Agricultural Sciences Journal
Available online at http://asj.mnsuam.edu.pk/index.php
ISSN 2707-9716 Print
ISSN 2707-9724 Online
https://doi.org/10.56520/asj.v6i3.423

Research Article

ASSESSMENT OF GENETIC DIVERSITY BY USING AGROMORPHOLOGICAL PARAMETERS IN LOCAL SAFFLOWER GENOTYPES UNDER RAINFED CONDITIONS OF POTHOHAR, PAKISTAN

Saadia[1], Ghulam Nabi[1], Muhammad Rizwan[2*], Muhammad Zeeshan[3], Wardah Muzaffar[2], Amjad Farooq[4], Muhammad Imran Khan[3], Jehanzeb Farooq[4], Hafiz Ghazanfar Abbas[4], Iram Sharif[4], Muhammad Asif[4]

[1]Groundnut Research Station, Attock, Pakistan
[2]Gram Breeding Research Sub-Station, Attock, Pakistan
[3]Barani Agricultural Research Station, Fatehjang, Pakistan
[4]Cotton Research Station, AARI, Faisalabad, Pakistan
**Corresponding Authors: muhammadrizwan29@gmail.com*

Abstract

Safflower (*Carthamus tinctorius* L.) is well known oilseed crop, cultivatedin major pockets of the world for superior quality vegetable seed oil. Study under discussion was planned to review Safflower germplasm (thirty-six lines) for genetic divergence by using agro-morphological parameters in rainfed environment. The research was organized using complete randomized design having three repeats in the 2022-23 Rabi growing season at Gram Breeding Research Sub-Station, Attock. Findings from variance analysis were significant among genotypeswith respect to days in flowers initiation, days for flower completion, days for maturity, plant height(cm), no. of capsules plant^{-1}, no. of branches plant^{-1}, 100 seed weight (g), plot yield, seed yield (kg/ha), oil contents (%), oil yield (kg/ha), biological yield (kg/ha), harvest index% and non-significant for days to maturity. The extent of Phenotypic variance co-efficient (PCV) was higher than Genotypic variance co-efficient (GCV) in almost all parameters. However, both values were same in biological yield and plot yield. Higher heritability together with higher genetic advance in biological yield, seed yield, and plot yield implied that genetic factors in comparison with environmental conditions are more effective and should be amenable to selection by breeders. As higher genetic variation was depicted in safflower germplasm for agro-morphological parameters. Therefore, it may be utilized in germplasm execution and potential safflower breeding objectives.

Keywords: *Safflower, heritability, genetic diversity, germplasm, rainfed*

(Received: 13- Sept-2024 Accepted: 22- Jan-2025) Cite as: Saadia., Nabi. G., Rizwan. M., Zeeshan. M., Muzaffar. W., Farooq. A., Khan. M. I., Farooq. J., Abbas. H. G., Sharif. I., Asif. M., 2024. Assessment of genetic diversity by using agromorphological parameters in local safflower genotypes under rainfed conditions of Pothohar, Pakistan. Agric. Sci. J. 6(3): 1-10

1. INTRODUCTION

Every year Pakistan imports 3-4 billion dollars of edible oil due to presence of disparity between local production and domestic oil consumption which creates a huge burden on national economy through its imports. Edible oil production has been a high priority in recent years. Cultivation of oilseed crops is essential to increase oil production and contribute to meet the local oil demands. Safflower (*Carthamus tinctorius*) is reported as most ancient and underutilized oilseeds crop that may be used as an alternative for oil production (Lira *et al*., 2021; Ali *et al*., 2020; Pavithra *et al*., 2015). According to an estimate, safflower is grown in twenty countries, covering 1,140,002 ha area and production of 948,516 tonnes (Ali *et al*., 2020). Major safflower producing countries include; Kazakastan, India, Mexico, Turkey, USA, China and Russia, (Pelin *et al*., 2020; Emongor and

Oagile, 2017). Moreover, America and Asia contributes to 93% of total Safflower production (Pelin *et al*., 2020). Safflower edible oil is human health friendly due to high levels of monounsaturated (oleic acid 11-87%) and polyunsaturated (linoleic acid 70-87%) fatty acids, that are much higher if compared with groundnut, olive, soybeans, corn and seed cotton (Reza *et al*., 2013). In recent years, demand of crop genotypes having high level of linoleic acid isincreased, owing to health benefits on human. Safflower is a drought and salt tolerant rabi crop and due to deep taproot system, it can also be grown successfully on soil with poor fertility and low irrigation (Hojati *et al*., 2011). It has been studied mainly in research centers (Lira *et al*., 2021), that exemplified the existence of genetic divergence among strains of Carthamus tinctorius (Pearl and Burke, 2014). The genetic assets and their assessment for genetic divergence in different crops species is very vital step to apply in plant breeding strategies i.e. selection, reduction of crossing cost and parental selection in hybridization programs. In any crop, existence of variation is one of the most important factor for evaluation of genotypes which can generate further variability and eventually helpful in selection of desirable genotypes (Kose *et al*., 2018). Generally, breeding program will be successful only if there is enough diversity in the germplasm for agronomically important traits which allow plant breeders for development of better performing varieties. Conventionally, both agronomic as well as morphological parameters are being used for measuring genetic divergence but infact many vegetative parameters are inclined by environment, due to which they show constant variation. Yield is the most important and complex quantitative trait influenced by different parameters. Therefore, direct selection will mislead for seed yield, while it will be more beneficial if researchers focus on a range of traits that contribute towards safflower yield asreportedly (Ali *et al*., 2020). Consideration of traits that indirectly contribute to seed as well as oil yield in existing safflower genotypes is very significant (Golparvar, 2011). Heritability is the extent to which a phenotype is genetically determined (Lourenco *et al*., 2017). It is usually estimated from phenotypic values of parameters that is attributable to the average effects of genes and environmental effects. Thus, heritability assessment seems very supportive for selecting appropriate strains amongst different environmental conditions, especially for those breeding programs which are designed to build up high-yielding strains (Tahernezhad *et al*., 2018). Generally in breeding programs, information regarding genetic advance and heritability is useful as it provide guideline for selecting promising lines (Bahmankar *et al*., 2014). Genotypes selection is considered as essential part of any research. Lack of variation between phenotypic and genotypic difference is the result of genetic factors and is less influenced by environmental factors. Therefore, this research was planned to evaluate genetic divergence among safflower genotypes based on different agronomic parameters by collecting and screening diverse genetic material. The superior genotypes may be incorporated in future breeding programs enabling the safflower plant breeders to maintain and improve the genetic makeup of their breeding material.

OBJECTIVES:

- The key intention of current study is estimation of genetic diversity and exploitation of its findings in selecting of desirable parents which will be utilized for scheduling and implementation of potential breeding agenda in safflower crop.

2. MATERIALS AND METHODS

The following research was executed to estimate genetic diversity, considering the importance of Safflower. Research was conducted at experimental farm of Gram Breeding Research Sub-Station, Attock, Pakistan during rabi season of 2022-23 under rainfed conditions. The experimental area was situated at 31° North latitude, 73° East longitude along with altitude of 184 m above sea and annual rainfall 528 mm. The research area soil was clay-loam, having less organic matter (0.61%), pH was 7.9, EC (0.25 dS/m), nitrogen (0.038 %), phosphorus (11.5 ppm) and potassium (145ppm). Thirty-six safflower genotypes cultivating in diverse climatic conditions of Pakistan were used. Design used was randomized complete block with three (03) replicates by maintaining row-to-row and plant-to-plant distances of 60 cm and 10 cm, respectively. Each of the studied plot consisted four (4) rows with length of 5m. All agronomic practices required time to time were adopted to maintain crop health. When crop reached at maturity, data regarding thirteen (13) yield related parameters was recorded which includes: No. of days upto (flower initiation, flower completion and maturity), plant height(cm), capsules plant^{-1}, branches plant^{-1}, 100 seeds wt (g), plot yield(g), seed yield (kg/ha), oil yield, oil contents (%), biological yield (kg/ha) and harvest index. Second and third rows of each one plot were used for determination of above mentioned traits. Oil contents in seed samples was determined by Nuclear magnetic resonance (NMR) apparatus. The calculated Oil contents were multiplied with seed yield to obtain oil yield of each strain. As analysis of variance determines the existence of significant differences in studied parameters while heritability estimates reflects the potential of studied genotypes and characters to respond to selection, so both these statistical techniques were used. To compute Analysis of variance (ANOVA), the statistical procedures defined by Steel *et al*., (1997) were followed; while for estimation of phenotypic (PCV), genotypic (GCV), coefficients of variance and broad sense heritability (h^2) were calculated using the technique formulated by Singh and Chaudhry (1985).

3. RESULTS AND DISCUSSION:

Data for all the thirteen traits were analyzed statistically. Means and least significant differences (Lsd) are presented inTable-1, while frequency distribution is depicted in Fig-1. The analysis confirmed the presence of substantial variation in studied genotypes which provide greater prospect of selection. Means of oil yield varied between 54.39 to 342.81 (kg ha^{-1}). The data of seed yield was maximum for genotype L-1 (1095.56 kg ha-1) followed by L- 30 (1019 kg ha^{-1}), while harvest index (%) was maximum for genotype L-1 (51%) followed by L-26 and L-30 (48%). Maximum oil content (34%) was depicted in genotypes L-3, L-19, L-23, L34 and L-36, while 100 seed weight was maximum for genotypes L-13 followed by L-10 and capsules plant^{-1} were maximum for Genotype L-12 (41) followed by L-1 (39) As reported by Ali *et al*., (2020), enough variation is important for the genetic studies as well as success of breeding programs. Ali *et al*., (2020) also reported significant results for No. of days upto (flower initiation, 50% flowering and flower completion), plant height, branches plant^{-1} and 100 seeds wt (g). Significant results for seed yield, harvest index, oil contents, 100 seed wt and capsules per plant were mentioned in previous studies of Muhammad *et al*., (2020).

Combined ANOVA exposed remarkable difference between the strains for days taken to (flower initiation, flower completion and maturity), plant height, capsules plant^{-1}, branches plant^{-1}, 100 seeds wt (g), plot yield, seed yield, oil contents, oil yield, biological yield, harvest index (%) and non-significant differences for days in maturity (Table 2). To increase seed yield and oil yield of safflower genotypes, the character's like branches plant^{-1}, Plant height, capsules plant-1, weight 100 seeds and oil content% are considered as imperative parameters (Hussain *et al*., 2014, Karimi *et al*., 2013; Golparvar, 2011a; Golkar *et al*., Topal *et al*., 2010 and Arslan, 2007). Higher variance

Table1: Mean and Least Significant difference (Lsd) value of different characters of thirty six Safflower genotypes

Sr. No.	Genotypes	DFI	DFC	DM	PH	BR/P	CAP/P	100SW	PY	SY	Oil	OY	BY	HI
1	L1	179	191	222	132	7	39	18	986	1096	31	343	2138	51
2	L2	185	192	223	194	6	19	10	846	940	33	308	2044	46
3	L3	180	195	226	173	6	18	13	557	619	34	208	1867	33
4	L4	178	190	188	191	6	14	21	681	757	33	247	1659	46
5	L5	177	190	221	199	6	25	18	730	811	32	258	1926	42
6	L6	176	191	222	188	5	17	17	856	951	32	302	2073	46
7	L7	175	189	214	168	5	12	16	659	732	33	241	2035	36
8	L8	178	188	213	177	5	21	15	363	404	33	132	1663	24
9	L9	177	191	216	175	8	35	18	335	372	30	113	1616	23
10	L10	178	190	221	180	6	23	22	549	610	27	164	1874	33
11	L11	173	194	223	191	6	24	17	631	701	31	219	1725	41
12	L12	172	192	222	164	8	41	16	195	217	31	68	927	23
13	L13	181	191	221	164	4	14	26	806	896	30	270	2027	44
14	L14	177	191	220	169	4	14	7	697	774	27	211	1742	44
15	L15	178	190	219	165	4	19	15	244	271	30	82	1388	20
16	L16	182	194	224	180	4	19	18	158	176	31	54	691	25
17	L17	178	189	219	199	5	28	16	385	428	32	138	1286	33
18	L18	179	193	222	172	5	22	15	667	741	33	246	1582	47
19	L19	178	190	220	188	5	23	15	676	751	34	252	1658	45
20	L20	183	193	222	170	3	14	12	748	831	31	259	1969	42
21	L21	180	189	219	198	3	11	10	706	784	33	261	1763	44
22	L22	182	190	221	185	4	16	17	580	644	33	211	1565	41
23	L23	181	192	223	178	5	15	18	683	759	34	255	1979	38
24	L24	181	191	222	182	4	12	16	301	334	32	106	1377	24
25	L25	177	189	217	187	6	25	11	172	191	31	59	1039	18
26	L26	178	188	216	171	5	19	16	860	955	33	313	1987	48
27	L27	175	187	216	130	5	18	16	697	775	33	252	1843	42
28	L28	176	184	215	186	7	37	11	376	418	33	136	1550	27
29	L29	177	188	217	175	4	17	14	816	907	33	297	2067	44
30	L30	176	187	215	180	3	14	18	917	1019	30	310	2108	48
31	L31	184	196	224	206	3	16	15	866	962	33	313	2099	46
32	L32	182	192	222	194	5	22	16	628	697	33	234	1570	44
33	L33	182	194	225	189	6	27	19	467	519	32	163	1466	35
34	L34	178	188	217	175	4	16	16	715	794	34	267	1956	41
35	L35	176	186	215	158	6	25	16	750	833	33	276	2080	40
36	L36	179	189	218	182	5	19	17	277	307	34	103	1371	22
Lsd		**3.56**	**3.52**	**16.86**	**12.49**	**0.67**	**3.41**	**0.59**	**37.47**	**13.88**	**0.71**	**5.97**	**50.81**	**2.61**

DFI: Days to Flower Initiation, DFC: Days to Flower Completion, DM: Days to maturity, PH: Plant height (cms),

BR/P: Number of branches per plant, CAP/P: Number of capsules / plant, 100SW: 100 seed weight(gms), PY: Plot Yield (gms),

SY: Seed Yield (kg/ha), Oil: Oil Content (%), OY: Oil Yield (Kg/ha), BY: Biological Yield (Kg/ha), HI: Harvest index(%).

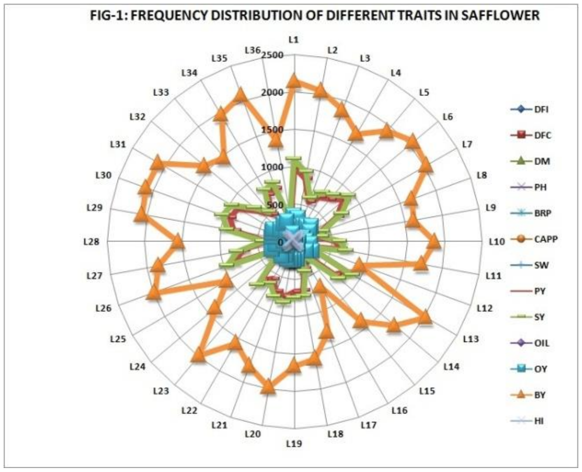
FIG-1: FREQUENCY DISTRIBUTION OF DIFFERENT TRAITS IN SAFFLOWER

was mentioned for seed yield by Sarang*et al*., (2004); branches plant^{-1} by Golkar *et al*., (2012) and Reddy *et al*., (2003) while for capsules plant^{-1} by Reddy *et al*., (2003); Lakshyadeep *et al*., (2005). As reported by Zheng *et al*., (1993), safflower genotypes having more plant height exhibit longer duration of flowering; these results are in consistent with our current study. According to previous studies, the safflower strains which mature early may compete with existing cash crops such as wheat and provides an escape mechanism from insects and disease (Golkar *et al*., 2011). The values of Mean, Range and genetic parameters viz., genotypic and phenotypic variation, coefficients of genotypic(GCV) and phenotypic variance(PCV), broad sense heritability(h^2bs), genetic advance(GA) and genetic advance as % of mean (GAM) were estimated for thirteen traits under study and presented in Table 3.

Table 2: Combined analysis of variance for studied characters of Safflower

Sov	df	DFI	DFC	DM	PH	BR/P	CAP/P	100SW	PY	SY	Oil	OY	BY	HI
Rep	2	21	0.6204	42.11	244.009	0.12	9.194	0.8307	2538	3134	0.985	352.5	2948	5.222
Gen	35	25.79*	18.13*	117.73	953.77*	4.57*	174.35*	36.73*	158071*	195148*	7.58*	20436.3*	374744*	272.361*
Error	70	4.7714	4.6775	107.197	58.809	0.16799	4.375	0.1317	530	654	0.19071	80.8	974	2.573

DFI: Days to Flower Initiation; DFC: Days to Flower Completion; DM: Days to maturity, PH: Plant height(cms), BR/P: No. of branches per plant, CAP/P: Number of capsules / plant, 100SW: 100 seed weight(gms), PY: Plot Yield (gms), SY: Seed Yield (kg/ha); Oil: Oil Content(%), OY: Oil Yield(Kg/ha), BY: Biological Yield(Kg/ha), HI: Harvest index(%).

Coefficients of Genotypic (GCV) & Phenotypic (PCV) Variation:

The selection of character or trait is feasible when the value of the genetic coefficients of variance is high indicating that the environmental factors are less likely to be affected. Whereas the high value of phenotypic coefficients of variation show that the effect is influenced by environmental factors as well as by genetic factors. In almost all of the parameters, the magnitude of PCV was more than GCV; however, both values were same in biological yield and plot yield. The uppermost extent of GCV and PCV was depicted for oil yield (38.88%, 38.65%) and seed yield (38.88%, 38.65%), subsequently capsule per plant (37.50%, 36.13%), indicating that those parameters are controlled genetically (Table 3). Khattab *et al*., (2018); Minnie *et al*., (2018) and Arslan (2007) also reported highest values of PCV and GCV related to capsules per plant and seed yield. The lack of variation between the phenotypic and genetic difference is the result of genetic factors and low impact of environment for the expression of different traits that give a greater chance of selection for desirable traits. The trait plant height has moderate magnitude of PCV (10.62%) and low GCV (9.71%). Days to flower completion (1.59%, 1.11 %) and days to maturity (4.81%, 0.86%) presented lesser magnitude of both PCV and, GCV, respectively and comparable outcome was reported earlier by Minnie *et al*., (2018). Tahernezhad *et al*., (2018) also found highest values of PCV (29.04%) related to harvest index while lowest for days to maturity (5.33%). Maturity is an important parameter as it enables to develop cultivars with different photoperiod and thermo-sensitivity for various agroecological zones (Rehman *et al*., 2009). Omidi *et al*. (2009) also report low value of GCV with respect to days taken to maturity. The divergences between PCV (4.81%) and GCV (0.86%) for days taken to maturity was high as compared to other parameters which indicate the highest influence of environment and low estimate of heritability in this trait.

Table 3: Genetic Parameters for yield and related components in 36 genotypes of Safflower

Traits	**Range**	**Mean**	**Genotypic variation**	**Phenotypic variation**	**Genotypic Coefficients of Variance (%)**	**Phenotypic Coefficients of Variance (%)**	**Heritability (broad sense)**	**Genetic Advance**	**Genetic Advance as mean (%)**
	1	2	σ^2G	σ^2P	GCV (%)	PCV (%)	h^2 bs (%)	GA	GAM(%)
DFI	172-185	178.56	7.01	11.68	1.48	1.91	0.59	4.22	2.36
DFC	186-195	190.31	4.48	9.16	1.11	1.59	0.49	3.05	1.6
DM	213-226	218.89	3.51	110.71	0.86	4.81	0.03	0.69	0.31
PH (cm)	130-205.5	177.93	298.32	357.13	9.71	10.62	0.84	32.52	18.28
BR/P	3.33-8	5.10	1.47	1.63	23.74	25.02	0.90	2.36	46.32
CAP/P	11-41.33	20.83	56.66	61.03	36.13	37.50	0.93	14.94	71.71
100SW (g)	6.81-25.64	15.79	12.20	12.33	22.12	22.23	0.99	7.16	45.31
OIL (%)	26.96-33.62	31.93	2.47	2.66	4.92	5.11	0.93	3.12	9.76
BY (kg/ha)	691.33-2137.67	1714.11	124590.0	125564.0	20.59	20.67	0.99	724.29	42.26
HI (%)	18.44-51.27	37.50	89.93	92.50	25.29	25.65	0.97	19.26	51.36
PY (g)	158-986	599.42	52513.7	53043.7	38.23	38.42	0.99	469.7	78.36
SY (kg/ha)	175.56-1095.56	666.02	64831.3	65485.3	38.23	38.42	0.99	521.89	78.36
OY (kg/ha)	54.39-342.81	213.15	6785.2	6865.9	38.65	38.88	0.99	168.68	79.14

DFI: Days to Flower Initiation; DFC: Days to Flower Completion; DM: Days to maturity, PH: Plant height (cms), BR/P: No. of branches per plant, CAP/P: Number of capsules / plant, 100SW: 100 seed weight(gms), PY: Plot Yield (gms), SY: Seed Yield (kg/ha), Oil: Oil Content (%), OY: Oil Yield (Kg/ha), BY: Biological Yield (Kg/ha), HI: Harvest index(%).

Heritability& Genetic Advance:

In Plant Breeding, broad sense heritability is often calculated from the proportion of genotypic as well as phenotypic variation. Thus, heritability assessment seems very supportive for selecting appropriate strains amongst different environmental conditions, especially for those breeding programs which are designed to build up high-yielding strains (Tahernezhad *et al*., 2018). Depending on magnitude (%), Reddy *et al*., (2013) classified broad sense heritability into low (0-30%), medium (30-60%) and high (>90%). Low heritability was found for days to maturity (30%) whereas, moderate was for days taken to flower initiation and completion (49 and 59% respectively). On the Contrary, Wakjira, (2011) mentioned higher heritability (91%) for days taken to flowering. Present results depicted that magnitude of heritability was more than 90% for capsules per plant, oil content, Seed yield, oil yield, 100SW, biological yield, harvest index and plot yield parameters (Table 3), indicating high transmittance percentage. Interestingly, these parameters are less influenced by environment so they can be improved by selection owing to the occurrence of additive genes action. Such high heritability estimate has been pointed out by Sarang *et al*., (2004) for seed yield and100SW; plant height traits by Reddy *et al*., (2013). On the Contrary, Camas and Esendal (2006) reported moderate heritability related to seed yield, branches plant-1 and oil contents (35%, 45% and 59% respectively) indicating moderately affected by environmental conditions. Inheritance/ heritability for plant height is 84% in our study. On the other hand, Camas and Esendal (2006) found 93% heritability.

The genetic advance estimates ranged between 0.69 to 724.29 % with higher values for seed yield, plot yield and biological yield. Generally, in breeding programs, information regarding the heritability along with genetic advance of related traits is useful because it furnishes information regarding assortment of promising lines (Bahmankar *et al*.,2014). Higher heritability in addition to higher genetic advance was present in seed yield, plot yield and biological yield (Table 3) implied that genetic factors in comparison with environmental conditions are more effective and amenable to selection by breeders. Such a higher heritability along-with higher genetic advance was mentioned by Minnie *et al*., (2018) in seed yield, capsules plant^{-1} and 100SW, Bahmankar *et al*., (2014) in plant height and 100 seed weight, Ottai *et al*., (2012) and Kandil *et al*., (2012) in capsules/plant and for seed yield by Reddy *et al*., (2003), Sarang *et al*., (2004); and Choulwar *et al*., (2005). This all revealed that in Safflower plant height, branches per plant, capsule per plant and 100SW are important traits which was also reported by (Kose *et al*., 2018). The genotypes good for capsules per plant, oil content, Seed yield, oil yield, 100SW, biological yield, harvest index and yield parameters can be selected as parents for transfer of these characters in future breeding strategies.

CONCLUSION:

Highest estimate of genetic advance and heritability was observed for capsule per plant, oil content, Seed yield, oil yield, 100SW, biological yield, harvest index and plot yield as these characters are least effected by environmental conditions due to the reason early and direct selection is valuable. The genotypes good for capsules per plant, oil content, Seed yield, oil yield, 100SW, biological yield, harvest index and yield parameters can be selected as parents for transfer of these characters in future breeding strategies.

CONFLICT OF INTEREST:

The authors didn’t showed any conflict of interests.

4. REFERENCES

Ali, F., M. A. Nadeem, M. Barut, E. Habyarimana, H. J. Chaudhary, I. H. Khalil, A. Alsaleh, R.Hatipoglu, T. Karakoy, C. Kurt, M. Aasim, M. Sameeullah, N. Ludidi, S. H. Yang, G. Chung and F. S. Baloch. 2020. Genetic Diversity, Population Structure and Marker-Trait Association for 100-Seed Weight in International Safflower Panel Using Silico DArT Marker Information. Plants. 9(5):652.

Ali, F., A. Yilmaz, H. J. Chaudhary, M. A. Nadeem, M. A. Rabbani, Y. Arslan, M. A. Nawaz, E. Habyarimana, F. S. Balochi. 2020. Investigation of morpho-agronomic performance and selection indices in the international safflower panel for breeding perspectives. Turkish J. Agri. and Forestry. 44: 103-120.

Arslan, B. 2007. Assessing of heritability and variance components of yield and some agronomic traits of different Safflower (*Carthamus* *tinctorius* L.) cultivars. Asian J. Plant Sci. 6(3): 554-557.

Bahmankar, M., M. R. Raij, A. R. Seloki, K. Shirkool. 2014. Assessment of broad sense heritability and genetic advance in safflower. Int. J. of Biosci. 4(8): 131-135.

Camas, N. and E. Esendal. 2006. Estimates of broad-sense heritability for seed yield and yield components of safflower (*Carthamus tinctorius* L.). Hereditas., 143: 55-57.

Choulwar, S. B., R. R. Dhutmal, I. Madrap and B. M. Joshi. 2005. Genetic variability for yield and yields related traits in F2 population of safflower. J. Maharashtra Agri. Univ. 30(1):114-116.

Emongor, V. E. and O. Oagile. 2017. Safflower production. The Botswana University of Agriculture and Natural Resources, Gaborone Botswana. 1-67.

Golkar, P., A. Arzani and A. M. Rezai. 2012. Genetic analysis of agronomic traits in safflower (L.). African J. Agri. Res. 6(14): 3264-3271.

Golkar, P., A. Arzani and A. M. Rezaei. 2011. Determining relationships among seed yield, yield components and morpho-phenological traits using multivariate analyses in safflower (*Carthamus tinctorious* L.). Annals of Bio. Res. 2:162-69.

Golparvar, A. R. 2011. Assessment of relationship between seed and oil yield with agronomic traits in spring safflower cultivars under drought stress condition. J. Res. Agric. Sci., 7:109-113.

Hojati, M., S. A. M. Modarres-Sanavy, M. Karimi and F. Ghanati. 2011. Responses of growth and antioxidant systems in *Carthamus tinctorius* L. under water deficit stress. Acta Physiol. Plant. 33: 105-112.

Houmanat, K., J. Charafi, H. Mazouz, M. El Fechtali and A. Nabloussi, 2016. Genetic diversity analysis of safflower (*Carthamus tinctorius*) accessions from different geographic origins using ISSR markers. Int. J. Agric. Biol., 18: 881–887.

Hussain, T., M. A. Tariq, I. Ahmad, M. Saghir, M. Batool, M. Safdar and M. Tariq. 2014. Characters association analysis in Safflower (*Carthamus tinctorius* L.). J. Biol., Agric. And Healthcare. 4: 63-65.

Kandil, A. A., A. E. Sharief, T. A. Abo-Zaied and A. G. T. Moussa. 2012. Multivariate analysis of some economic characters in flex. Pak. J. Biol. Sci., 15:85-91.

Karimi, M., A. R. Golparvar and M. Shams. 2013. Multivariate regression and path coefficient analysis of seed and oil yield in spring safflower (*Carthamus tinctorius* L.) cultivars. App. Sci. Report. 4:184-186.

Khattab, M. N. 2018. Variance, Heritability, Genetic Advance and Correlation of Some Phenological, Morphological and Productivity Traits in Some Safflower (*Carthamus tinctorius*L.) Genotypes. Syrian J. Agri. Res. 5(4): 297-307.

Lakshyadeep, S. P. and S. S. Shanna. 2005. Genetic variability and correlation studies in safflower, *Carthamus tinctorius* L. J. Oilseeds Res. 22(1): 180-182.

Lourenco, V. M., P. C. Rodrigues, A. M. Pires and H. P. Piepho. 2017. A robust DF-REML framework for variance components estimation in genetic studies. Bioinformatics. 33: 3584-3594.

Minnie, C. M., S. Sandeep and K. Sujatha. 2018. Genetic Variability, Heritability and Genetic Advance Studies in Safflower (*Carthamus* *tinctorius* L.). Int J. Cur. Microbiol. App. Sci., 7(12): 3714-3718.

Muhammad, R. W., H. M. W. Ali, A. Hamza, M. Q. Ahmad, A. Qayyum, W. Malik and E. Noor. 2020. Estimation of different genetic parameters in various safflower (*Carthamus tinctorius* L.) genotypes under field condition. Pak. J. Agri. Res., 33(4): 849-857.

Kose, A., O. Onder, O. Bilir and F. Kosar. 2018. Application of multivariate statistical analysis for breeding strategies of spring safflower (*Carthamus tinctorius* L.). Turk. J. Field crops. 23(1): 12-19.

Lira, J. P. E., M. A. A. Barelli, V. P. da Silva, R. Felipin-Azevedo, D. T. dos Santos, C. Galbiati, R. O. de Sa and J. P. Poletine. 2021. Safflower genetic diversity based on agronomic characteristics in Mato Grosso state, Brazil, for a crop improvement program. Genetics and Mol. Res., 20(1): 1-11.

Omidi, A. H., H. Khazaei and S. H. Hongbo. 2009. Variation for some important agronomic traits in 100 spring safflower (*Carthamus tinctorius* L.) genotypes. American-Eurasian J. Agric. Environ. Sci. 5(6): 791-795.

Ottai, M. E. S., M. A. A. Al-Kordy, R. M. Hussein and M. S. Hassanein. 2012. Genetic diversity among Romanian fiberflax varieties under Egyptian conditions. Aust. J. Basic Applied Sci., 6: 162-168.

Pavithra, K. P., S. P. Rajesh, H. Yallappa and G. K. Nishanth. 2015. Assessment of genetic diversity in safflower (*Carthamus tinctorius* L.) Germplasms. Int. J. Agric. Res., 5: 151-157.

Pearl, S. A. and J. M. Burke. 2014. Genetic diversity in *Carthamus tinctorius* (Asteraceae; Safflower), an underutilized oilseed crop Am. J. Bot., 101: 1640-1650.

Pelin, G., E. Zeynepand A. Ozbek. 2020. Cold Pressed Oils Chapter 29 - Cold pressed safflower (*Carthamus tinctorius* L.). Seed oil., 323-333.

Reddy, M. P., B. N. Reddy, B. T. Arsul and J. J. Maheshwari. 2013. Genetic variability, heritability and genetic advance of growth and yield components of linseed (*Linum usitatissimum* L.). Int. J. Curr. Microbiol. App. Sci. 2(9): 231-237.

Reddy, M. V., P. Chand and V. Band. 2003. Analysis of variability parameters for yield and its components in the F3 generation of safflower (*Carthamus tinctorius* L.). Prog. Agri. 3(1/2): 143-144.

Rehman, A. U., I. Habib, N. Ahmad, M. Hussain, M. A. Khan. 2009. Screening wheat germplasm for heat tolerance at terminal growth stage. Plant Omics J. 2(1): 9-19.

Reza, A. M., M. J. Mirhadi, B. Delkhosh and A. Omidi. 2013. Evaluation of native and exotic safflower (*Carthamus tinctorius* L.) genotypes for some important agronomic traits and fatty acid composition. Ann. Biol. Res., 4(6): 200-204.

Sarang, D. H., A. A. Chavan, A. S. Gunjkar, V.N. Chinchane and S.P. Pole. 2004. Study of genetic variability following hybridization in Safflower. Annals Plant Physiology. 18(1): 68-70.

Singh, R. K. and B. D. Chaudhry, 1985. Biometrical methods in quantitative genetic analysis (revised). Kalyani publishers. New Dehli, India.

Steel, R. G. D., J. H. Torrie and D. A. Dicky. 1997. Principles and Procedures of Statistics, A biometrical approach McGraw-Hill Book Co., New York.

Tahernezhad, Z., J. Saba, M. Zeinalabedini, S. S. Pourdad and M. R. Ghaffari. 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 J. Bot. 47(3): 501-508.

Topal, M., M. E. Ozturk and T. Polat. 2010. Path analysis of seed yield components using different correlation coefficients in safflower (*Carthamus tinctorius* L.). The JAPS. 20: 220-224.

Wakjira, A. Terefe, G., A, Wakjira and D. Gorfu 2011. Genetic variability among linseed collections. In: Oilseeds-Engine for economic development, (Eds.). Ethiopian Institute of Agricultural Research, Addis Ababa, Ethiopia. pp: 61-72.

Zheng, N. C., C. Futang, S. Xinchun and W. Yancai. 1993. Path analysis of correlated characters on flower yield of safflower individuals. In: Proceedings of the 3rd International Safflower Conference, 14-18 June 1993, Beijing, China.