
PH	-0.0020	-0.0044	0.0017	-0.0093	0.0072	0.0215	-0.0137	-0.0042	-0.0097	0.2127	0.0284	0.1707	-0.0215	0.1041	0.3775
NPB/P	-0.0003	0.0012	-0.0009	0.0025	0.0128	0.0111	-0.0350	-0.0119	-0.0016	0.2982	0.0243	0.0380	0.0102	0.1715	0.3487
NSB	0.0014	0.0018	-0.0008	0.0074	0.0023	-0.0030	-0.0100	-0.0394	-0.0015	0.1673	0.0121	-0.0294	-0.0008	0.0866	0.1073
CD	-0.0017	-0.0015	0.0007	0.0075	-0.0148	0.0069	-0.0032	-0.0065	-0.0142	0.1054	0.0103	0.2155	-0.0371	0.0917	0.2673
NCP/P	-0.0022	0.0013	-0.0001	0.0115	-0.0071	0.0083	-0.0203	-0.0174	-0.0068	0.7059	0.0114	-0.0109	-0.0875	0.3268	0.5864
LLPB	-0.0045	-0.0040	0.0022	-0.0006	0.0082	0.0044	-0.0112	-0.0071	-0.0065	0.0666	0.0723	0.1215	0.0758	0.1365	0.3172
NS/C	-0.0029	-0.0023	0.0013	-0.0040	0.0064	0.0000	-0.0050	-0.0014	-0.0137	0.0261	0.0182	0.5917	-0.1159	0.2213	0.4987
HSW	0.0007	0.0011	-0.0008	-0.0096	0.0092	-0.0027	-0.0014	-0.0006	0.0028	-0.0701	0.0075	-0.1411	0.5043	-0.0495	0.2995
PY/P	-0.005	0.003	-0.001	0.0126	-0.0119	0.0221	-0.0201	-0.0098	-0.0009	0.3290	0.0164	0.1681	-0.1444	0.3498	0.7077

Residual effect = 0.2255

and height up to main capitulum (0.1463).The traits, number of capitula/plant, number of seeds/capitulum and hundred seed weight exhibited high direct effects on yield appeared to be the main reasons for their strong association with grain yield. Hence, direct selection for these traits would be effective.Rathod *et al.* (2021), Mali *et al.* (2022) and Divya *et al.* 2022 also reported similar results. In the present study, the residual effect is 0.2255 showing that the characters involved in current study contributed almost 78% of variability influencing to the dependent variable i.e., seed yield/plant.

Higher values of PCV were observed than GCV, though the difference was very narrow between them for almost all the traits studied indicating the least influence of the environment.However, the characters, seed yield/plant, number of capitula/plant, plant height and height upto main capitula showed a wide range of variation. High heritability with high GAM was expressed by most of the traits except flowering traits. Due to a significant and positive association with yield, the traits, number of capitula/plant, number of seeds/capitulum, height up to the main capitulum, plant height, number of primary branches/plant, capitulum diameter, and hundred seed weight have to be considered as major characters while selecting the genotypes for yield improvement. Direct positive association towards grain yield was contributed by the traits number of capitula/plant,number of seeds/capitulum, hundred seed weight and petal yield/plant. Selection for these traits would be effective to enhance the yield potential of seed and petals.

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