Genetic variability and character association studies in trait specific safflower (*Carthamus tinctorius* L.) germplasm lines.

Abstract

Sixty one safflower trait specific germplasm were evaluated in a Randomized Block Design (RBD) at ICAR- IIOR, during rabi 2023-24 to determine the genetic variability, heritability and genetic advance, character association and path analysis studies for twelve quantitative traits. Analysis of variance showed that significant variation was present in the genotypes studied for all the traits. The phenotypic coefficient of variation was found to be higher than the genotypic coefficient of variation for all the traits. High level of GCV and PCV was recorded for seed yield per plant, number of seeds per primary capitula. Heritability was high for days to 50% flowering, days to maturity, plant height, no.of capitula per plant, capitula diameter, no. of seeds per primary capitula,1000 seed weight, plant dry weight , seed yield, harvesting index, oil content. GA (% mean) was high for all the traits except for days to maturity. High heritability coupled with high genetic advance as percent of mean was recorded for days for flowering, plant height, no.of capitula per plant, capitula diameter,1000 seed weight, plant dry weight, seed yield, harvesting index, oil content. The character's productive branches per plant, no.of capitula per plant,1000 seed weight, plant dry weight, harvesting index showed a positive significant correlation with the total yield. The path coefficient analysis indicates that the utmost positive direct effect on total yield was plant dry weight. Hence, it was concluded that selection for traits The plant dry weight, harvesting index, oil content, days to maturity, no. of capitula per plant, no.of seeds per primary capitula, 1000 seed weight and capitula diameter beneficial in yield improvement programs of safflower.

Keywords: Safflower, trait-specific germplasm, Character association, Path analysis, heritability, genetic advance

1. Introduction

Safflower (*Carthamus tinctorius* L.) is an annual oil-seed crop with several uses, which includes natural dyes, pharmaceuticals, and vegetable oil. Safflower has a wide variety of agroclimatic adaptations and is thought to have originated in the Fertile Crescent around 4000 years ago. Safflower has emerged as an important source for the production of edible oils, primarily due to its high-quality oil, which contains a substantial proportion of oleic and linoleic acid (70–75%). This fatty acid is particularly beneficial for lowering blood cholesterol levels. Intensive breeding programs in safflower has resulted in increased seed and oil yielding cultivars with narrow genetic base (Kadirvel *et al*. 2017). Currently, safflower is commercially grown in 15 countries including

India, Mexico, Iran, Egypt, Pakisthan, USA, Argentina and Mediterranean countries. In India, it is grown in an area of 1.09 lakh ha, with a production of 90000 tonnes and productivity of 826kg/ha and in Telangana is 9000ha, 8000 tonnes, 900 kg/ha (Indiastat 2023-24). In India, it is mainly cultivated in Karnataka, Maharashtra, Telangana, etc. Safflower is grown as a rainfed crop during rabi in Vikarabad, Sangareddy, Nizamabad, Kamareddy and Nirmal districts in Telangana. The productivity is still low and there is a need to improve yield traits.

To improve the qualitative traits in seed yield and oil content, it is crucial to understand genetic nature, association and heritability of the traits. Studies on correlation coefficients provide valuable insights into the nature and strength of associations among different traits, while path coefficient analysis elucidates the direct and indirect effects of these traits on one another, thereby establishing causal relationships between variables. Understanding variability, heritability, and genetic advance is fundamental for the effective utilization of genetic resources and is critical for the success of plant breeding programs which aimed at developing future varieties with a broad genetic base. Information on variability is useful in assessing the genetic composition of germplasm and predicting the potential genetic gains. Hence the present investigation has been carried out to assess the magnitude of phenotypic and genotypic variability, phenotypic coefficient of variation and genotypic coefficient of variation, heritability in broad sense, correlation coefficient and path analysis among safflower genotypes.

2. Materials and methods

The experiment was conducted at the ICAR-Indian Institute of Oilseeds Research (ICAR-IIOR), Rajendranagar, Hyderabad. The city is nestled on the Deccan Plateau and is positioned at a 17°15’16’’ N latitude and 78°18’30’’ E longitude during Rabi, 2023-24. Sixty one trait specific germplasm lines (includes high seed yield, oil content, biotic and abiotic stress tolerant lines) were evaluated in an Randomized block design (RBD) with three replications and all recommended agronomic practices were adopted to raise a good crop. The genotypes were evaluated for the following traits: days to 50% flowering (DFF), days to maturity (DTM), plant height (PH) (cm), number of branches per plant (PBP), number of capsules per plant (NCP), capitula diameter (CD)(cm), no. of seeds/primary capitula (NSC), 1000 seed weight (TWT) (g), plant dry weight (PWD) (g), seed yield per plant (SY) (g), harvest index (HI) and oil content (OC) (%). The analysis of variance for the design of the experiment was carried out according to the procedure outlined by Panse and Sukhatme *et al.* (1985). The phenotypic and genotypic coefficients of variation were estimated according to the method suggested by Burton and de Vane *et al.* (1953). Broad sense heritability (h2) expressed as the percentage of the ratio of the genotypic variance (σ2g) to the phenotypic variance (σ2p) and was estimated on genotype mean basis as described by Allard *et al.* (1960). and Genetic advance (GA) and Genetic advance percent of mean (GAM), assuming selection of superior 5% of the genotypes was estimated in accordance with the methods illustrated by Johnson *et al.* (1955). Variance and covariance components for each pair of characteristics were estimated using the methods of Al-Jibouri *et al.* (1958) to calculate phenotypic and genotypic correlation coefficients. The significance of correlation coefficients was tested by comparing the estimated values with table values at 5 percent and 1 percent significant levels. Path coefficient analysis, as proposed by Wright *et al.* (1921). and detailed by Dewey and Lu *et al.* (1959) was used to distinguish the direct and indirect effects of independent factors on the dependent variable. Analysis of variance was performed by using the INDOSTAT software.

3. Results and Discussions

1) Genetic variability parameters

The analysis of variance showed significant differences among the genotypes for all the traits viz., days to 50% flowering, days to maturity, plant height, number of branches per plant, number of capitula per plant, capitula diameter, number of seeds per primary capitula, 1000 seed weight, plant dry weight, harvesting index, oil content and seed yield per plant and oil content indicating the presence of considerable genetic variability among the experimental material under study reported similarly by Bahmankar *et al.*,(2014) (Table 1).

The value of Genotypic Coefficient of variation (GCV) ranged from 6.22 for days to maturity to 64.71 for no. of seeds per primary capitula. High GCV was observed for no. of seeds per primary capitula (64.71), seed yield (38.54). Tariq et al.,(2014) reported high GCV for seed yield , Shivani *et al.*,(2011) and Kattab *et al.*,(2018) also reported higher estimates of GCV for seed yield per plant and number of seeds per primary capitula. Moderate GCV was observed for harvesting index. Tahernezhad *et al.*,(2018) also reported moderate GCV for harvesting index. Low GCV was observed for days to maturity which was also reported by Shivani *et al.,* (2011) Tahernezhad *et al.*,(2018) and Khattab *et al.*,(2018)

The Phenotypic Coefficient of Variation (PCV) was found high for. no. seeds per primary capitula (67.49), seed yield (39.91),productive branches per plant (32.88), plant dry weight (32.45) no.of capitula per plant (31.74) ,1000 seed weight (31.51), harvesting index (21.87) ,oil content (21.3), plant height (20.6), capitula diameter (14.45), days for 50% flowering (10.63), days to maturity (6.45). Moderate PCV was observed for days to 50% flowering, capitula diameter. Low PCV was observed for days to maturity which was similarly reported by Tariq *et al*., (2014) The

PCV estimates were higher than the GCV for all traits studied, indicating the additive influence of the environment on trait expression. These findings suggest that selection based on these traits could be effective, with their phenotypic expression serving as a reliable indicator of their genetic potential. According to Shivani *et al*.,(2011) Tahernezhad *et al*.,(2018) and Khattab *et al*.,(2018) days to maturity showed low genotypic and phenotypic coefficient of variation.

High heritability was obtained for 1000 seed weight (99.3), days for 50% flowering (98.6), plant dry weight (96.7), plant height (95.6), oil content (94.7) seed yield (93.3), days to maturity (93), no. seeds per primary capitula (92.0), no. of capitula per plant (81.1), capitula diameter (78.1), harvesting index (67.7). Similar results are also reported by Khattab *et al*., (2018) and Sathees *et al*., (2023). moderate heritability was reported in productive branches per plant.

The highest estimate of genetic advance as percent of mean was recorded for number of seeds per primary capitula (127.85), seed yield (76.67), plant dry weight (64.64),1000 seed weight (64.46), no .of capitula per plant (53.03), oil content (41.53), plant height (40.57), productive branches per plant (38.36), harvesting index (30.51), capitula diameter (23.26), days for 50% flowering (21.6) Sathees *et al*.,(2023) and Neelima *et al* ., (2021) also reported highest estimate of genetic advance as percent of mean for these traits. High heritability coupled with high genetic advance as percent of mean was recorded for days to 50% flowering, plant height, no. capitula per plant, capitula diameter, no. seeds per primary capitula, 1000 seed weight, productive branches per plant, seed yield, harvesting index and oil content showed that these traits were controlled by additive genetic influences. Similar results are also reported by Shivani *et al*., (2011), Pushpavalli *et al*., (2017), Khattab *et al*., (2018), Neelima *et al*., (2021), Sathees *et al*., (2023). found high heritability with high genetic advance on oil content.

2) Character association studies

Seed yield is a complex trait governed by a multitude of characteristics, and genetic diversity in these traits is crucial for breeders aiming to enhance yield potential. In this investigation, correlation and path coefficient analyses were employed to explore the associations among yield-related traits and their connection to overall yield.

Yield is a multifaceted trait influenced by various contributing characters that can exhibit positive or negative associations both with yield and among themselves. The correlations computed using the Pearson correlation coefficient offer valuable insights for indirect selection strategies to enhance seed yield. The results of the Pearson correlation analysis depict relationships between yield and its contributing characters (Table 2).

The results revealed that the traits productive branches per plant (0.37**), no. of capitula per plant (0.69**), 1000 seed weight (0.32*), plant dry weight (0.83**), harvesting index (0.58**) have the significant positive correlation with the seed yield indicating that these attributes were influencing more on seed yield in safflower and therefore selection for these traits will improving seed yield. A non-significant positive correlation was registered for the plant height (0.02), oil content (0.13) and capitula diameter (0.16) and plant height (0.02) while days to 50 percent flowering(-0.16) exhibited a non-significant negative correlation with seed yield and significant negative correlation was seen in days to maturity(-0.26*) which is similarly reported by Pattar *et al.*, (2020) and it is highly useful in developing short-duration varieties that require negative selection for flowering without compromising the seed yield. These kinds of correlations were similar to the findings of Shivani *et al*., (2011), Dambal *et al*., (2015), Sirel *et al*., (2016), Pushpavalli *et al.*, (2017), Muhammad *et al*., (2020), Dhage *et al.*, (2020), Mali *et al,* (2022), Sathees *et al.*, (2023), and Naziha *et al.*, (2023).

To gain a comprehensive understanding and enable effective manipulation of the characters, path coefficients were employed alongside correlation coefficients. Path analysis allows for the dissection of correlations into direct and indirect effects, providing insights into the relative significance of the causal factors involved (Dewey and Lu, 1959). In the present study, twelve characters were taken and partitioned into direct and indirect effects using seed yield per plot as a dependent variable. The information about the direct and indirect effects of eleven variables on seed yield per plot in sixty one germplasm lines of safflower is described below (Table 3, Figure 1).

The plant dry weight (0.8239) and harvesting index (0.5316) have a high positive direct effect on seed yield, while days to maturity (0.0619), oil content (0.0523), no.of seeds per primary capitula (0.0337) plant height (0.0184) and 1000 seed weight (0.0107), no. of capitula per plant (0.0030), have a low positive direct effect on seed yield. Due to the positive direct effect on seed yield these traits can be considered for selections in crop improvement program of safflower. Days to 50 percent flowering (-0.0737), number of branches per plant (-0.0600) and capitula diameter (-0.0526) have negative direct effects. Golkar *et al.*, (2011), Dambal *et al.*, (2015), Pushpavalli *et al.*, (2017), Neelima *et al*., (2021), Sathees *et al.*, (2023) findings were similar to the present study. Residual effect was recorded as 0.038, which indicates maximum variability was contributed by the studied traits for the seed yield in safflower.

4. Conclusion:

Greater genetic variability enhances the likelihood of selecting superior genotypes. High estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) on seed yield per plant, number of capitula per plant, number of branches per plant, no. seeds per primary capitula ,1000 seed weight, plant dry weight, oil content, harvesting index and plant height gives us an idea about the magnitude of variability present in these characters in the germplasm lines. High heritability along with high genetic advance as percent of mean for days for 50% flowering, capitula diameter, seed yield per plant, 1000 seed weight, number of capitula per plant, number of seeds per primary capitula, plant dry weight, harvesting index, oil content and plant height indicated additive gene action predicting genetic gain under selection than heritability estimates alone. Correlation studies revealed that traits productive branches per plant, no. of capitula per plant, 1000 seed weight, plant dry weight, harvesting index define seed yield of safflower where path analysis revealed that plant dry weight and and harvesting index showed high direct positive effect on seed yield. Therefore, plant breeding efforts should focus on manipulating existing genetic diversity in the desired direction through appropriate crop improvement programs to develop safflower with enhanced seed yield and oil content.

FUTURE SCOPE

Through comprehensive research on genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), genetic advance as a percentage of mean, heritability, correlation, and path coefficient analysis, key desirable traits for yield enhancement in safflower have been identified. These findings provide critical insights for improving seed yield and oil content simultaneously in future safflower breeding programs.

Source of Variation	Mean sum of squares												
	df	DFF	DTM	PH (cm)	PBP	NCP	CD (cm)	NSC	TWT	PDW	SY(g)	HI (%)	OC
Replications	**2**	1.52	1.66	5.39	0.04	0.2	2.25	0.58	0.89	8.94	1.29	4.14	0.11
Genotypes	**60**	188.28**	147.34 **	803.22**	16.14**	136.98**	21.53**	201.9**	747.03**	1335.07*	115.73**	68.29**	121.89 **
Error	**120**	0.90	3.6	12.09	3.28	9.88	1.84	5.69	1.81	15.06	2.73	8.84	2.24
Total	**182**	62.68	50.98	274.19	7.49	51.67	8.34	70.32	247.48	450.16	39.97	27.07	41.66

TABLE 1: Analysis of variance of sixty one genotypes of safflower

*-Significance at 5% level of probability

**-Significance at 0.1% level of probability

Table 2. Genetic parameters for yield components in sixty one genotypes of safflower

S.No.	Trait	Range		Mean±SEm	Variance		Coefficient of Variation		h^2 (%)	GAM (%) at5%
		Min	Max		Genotypic	Phenotypic	GCV (%)	PCV (%)		
1	Days for 50% flowering	64.33	103.33	74.87±**0.54**	62.46	63.37	10.55	10.63	98.6	21.6
2	Days to maturity	95.66	127.66	111.27±**1.08**	47.93	51.52	6.22	6.45	93.0	12.36
3	Plant height (cm)	60.23	153.86	80.63±**2.0**	263.71	275.80	20.14	20.6	95.6	40.57
4	Productive branches per plant	4.33	14.00	8.36±**1.03**	4.29	7.57	24.74	32.88	56.6	38.36
5	Number of capitula/plant	9.8	46.93	22.77±**1.8**	42.37	52.24	28.59	31.74	81.1	53.03
6	Capitula diameter (cm)	14.45	26.43	20.05±**0.8**	6.56	8.40	12.77	14.45	78.1	23.26
7	No. of seeds per primary capitula	0	46.33	12.5±**1.37**	65.40	71.1	64.71	67.47	92.0	127.85
8	1000 seed weight (g)	20.46	82.50	50.19±**0.8**	248.41	250.22	31.40	31.52	99.3	64.46
9	Plant dry weight (g)	28.03	124.83	65.74±**2.2**	440.00	455.06	31.91	32.45	96.7	64.64
10	Seed yield (g)	5.73	32.06	15.92±**0.94**	37.67	40.4	38.54	39.91	93.3	76.67
11	Harvesting index (%)	14.35	36.46	23.87±**1.7**	18.49	27.32	18.01	21.9	67.7	30.51
12	Oil content (%)	21.58	45.04	30.47±**0.86**	39.88	42.13	20.72	21.3	94.7	41.53

	DFF	DTM	PH (cm)	PBP	NCP	CD (cm)	NCP	TWT	PDW	HI (%)	OC	SY(g)
DFF	**1.00**	0.73**	0.68 **	-0.10	-0.25	0.26 *	0.60 **	-0.29 *	-0.15	-0.04	-0.07	-0.16
DTM		**1.00**	0.50 **	-0.21	-0.32 *	0.13	0.53 **	-0.27 *	-0.28 *	-0.09	-0.30 *	-0.26*
PH (cm)			**1.00**	-0.06	-0.07	0.22	0.57**	-0.21	0.08	-0.10	-0.09	0.02
PBP				**1.00**	0.53 **	-0.18	-0.14	0.45 **	0.43 **	0.14	-0.22	0.37 **
NCP					**1.00**	-0.04	-0.25	0.41**	0.80 **	0.12	0.05	0.69 **
CD (cm)						**1.00**	0.51 **	-0.23	0.14	0.10	0.21	0.16
NSC							**1.00**	-0.38 **	-0.10	0.08	0.14	-0.02
TWT								**1.00**	0.35 **	0.13	-0.28 *	0.32 *
PDW									**1.00**	0.09	0.05	0.83 **
HI (%)										**1.00**	0.09	0.58 **
OC											**1.00**	0.13
SY(g)												**1.00**

Table 3: Correlation coefficients of yield attributing traits in safflower germplasm lines

**Significant at 0.5% level of probability ; * Significant at 5% level of probability

Table 4: Path coefficient analysis of yield attributing traits in the germplasm lines of safflower studied during *Rabi 2023-24*

	DFF	**DTM**	**PH**	**PBP**	**NCP**	**CD**	**NSC**	**TWT**	**PDW**	**HI**	**OC**
DFF	**-0.0737**	-0.0547	-0.0503	0.0082	0.0189	-0.0206	-0.0453	0.0221	0.0113	0.0031	0.0052
DTM	0.0459	**0.0619**	0.0318	-0.0151	-0.0208	0.0083	0.0340	-0.0171	-0.0176	-0.0067	-0.0192
PH	0.0126	0.0095	**0.0184**	-0.0015	-0.0013	0.0042	0.0106	-0.0039	0.0016	-0.0020	-0.0018
PBP	0.0067	0.0147	0.0048	**-0.0600**	-0.0374	0.0144	0.0102	-0.0301	-0.0292	-0.0088	0.0151
NCP	-0.0008	-0.0010	-0.0002	0.0018	**0.0030**	-0.0001	-0.0008	0.0013	0.0025	0.0004	0.0001
CD	-0.0147	-0.0070	-0.0119	0.0126	0.0022	**-0.0526**	-0.0291	0.0124	-0.0074	-0.0071	-0.0116
NSC	0.0207	0.0185	0.0194	-0.0057	-0.0091	0.0186	**0.0337**	-0.0130	-0.0035	0.0029	0.0049
TWT	-0.0032	-0.0029	-0.0023	0.0053	0.0045	-0.0025	-0.0041	**0.0107**	0.0037	0.0014	-0.0031
PDW	-0.1263	-0.2346	0.0721	0.4010	0.6936	0.1166	-0.0863	0.2896	**0.8239**	0.0931	0.0411
HI	-0.0227	-0.0575	-0.0589	0.0781	0.0690	0.0716	0.0457	0.0702	0.0600	**0.5316**	0.0567
OC	-0.0037	-0.0162	-0.0051	-0.0131	0.0024	0.0116	0.0076	-0.0150	0.0026	0.0056	**0.0523**
SY	-0.1591	-0.2694	0.0180	0.4116	0.7251	0.1696	-0.0239	0.3271	0.8479	0.6134	0.1398
Partial R	0.0117	-0.0167	0.0003	-0.0247	0.0021	-0.0089	-0.0008	0.0035	0.6986	0.3261	0.0073

R SQUARE = 0.9986; RESIDUAL EFFECT = 0.038

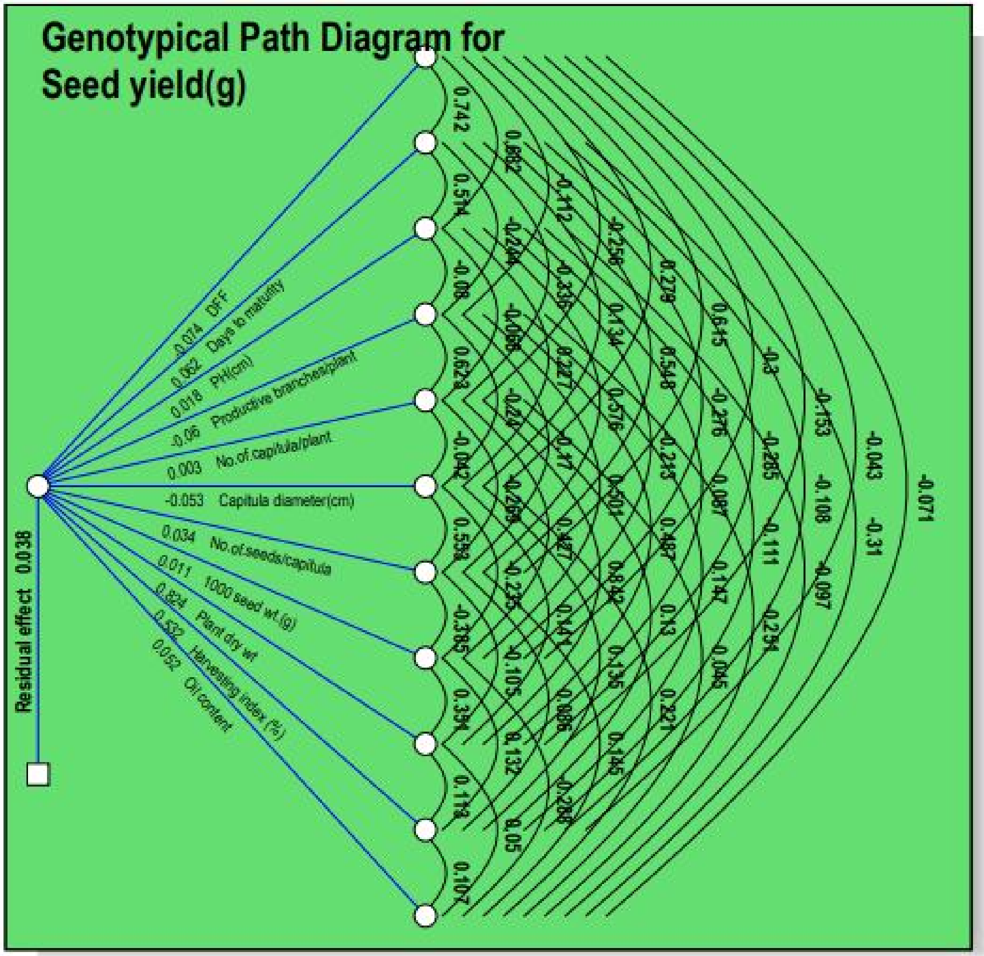

Fig. 1. Genotypical path diagram of various traits with seed yield per plot in safflower.

References:

Al-Jibouri, H. A., Miller, P. A and Robinson, H. F. 1958. Genotypic and environmental variation and correlation in upland cotton cross of interspecies origin. *Agronomy Journal.* 50: 633-636.

Allard RW. Principles of Plant Breeding. John Wiley & Sons, New York, 1960.

Bahmankar, M., Nabati, D.A and Dehdari, M. 2014. Correlation, multiple regression and path analysis for some yield-related traits in safflower. *Journal of Biodiversity and Environmental Sciences*. 4 (2): 111-118.

Burton, C. W and De Vane, E. H. 1953. Estimating heritability in tall Festuca (Restucaarundinacae) from replicated clonal material. *Agronomy Journal.* 45: 1476-1481.

Dambal, G.I and Patil, R.S. 2015. Correlation and path analysis in safflower germplasm (*Carthamus tinctorius* L.).

Dewey, J. R and Lu, K. H. 1959. Correlation and path coefficient analysis of components of crested wheat grass seed production. *Agronomy Journal.* 51: 515- 518.

Dhage, P., Ratnaparkhi, R.D., Sonone, M and Fatak, S. 2020. Correlation studies in safflower (*Carthamus tinctorius* L.) for seed yield and yield related traits. *International Journal of Chemical Studies*. 8 (4): 2515-2517.

Golkar, P., Arzani, A and Rezaei, A.M. 2011. Determining relationships among seed yield, yield components and morpho-phenological traits using multivariate analyses in safflower (*Carthamus tinctorious* L.). *Annals of Biological Research*. 2 (3): 162-169.

Indiastat. 2023-2024. https://www.indiastat.com/default.aspx

Johnson, H. W., Robinson, H. F and Comstock, R. E. 1955. Estimates of genetic and environmental variability in Soybean. *Agronomy Journal.* 47: 314-318

Kadirvel, P., Ravi, D., Mukta, N., Montoya-Coronado, M.C.L., Ghuge, S.B., Singh, J., Singh, V., Shinde, S.K., Deshmukh, S.N., Yadav, P and Varaprasad, K.S. 2017. Genetic distinctiveness of safflower cultivars of India and Mexico as revealed by SSR markers. *Plant Genetic Resources*. 15 (6): 474-487.

Khattab, M.N. 2018. Variance, heritability, genetic advance and correlation of some phonological, morphological and productivity traits in some safflower (*Carthamus tinctorius* L.) genotypes. *Syrian J Agric Res (SJAR)*. 5 (4): 297-307.

Mali, B.B., Wadikar, P.B., Gorte, A.S and Yadav, U.V. 2022. Relationship among traits using correlation and path coefficient analysis in safflower (*Carthamus tinctorius* L.). *Journal of Agriculture Research and Technology*. 47: 39-42.

Muhammad, R.W., Ali, H.M.W., Hamza, A., Ahmad, M.Q., Qayyum, A., Malik, W and Noor, E. 2020. Estimation of Different Genetic Parameters in Various Safflower (*Carthamus tinctorius* L.) Genotypes under Field Condition. *Pakistan Journal of Agricultural Research*. 33(4).

Naziha, E.L and Kurt, O. 2023. Correlation and path coefficient analysis for seed yield and yield contributing components, phenological and some morphological traits in Safflower (*Carthamus tinctorius* L.). *International Journal of Phytology Research*. 3 (1): 01-06.

Neelima, S., Prabhakar, K and Ramanamma, K.V. 2021. Genetic variability, heritability, association and divergence studies in safflower (*Carthamus tinctorius* L.) genotypes. *Indian Society of Oilseeds Research*. 38: 265-269.

Panse, V. G and Sukhatme, P. V. 1985. Statistical methods for agricultural workers, ICAR, New Delhi.

Pattar, V.K and Patil, R. 2020. Correlation and path analysis in safflower (*Carthamus tinctorius* L.) genotypes. *Journal of Pharmacognosy and Phytochemistry*. 9 (4): 1717-1719.

Pushpavalli, S.N.C.V.L and Kumar, G. 2017. Study of genetic variability, correlation and path analysis of safflower genotypes. *Research Journal of Agricultural Sciences*, 8 (3): 706-709.

Sathees, N., Vanniarajan, C., Yuvaraja, A., Renuka, R and Mini, M.L. 2023. Genetic variability and character association studies among seed yield and yield component traits in safflower (*Carthamus tinctorius* L.) genotypes. *Electronic Journal of Plant Breeding*. 14 (1): 217-225.

Shivani, D., Sreelakshmi, C and Kumar, C.S. 2011. Genetic divergence and variability studies for yield and yield component traits in safflower. *Andra Agric J*. 5 (4): 419-423.

Sirel, Z and Aytac, Z. 2016. Relationships between the seed yield and some agronomic characteristics of safflower (*Carthamus tinctorius* L.) under semi-arid conditions. *Turkish Journal of Field Crops*. 21 (1): 29-35.

Tahernezhad, Z., Saba, J., Zeinalabedini, M., Pourdad, S.S and Ghaffari, M.R. 2018. Estimation of broad-sense heritability and variance components for seed yield and agronomic traits in native and exotic safflower (*Carthamus tinctorius* L.) genotypes. *Bangladesh Journal of Botany*. 47 (3): 501-508.

Tariq, M., Tariq, M.A., Shah, M.K.N., Ijaz, M., Hassan, M.F., Aftab, M., Aadal, N.K and Hussain, T. 2014. Genetics and interrelationship of yield and yield related attributes in some genotypes of safflower (*Carthamus tinctorius* L.) under rainfed conditions. *Genetics*. 4 (3): 1-8.

Wright, S. 1921. Correlation and causation. *Journal of Agricultural Research*. 20: 557-585.