Biological Forum – An International Journal **15(4): 479-486(2023)**

ISSN No. (Print): 0975-1130
ISSN No. (Online): 2249-3239

Study of Genetic Diversity and Relationships between Agronomic Traits in Large Safflower (*Carthamus tinctorius* L.) Germplasm Collection

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(Received: 20 February 2023; Revised: 15 March 2023; Accepted: 19 March 2023; Published: 20 April 2023)
(Published by Research Trend)

ABSTRACT: Safflower (*Carthamus tinctorius* L.), a member of the family Compositae, is a multi-purpose crop for oil, medicative and industrial uses. Despite its importance, safflower production and productivity are constrained by the low yielding varieties, poor cultural conditions and susceptible to biotic and abiotic stresses. The objective of the present study is to establish the level of genetic diversity of 315 germplasm accessions of safflower for major agronomic traits from 21 countries along with 5 released varieties. The data was recorded for 9 agronomic traits for two seasons. Analysis of variance revealed highly significant differences for the quantitative traits measured indicating the existence of wide genetic variation among the accessions. The accessions clustered into seven groups and there was no clear grouping of accessions according to their geographical origin probably due to gene flow. Correlation studies revealed thatnumber of branches per plant (r=0.29), number of capitula per plant (0.51**), number of seeds per capitula (0.35*), 100-seed weight (0.10*) and hull content (0.19*) are significantly positive correlated with seed yield per plant. The results indicated a large genetic diversity among the accessions evaluated and the correlation studies established that wide diversity in the crop and it is possible to increase the seed yield and oil content. The promising germplasm accessions identified could be useful in future safflower breeding programs.**

Keywords: Safflower, Genetic diversity, Agronomic traits, Correlation.

INTRODUCTION

Safflower (*Carthamus tinctorius* L., 2n=24) member of the compositae family is one of the ancient oilseed crop grown throughout the world. Kazakhstan (38.6%), Russia federation (21.4%), India (10.5%), Unites states of America (6.2%) and Mexico (6.1%) are the major safflower producing regions of the world that together contributed 83% of the world's safflower production during 2021. Globally, safflower is cultivated on 8.5 lakh ha in ~22 countries with an annual production of 0.63 m t. The global yield of safflower in 2021 was only 742 kg/ha, which is rather low. There were severe regional imbalances in the yield of safflower which varied from 2576.9 kg/ ha in Pakistan, 1690.1 kg/ ha in Mexico, 774.7 kg/ ha in India to 505.2 kg/ha in the Ukraine. The cultivation of safflower under diverse climatic conditions in different countries over a period of 4000 years, suggests that sustainability of the crop is very high. In India, it is continued cultivation due to multipurpose nature of crop i.e., producing natural coloring dye (carthamin), medicine, industrial and quality oil rich in poly and monounsaturated fatty acids, coupled with varietal development for yield and resistance to pests and diseases in addition to its drought tolerance. Under changing climate and production scenarios, safflower varieties with low yield and oil content are not able to maintain its edge over competing crops resulting in a reduction in its areal extent and production the world over. In addition, shifting of these oilseed crops to marginal soils which have poor nutrient levels and water holding capacities, thus, causing a further decline in their productivity and profitability. The recent increasing health consciousness and the consumption of organic and naturally processed vegetable oils provides ample scope for safflower in attracting greater attention of the industry considering the health benefits of consuming safflower oil due to prevalence of omega-6 fatty acid, high linoleic acid, higher anti-oxidant properties, minerals, tocopherols etc. The development of safflower with high oleic content (which enhanced the shelf life of safflower oil and was suitable for deep and refrying with all the advantages of polyunsaturated fatty acid oil) in the United States further widened its utilization and hence sustainability. So, to restore the crop, highest priority has to be given to seed yield enhancement, increase in oil yield per unit area along with improving the quality traits for health benefits and nutrition. It also makes safflower crop more suitable for sustainable production resulting in an increased area and production.

A large collection of diverse germplasm accessions as well as related wild species available in this crop [IIOR (~7000); USDA (~2300)]. The present scenario of increased demand for oilseeds in the face of increase economic value, industrial requirements and nutritional demands presents a challenge and an opportunity to stimulate greater use of the available genetic variability by breeders and agronomists to look into new, diverse, and resilient germplasm through adequate characterization and screening for useful traits (Jaradat, 2015). Genetic variability for agro-morphological and biochemical traits has been well documented in safflower (Amini *et al.,* 2008; Mahasi *et al*., 2009; Elfadl *et al.,* 2010; Safavi *et al*., 2012; Majidi and Zadhoush 2014; Talebi and Abhari 2016; Kadirvel *et al.,* 2017; Ali *et al.,* 2020; Hassani *et al.,* 2020; Dhage *et al*., 2020; Lira *et al.,* 2021; Qin *et al.,* 2022; Rostami *et al.,* 2022; Culpan *et al.,* 2022; Sathees *et al.,* 2022). However, the genotypes screened are very few in these genetic diversity studies. It is widely recognized that DNA markers in combination with phenotypic descriptors provide better understanding of plant genetic resources. Substantial efforts are also made to analyse genetic diversity using DNA markers (Golkar *et al.,* 2011; Barati and Arzani, 2012; Panahi and Neghab 2013; Majidi and Zadhoush 2014; Lee *et al.,* 2014; Kumar *et al*., 2014; Pearl and Burke 2014; Usha Kiran *et al*., 2015; Talebi and Abhari 2016; Talebi *et al.,* 2018; Ali *et al.,* 2020; Rahimi 2021. Narrow genetic base of cultivars might result in increased risk of crop vulnerability, i.e., crop failure, due to insect pests and disease epidemics or unpredictable climatic effects. Low productivity and biotic/abiotic stresses coupled with limited genetic variation in the cultivated gene pool necessitates identification and utilization of germplasm for introduction of new variability for yield and yield related traits, improving oil content and quality. The aim of the present investigation was to characterize the diverse germplasm collection and identify genetically diverse multi-trait-specific germplasm sources, considering agronomic performance and oil content.

MATERIAL AND METHODS

Plant Material and Field Trials. Field experiments were conducted during Rabi 2016-17 and 2017-18 at experimental fields of ICAR-IIOR, Hyderabad, India representing the medium depth vertisols located at latitude of 17°51′ North and longitude of 78° 27’East.The experimental material for the present study comprised of 315safflower germplasm lines from 21 countries viz., India (185), USA (48), Mexico (31), Pakistan (20), Iran (7), Portugal (4), Italy, Afghanistan (3 each), Australia, China, Egypt, Israel, Turkey (2 each) and Belgium, Germany, Hungary, Japan Poland, Spain, Sudan, Ukraine, USSR, Uzbekistan (1 each) and 5 commercial varieties (A1, PBNS12, NARI57, NARI6) from India which are used as checks (Supplementary Table S1). The germplasm accessions used in the study are initially selected from the ~2000 safflower germplasm accessions based on the pre-evaluation data of germplasm management unit of ICAR-IIOR, Hyderabad, India to develop a germplasm mapping panel with diverse range for different traits. The trial was laid out in an augmented block design. The five checks used in this experiment were augmented with 10 randomly allocated germplasm accessions (entries) so that each block had 25 plots.

Evaluation of Agronomical Traits. Agronomic traits were scored onten randomly selected representative plants from each of the germplasm accessions for the morphometric traits *viz*., days to 50% flowering (DFY), days to maturity (DMY), number of branches per plant (NBP), number of capitula per plant (NCP), number of seeds per capitula (NSC), 100 seed weight (TW). Seed yield per plant (SY) was calculated on plot basis. Hull content (HC) was estimated as hull weight to the total seed weight expressed in percentage. A sample of 40 random seeds (for each germplasm line) was used to measure seed length (SL), seed breadth (SB) and seed thickness (ST).

Estimation of Oil content. The safflower seeds (10 g) were dried in oven at 50 to 60 °C for 24 h, estimated for its oil content using Oxford-bench top pulsed Nuclear Magnetic Resonance (NMR) MCQ-5 (London, UK) pre-calibrated for different oilseed crops (Yadav and Murthy 2016). The instrument had been calibrated earlier using safflower samples whose oil content had been estimated by Soxhlet extractor method using hexane as the solvent. Preloaded Easy-cal software was used for calibration of known samples as standards. The conditions of calibration included operating frequency of 5 MHz, sample probe of 40 mm diameter, 4 scans @ 1 s delay in recycle and magnetic box temperature of 40°C, and with the ambient room temperature maintained @ 25 ± 2°C.

Statistical Analysis. The statistical analyses were performed using appropriate procedures of the R program version 3.4.3 and SPSS v.16.0. The data recorded on quantitative traits were averaged and analyzed for simple statistical measures i.e. mean, minimum, maximum, standard deviation and coefficient of variation to determine the extent of genetic diversity among the studied germplasm. Simple Pearson correlation coefficients between all pairs of quantitative traits were obtained as per Steele and Torrie (1980) using mean values. The agronomic data were also used for multivariate analysis with the major objectives to display the variability among safflower germplasm on the basis of multiple traits, identify traits that are positively or negatively associated and determine the main characters that differentiate between accessions. Further, the data were subjected to cluster analysis according to the Sneath and Sokal (1973). For the eradication of scaling differences, the means of each trait were standardized using Z-scores before carrying out the cluster analysis. Estimates of Euclidean distance coefficients were carried out for all pairs of genotypes. The resulted matrices of Euclidean dissimilarity coefficient were applied to assess the genetic relationships between safflower germplasm with a cluster analysis through Ward method of variance.

RESULTS AND DISCUSSION

Agronomic traits. Analysis of variance revealed significant differences among the accessions for all traits analyzed, indicating a high level of phenotypic variability. All the traits contributed to the yield directly or indirectly and positively or negatively and possessed key genetic status for the identification of productive genotypes. The basic statistical data (mean, minimum, maximum, standard deviation, coefficient of variation and variance) for traits was calculated among all the germplasm accessions (Table 1). A high coefficient of variation (CV) (>20%) was observed for the traits, number of branches per plant, number of capitula per plant, number of seeds per capitula, 100-seed weight, seed yield, seed breadth, seed thickness while the traits, days to 50% flowering, days to maturity, hull content, seed length, oil content showed low CV. Maximum variability was observed for seed yield (142.32) followed by number of capitula per plant (137.82), days to maturity (91.58), number of seeds per capitula (86.49), days to 50% flowering (60.52) which suggested that these traits are amenable for selections to realize high yielding genotypes. The wide range of variability observed in the present study is in accordance with the earlier reports in safflower (Amini *et al.,* 2008; Arif *et al.,* 2016; Shinwari *et al.,* 2014; Bahmankar *et al.,* 2016; Karim *et al.,* 2017; Neelima *et al.,* 2021). Most of the studies reported the traits viz., 100 seed weight, number of effective capitula per plant and number of seeds per capitulum contributes to the seed yield in safflower (Bidgoli *et al.,* 2006; Pusphpavalli *et al.,* 2017).

Table 1: Variability of agronomic traits in safflower germplasm accessions^a.

Traits	Range	Mean	SD	CV%	Variance
Days to 50% flowering (No.)	63-106	82.28	7.78	9.45	60.52
Days to maturity (No.)	100-147	121.14	9.57	7.90	91.58
Number of branches per plant	2.40-20.60	9.61	2.72	28.35	7.40
Number of capitula per plant	5.80-68.0	28.21	11.74	41.63	137.82
Number of seeds per capitula	7.40-58.67	28.92	9.30	32.17	86.49
100-Seed weight (g)	2.10-7.97	4.36	0.98	22.50	0.96
Hull content (%)	24.43-57.52	45.25	4.45	9.83	19.80
Seed yield (g)	2.50-83.20	23.33	11.93	51.14	142.32
Seed length (mm)	1.38-9.92	7.68	1.35	17.55	1.82
Seed breadth (mm)	0.34-5.29	4.05	1.03	25.54	1.06
Seed thickness (mm)	0.24-6.86	3.35	0.91	46.86	0.83
Oil content (%)	23.59-46.4	33.44	0.36	12.58	0.13

^{a}Trait value is averaged from the data from two years. SD, standard deviation. CV, coeffficient of variation.

Genetic diversity. Ward's method was used to quantify the genetic divergence between the germplasm accessions (hierarchial cluster analysis) to identify diverse clusters (germplasm) with desirable yield attributing and improved seed quality traits. In this multi-step approach of grouping, at each step the pair of clusters with minimum between cluster distances are merged, so that there will be minimum increase in total within-cluster variance after merging. Thus, this exercise categorizes the tested genotypes into the least number of clusters so that suitable genotypes with enough variability to provide genetic gain are identified for the breeding exercises that try to harness the variability. At the Euclidean distance of 18, the 320 accessions were grouped into seven clusters (Fig. 1) and the cluster means were given in Table 2 and grouping of germplam accessions were given in Table 3. The promising accessions of safflower identified on the basis of traits for future use were listed in Table 4. Cluster I comprised of 14 (14.38%) genotypes grouped together and had unique attributes such as the small seed size i.e., less seed length (4.14), less seed breadth (0.81), less seed thickness (0.34). Cluster II consisted of 27 (8.44%) genotypes grouped together due to their high oil content (41.18), high oleic acid (72.14), more number of branches per plant (11.41), number of capitula per plant (40.17), number of seeds per capitula (31.92) and low 100-seed weight with medium grain yield per plant (24.03). Cluster III was having 57 (17.81%) genotypes converged due to distinguishing features such as best seed characteristics like more seed length (8.14), seed breadth (3.99), seed thickness (3.30), moderate 100-seed weight (4.77) and highest grain yield per plant (26.73). The oil content of this group is 32.90. Cluster IV comprised of 25 (7.81%) accessions with prominent features like low number of seeds per capitula (29.54), low seed length (4.95) and the low oil content (31.17). Cluster V consisted of 82 (25.63%) genotypes which clustered together on the basis of highest 100-seed weight (5.05), more seed length (8.25), seed breadth (4.52) and seed thickness (3.81), low oil content (31.05). Cluster VI consisted of 40 (12.5%), genotypes which clustered together on the basis of highest number of branches per plant (11.94), number of capitula per plant (43.33), number of seeds per capitula (32.0). Cluster VII consisted of 75 (23.44%) genotypes which clustered together on the basis of lowest number of branches per plant, number of capitula per plant, seed yield (18.65).

Genetic divergence has been considered as an important factor in discriminating the genetically diverse parents for an efficient and successful hybridization programme in order to get potential transgressive segregants. Lack of a relationship between genetic diversity and geographical origin suggests a similarity in their genetic constitution and a free exchange of breeding material over places (Sharma, 2005). Cluster II and V were highly diverse for different traits. Cluster II was highly diverse group consisting of mostly collections with high oil lines including those from Mexico and USDA collection. Cluster V was the largest group with good seed yield traits. Development of varieties with high seed oil yield coupled with better quality traits is the top priority in safflower research. Genetic enhancement of safflower for oil yield and quality requires simultaneously improvement in seed yield, oil content and unsaturated fatty acids. Even though fatty acid content can be easily manipulated in breeding programmes, it is a greater challenge to combine seed yield related traits and seed quality traits to get high yielding safflower genotypes with better oil quality. Only a few studies have explored the relationships among seed yield components and seed quality traits in safflower. Most of the genetic diversity studies have documented variability in agro-morphological traits in cultivated germplasm accessions of safflower (Arif *et al.,* 2016; Karim *et al.,* 2017; Kumari *et al*., 2017; Safavi *et al.,* 2017; Ali *et al*., 2020; Hassani *et al.,* 2020; Dhage *et al*., 2020; Lira *et al.,* 2021; Qin *et al.,* 2022). There are only a few studies on genetic variation in the wild species of safflower, including *C. lanatus* and *C. oxyacanthus* as well as C. tinctorius landraces from Iran (Amini *et al*., 2008; Sabzalian *et al.,* 2008). Based on our comprehensive study, clustering pattern could be utilized by choosing combinations of germplasm lines to generate the highest possible variability in the seed yield and oil content.

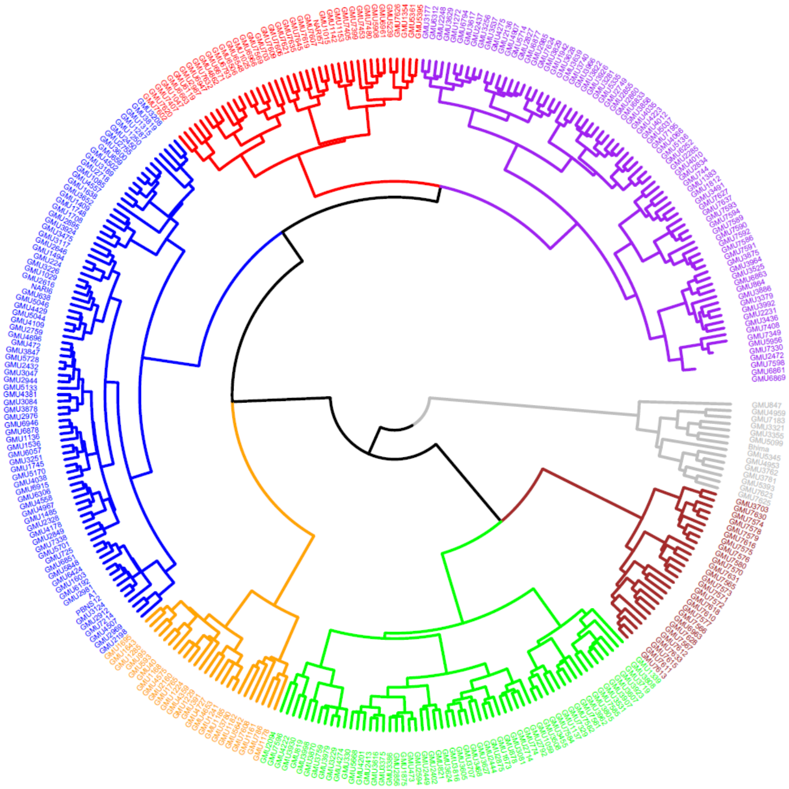


Fig. 1. Dendrogram showing the genetic relationship among safflower germplasm accessions based on agronomic traits.

Table 2: Cluster means of germplasm accessions for traits included in different clusters.

Traits	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Days to 50% flowering (No.)	85.33	87.37	82.17	81.50	82.00	75.2	8425
Days to maturity (No.)	121.33	125.11	119.27	117.20	120.00	110.5	117.0
Number of branches per plant	8.67	11.41	9.47	10.14	9.77	11.94	7.65
Number of capitula per plant	22.84	40.17	24.13	28.26	27.49	43.33	20.70
Number of seeds per capitula	31.18	31.92	28.99	29.54	24.83	31.99	30.02
100 Seed weight (g)	3.97	3.20	4.77	4.63	5.05	3.68	4.08
Hull content (%)	21.94	24.03	26.73	22.58	25.44	23.41	18.65
Seed Yield (g)	45.0	32.8	46.89	47.00	49.00	44.0	45.25
Seed length (mm)	4.14	8.14	8.12	4.95	8.25	7.94	7.97
Seed breadth (mm)	0.81	3.99	4.53	2.11	4.52	4.30	4.30
Seed thickness (mm)	0.34	3.30	3.68	1.80	3.81	3.56	3.58
Oil content (%)	32.92	41.18	32.90	31.17	31.05	34.13	34.16

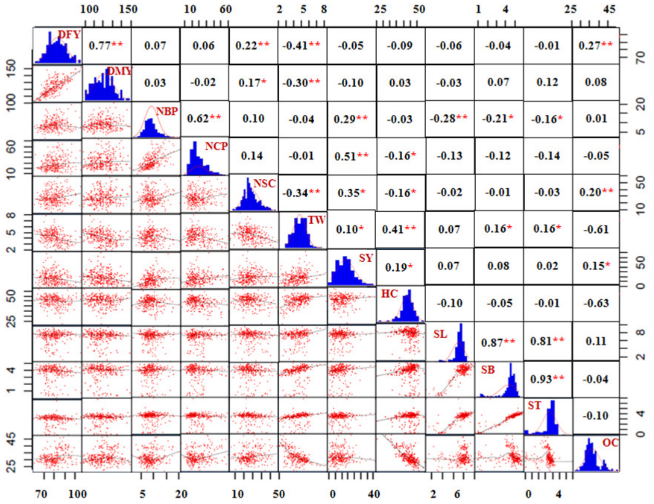
Table 3: Total number of germplasm per cluster, percentage and prominent features of safflower germplasm separated into clusters.

Cluster	No. of germplasm	% of germplasm	Names of the germplasm in the cluster	Important characteristics of the germplasm grouped
Cluster I	14	4.38	GMU847, GMU4959, GMU7183, GMU3321, GMU3355, GMU5099, Bhima, GMU5345, GMU4953, GMU3762, GMU3781, GMU5393, GMU7623, GMU7625	Small seed size characteristics viz., less seed length, seed breadth, seed thickness
Cluster II	27	8.44	GMU3703, GMU7630, GMU7574, GMU7578, GMU7579, GMU7616, GMU7575, GMU7576, GMU780, GMU7570, GMU7631, GMU7565, GMU7573, GMU71, GMU7572, GMU7618, GMU7610, GMU7577, GMU7566, GMU6963, GMU7628, GMU7567, GMU7612, GMU7633, GMU7615, GMU7611, GMU7613	Highest number of branches per plant, number of capitula per plant, number of seeds per captula, low test weight, large seed length, high oil content
Cluster III	57	17.81	GMU1339, GMU3808, GMU3719, GMU3923, GMU3607, GMU3907, GMU3531, GMU7585, GMU3805, GMU3962, GMU7581, GMU7582, GMU7329, GMU1137, GMU7584, GMU3455, GMU3508, GMU1059, GMU2792, GMU774, GMU2714, GMU3081, GMU878, GMU1673, GMU2875, GMU2444, GMU3627, GMU3468, GMU3707, GMU3605, GMU3816, GMU3624, GMU821, GMU2402, GMU2449, GMU2594, GMU473, GMU1875, GMU2856, GMU3386, GMU6675, GMU3616, GMU2413, GMU4201, GMU5668, GMU330, GMU4274, GMU3229, GMU3979, GMU3759, GMU3870, GMU3998, GMU819, GMU3930, GMU4222, GMU7596, GMU 2094	High seed yield
Cluster IV	25	7.81	GMU1695, GMU1643, GMU1285, GMU95, GMU593, GMU40, GMU1168, GMU4575, GMU2160, GMU1765, GMU1224, GMU4359, GMU1229, GMU391, GMU4727, GMU4653, GMU1241, GMU1185, GMU3780, GMU1182, GMU5642, GMU7608, GMU1161, GMU786, GMU1178	Lowest number of seeds per capitula, low seed length, low oil content
Cluster V	82	25.63	GMU3208, GMU3819, GMU1315, GMU1287, GMU1250, GMU2450, GMU2755, GMU3600, GMU659, GMU4502, GMU3189, GMU2718, GMU1085, GMU4557, GMU1638, GMU3652, GMU1409, GMU1748, GMU1708, GMU2895, GMU3924, GMU3475, GMU3117, GMU2646, GMU1494, GMU224, GMU3226, GMU1029, GMU2616, NARI6, GMU638, GMU5046, GMU4429, GMU5044, GMU4109, GMU2759, GMU4696, GMU472, GMU3847, GMU5728, GMU2432, GMU3047, GMU2944, GMU5133, GMU4381, GMU3084, GMU3878, GMU2976, GMU6946, GMU6878, GMU1136, GMU1536, GMU6057, GMU3251, GMU1745, GMU5170, GMU4038, GMU6915, GMU6306, GMU4558, GMU4967, GMU1485, GMU2328, GMU4178, GMU2849, GMU7338, GMU5701, GMU725, GMU6851, GMU5848, GMU6424, GMU1603, GMU6192, GMU2981, A1, PBNS12, GMU3124, GMU2912, GMU7214, GMU4507, GMU2969, GMU2198	High test weight, seed yield, more seed length, seed breadth, seed thickness
Cluster VI	40	12.5	GMU7602, GMU7620, GMU7407, GMU1047, GMU6663, GMU6119, GMU2987, GMU6947, EC736516, GMU4862, GMU6671, GMU6793, GMU6506, GMU6548, GMU1025, GMU6966, GMU7569, GMU703, GMU7609, GMU7606, GMU7621, GMU7635, GMU7645, GMU7619, GMU7607, NARI57, GMU1015, GMU1142, GMU1153, GMU7405, GMU7399, GMU7453, GMU7480, GMU5908, GMU6961, GMU5239, GMU7626, GMU1354, GMU5361, GMU5395	Highest number of branches per plant, number of capitula per plant, number of seeds per captula
Cluster VII	75	23.44	GMU3177, GMU6312, GMU2248, GMU3629, GMU1272, GMU6794, GMU3617, GMU2437, GMU3256, GMU3537, GMU4275, GMU2136, GMU4907, GMU5714, GMU2827, GMU6877, GMU2985, GMU6508, GMU3829, GMU1942, GMU3628, GMU3639, GMU3740, GMU3966, GMU3822, GMU3926, GMU3281, GMU5335, GMU2749, GMU2855, GMU2860, GMU6833, GMU3858, GMU4035, GMU4223, GMU4012, GMU5037, GMU7195, GMU4066, GMU5136, GMU6252, GMU2285, GMU4010, GMU2834, GMU744, GMU1383, GMU1812, GMU3491, GMU7627, GMU7637, GMU7593, GMU7594, GMU7589, GMU7590, GMU7592, GMU7586, GMU7591, GMU3875, GMU3964, GMU3525, GMU6863, GMU864, GMU3886, GMU3379, GMU3992, GMU2231, GMU3436, GMU7408, GMU7349, GMU5956, GMU7330, GMU2472, GMU7598, GMU6861, GMU6869	Lowest number of branches per plant, number of capitula per plant

Table 4: Promising accessions of safflower identified on the basis of traits for future use.

Traits of Interest	Range	Accessions identified
Early maturing lines	< 105 days	GMU2981, GMU3475, GMU3858, GMU2860, GMU95, GMU2895, GMU2855, GMU40
Number of branches per plant	>15 no.	GMU7569, GMU7570, GMU7572, GMU703, GMU7596, GMU1047, GMU1178
Number of capitula per plant	>60 no.	GMU7620, GMU7399, GMU7609, GMU7602, GMU6663, GMU7596, GMU7214
Number of seeds per capitula	>50 no.	GMU7566, GMU7405, GMU7637, GMU1812, GMU1153, GMU7567, GMU1354
100 Seed weight	>6 g	GMU4507, GMU2969, GMU3081, GMU2198, GMU3819, GMU1485, GMU2849, GMU330
Seed yield	>50 g/plant	GMU1250, GMU1315, GMU4222, GMU3208, GMU 4359, GMU3930, GMU2402, GMU3819, GMU7619
Seed size	>9 mm	GMU6306, GMU2198, GMU4507, GMU3924, GMU2969, GMU3907, GMU2860, GMU1153, GMU7610
Hull content	>50 %	GMU3475, GMU3436, GMU5668, GMU1161, GMU4558, GMU1241, GMU6306, GMU3992, GMU7338, GMU593, GMU7579, GMU7330, GMU5701
Oil content	>40%	GMU7615, GMU7616, GMU7609, GMU7613 GMU7612, GMU7611, GMU7610, GMU7576, GMU7621, GMU7579, GMU7589, GMU7577

Correlation between Traits. The Pearson correlation coefficients calculated between pairs of variables revealed how some traits were inter-dependable, others independent, whereas a group of traits clustered together because of reciprocal tight correlation (Fig. 2). Seed yield showed positive correlation with yield related traits *viz.*, number of branches per plant (r=0.29**), number of capitula per plant (0.51**), number of seeds per capitula (0.35*), 100-seed weight (0.10*) and hull content (0.19*) reflecting the tendency of the germplasm having these traits to be more productive. The seed size related traits viz., seed length, seed breadth and seed thickness showed highly significant and positively correlated among themselves showing these traits are inter-dependable. A similar significant correlation between seed yield and other traits has also been reported in safflower (Nair *et al.,* 2006; Bidgoli *et al.*, 2006; Diwakar *et al.,* 2006; Mozaffari and Asadi 2006; Amir *et al.,* 2009; Shivani *et al.,* 2010; Shivani and Sreelakshmi, 2013; Shinwari *et al.,* 2014; Bahmankar *et al.,* 2016; Pushpavalli *et al.,* 2017). The number of seeds per capitula and 100-seed weight were negatively correlated (-0.34**) as germplasm lines with bold seed had fewer seeds per capitulum. In our results, seed yield and oil content (0.14*) were positively correlated in contrast to what has been earlier [Bagavan and Ravikumar (2001) (-0.068), Pahlavani (2005) (-0.26)] where negative correlation between seed yield and oil content had been observed. Oil content was negatively correlated with 100-seed weight (-0.61) and hull content (-0.63**) and consecutively 100-seed weight and hull content is positively correlated (0.41**). 100-seed weight and Hull content are more important traits which affect the seed yield in safflower. The selection of reduced seed hull would result in increase in oil content with reduction in 100-seed weight. This clearly indicated that breeders have to effect more recombinants to break this negative relationship realize lines with higher seed yield and higher oil content and to understand the existing relationships between seed yield and yield attributing traits which often arise because of either genetic linkage or pleiotropy.



** Correlation is significant at the 0.01 level; * Correlation is significant at the 0.05 level

Fig. 2. Correlation among agronomic traits of safflower.

CONCLUSIONS

A comprehensive diversity analysis for nine agronomic traits was taken up with 315 safflower germplasm accessions representing 21 countries. Our results showed significant diversity among the genotypes for most of the agronomic traits studied. The findings suggest that the economic traits can be efficiently improved by exercising appropriate recombination breeding approaches and selection procedures in this important oilseed crop. Cluster analysis based on ward minimum variance grouped the germplasm into seven distinct groups, with geographical origin of the germplasm not having any bearing on the categorization. Promising germplasm accessions identified for the traits can be exploited in future breeding programs for increase of seed oil yield.

FUTURE SCOPE

Food security and quality are major challenges in modern agriculture, which in the near future needs to focus on the increase of global population and general environmental changes. The global consumption of oil has increased in the past few years because of their use in processed products; effort has to be increased in breeding programs aimed to constitute new varieties with high Oil yield. Data generated in this study confirmed that safflower represents a wide phenotypic diversity for agronomic traits. Results reported in this work have highlighted that the potentiality of germplasm accessions and subdividing the accessions divergent for the phenotypic traits considered. The findings suggest that the economic traits can be efficiently improved by exercising appropriate recombination breeding approaches and selection procedures in this important oilseed crop.

Acknowledgement. Authors greatly acknowledge the financial support given by ICAR-Indian Institute of Oilseeds Research, Hyderabad-30, Telangana, India.

Conflict of Interest. None.

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How to cite this article: Usha Kiran B., Dinesh Kumar V. and Uma A. (2023). Study of Genetic Diversity and Relationships between Agronomic Traits in Large Safflower (*Carthamus tinctorius* L.) Germplasm Collection. *Biological Forum – An International Journal, 15*(4): 479-486.