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## Genetic diversity studies in safflower germplasm (*Carthamus tinctorius* L.)

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**Abstract**

The investigation on "Genetic diversity studies in safflower germplasm (*Carthamus tinctorius* L.)" was undertaken to estimate the extent of diversity and to estimate the contribution of each character towards genetic diversity. The set of 63 genotypes along with three checks 'A-1, PBNS-12, PKV Pink' were evaluated at the field of Oilseeds Research Unit, Dr. PDKV, Akola during *rabi* 2018-2019. Based on measurements of genetic diversity by Mahalanobis  $D^2$  distance and grouping by Tocher's method, these genotypes were grouped into ten clusters. Clusters VI and VIII (3896.92) had maximum average inter cluster distance followed by clusters X and VIII (3096.12), clusters III and VI (2772.88), clusters II and VIII (2383.65), clusters V and IV (2296.31). Seed yield per plant (25.69%) contributed maximum towards genetic divergence followed by days to maturity (18.41%), days to 50% flowering (16.08%), number of seeds per capitulum (12.82%) and plant height (10.58).

The present investigation projected the importance of GMU-7363, GMU-5135, GMU-5134 as parents for higher heterosis in F1 and potential transgressive segregants in subsequent generations for earliness as they have least mean for days to maturity whereas high mean of GMU-7448, GMU-5136, GMU-2648, GMU-2928, GMU-667, GMU-1798 GMU-2830 and GMU-7355 for characters viz plant height, number of branches per plant, number of capitula per plant, number of seeds per capitulum, 100 seed weight, volume weight, oil content and seed yield per plant respectively.

**Keywords:** Genetic diversity, safflower, variation, genotype, intra and inter cluster distance

**Introduction**

Oilseed crops are the main source of edible oils with healthy diet and compared to synthetic and animal fat and have become more popular with high demand among consumers. Safflower (*Carthamus tinctorius* L.) is one of such popular *rabi* crop which has a high adaptation to different conditions such as resistance to drought and it is suited to be grown in arid and semi-arid regions. Safflower is an important oilseed crop as it contains 78 per cent of PUFA (Linoleic Acid) which is useful for heart patients as it reduces blood cholesterol levels (Nimbkar 2002) [4]. Safflower possesses considerable diversity across different regions of the world (Knowels, 1969) [3]. In order to design an appropriate breeding programme, it is important to know how much the phenotypic variation of the trait is heritable, since the efficiency of selection programme is mainly dependent on the magnitude of genetic variation and heritability of the trait (Falconer and Mackay, 1996) [2]. The selection of parents for hybridization determines the success of breeding programme. The genetic diversity is the basis of plant breeding created due to inherent genetic differences in the plant species and is of major interest to plant breeder. The more diverse parent, the greater are the chances of obtaining higher amount of heterotic expression in F1 and broad spectrum of variability in segregating generations. The present study was undertaken to estimate the extent of diversity and to estimate the contribution of each character towards genetic diversity.

**Material and Methodology**

Sixty three germplasm lines of safflower along with three checks were sown in augmented design, in a single row plot of five metre length to assess genetic diversity for yield, yield attributing traits and oil content at the field of Oilseeds Research Unit, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola, during *rabi* season 2018-19. The experimental design consisted of seven block design with each block containing nine germplasm lines and three checks. The observations were recorded on five randomly selected plants for ten quantitative traits viz., days to 50% flowering, days to maturity, plant height (cm), number of branches per plant, number of capitula per plant, number of seeds per capitulum, volume weight (g/100ml), 100 seed weight (g), oil content (%) and seed yield per plant (g).

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The data was subjected to D<sup>2</sup> statistics as described by Rao (1952) [5] and genotypes were grouped into different clusters by following Tocher's method using Windstat statistical software.

### Result and Discussion

To analyze genetic diversity among these genotypes, D<sup>2</sup> analysis was carried out. The variation among the genotypes were significant for days to 50% flowering, days to maturity, plant height, number of branches per plant, number of capitula per plant, number of seeds per capitulum, 100 seed weight, volume weight, oil content, seed yield per plant indicating the presence of wide genetic variability for these characters. Variation among the entries was also significant for all characters. The 63 genotypes and 3 checks were grouped into ten clusters by the Tocher's method as shown in table 1. Cluster I was the largest involving 44 genotypes with checks A-1, PBNS-12 and PKV Pink. The next largest cluster was cluster II with 14 genotypes. Cluster III, IV, V, VI, VII, VIII, IX, X involved only one genotype in each cluster.

Average intra and inter cluster statistical distance among ten characters was calculated by Tocher's method and were presented in the table 2. The average inter cluster distance was maximum between cluster VI and VIII (3896.92), followed by cluster X and VIII (3096.12), cluster III and VI (2772.88), cluster II and VIII (2383.65), cluster V and IV (2296.31). The clusters having maximum distance were genetically divergent and hence genotypes in these clusters can be used as parents for hybridization in breeding programme to obtain maximum segregation.

The cluster means of all the 10 characters had presented in the table 3. For days to 50% flowering, least cluster mean was recorded by cluster VIII (64.38), For days to maturity cluster VIII (96.71) showed least cluster mean. In case of 100 seed weight, the highest cluster mean was observed in cluster IX (3.61), for oil content it was highest for cluster VI (36.08), for

seed yield per plant (g) highest cluster mean as cluster V (46.39) followed by cluster VIII (45.65).

The trait seed yield per plant had contributed maximum (25.69%) towards total divergence followed by days to maturity (18.41%), days to 50% flowering (16.08%), number of seeds per capitulum (12.82%), plant height (10.58%), volume weight (8.34%), number of capitula per plant (6.62%), oil content (0.98%) number of branches per plant (0.47%). While 100 seed weight has not shown any contribution towards genetic divergence in the present study. Similar results were also obtained by Tayade (2015) [6] and Atole (2018) [11].

The present study has helped to identify diverse parents for hybridization programmed based on mean performance and cluster formed. The genotypes identified for different characters for further breeding programme are given in Table 5. The present study projected the importance of GMU-7363, GMU-5135, GMU-5134 as parents for higher heterosis in F1 and potential transgressive segregants in subsequent generations as they have least mean for days to maturity, whereas high mean of GMU-7448, GMU-5136, GMU-2648, GMU-2928, GMU-667, GMU-1798, GMU-2830 and GMU-7355 for characters viz plant height, number of branch per plant, number of capitula per plant, number of seeds per capitulum, 100 seed weight, volume weight, oil content and seed yield per plant respectively for their further improvement in respect to yield contributing characters.

Based on maximum intercluster distance, ten different potential cross combinations have been suggested as mentioned in the table 6. GMU-7590 x GMU-972 for high oil with earliness and high yield potential, GMU-4914 x GMU-972 for earliness with moderate volume weight and high yield potential, GMU-590 x GMU-7590 for high plant height with high oil, GMU-2830 x GMU-972 for high oil with earliness, GMU-3438 x GMU-4914 for high hundred seed weight with earliness, GMU-7590 x GMU-6852 for high plant height and high oil with earliness.

**Table 1:** Grouping of genotypes into different clusters

Cluster	No. of Genotypes	Name of Genotypes
1	44	GMU-1758, GMU-5142, GMU-7351, GMU-7355, GMU-7359, GMU-1654, GMU-5149, GMU-2687, GMU-2648, PKV PINK, GMU-3266, GMU-5136, GMU-2347, GMU-2928, GMU-880, GMU-7363, GMU-7456, GMU-955, GMU-2644, A-1, GMU-1798, GMU-1067, GMU-2757, GMU-5135, GMU-5134, GMU-2273, GMU-3944, GMU-2424, GMU-2403, GMU-5133, GMU-667, GMU-1360, GMU-184, GMU-3206, GMU-5097, GMU-974, GMU-609, GMU-884, PBNS-12, GMU-1811, GMU-2486, GMU-2775, GMU-6891, GMU-7593
2	14	GMU-1731, GMU-7591, GMU-1397, GMU-7618, GMU-1894, GMU-7573, GMU-7448, GMU-7581, GMU-6926, GMU-753, GMU-4983, GMU-579, GMU-2830, GMU-589
3	1	GMU-590
4	1	GMU-7569
5	1	GMU-3438
6	1	GMU-7590
7	1	GMU-2380
8	1	GMU-972
9	1	GMU-6852
10	1	GMU-4914

**Table 2:** Average intra and inter cluster distance

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X
Cluster I	494.42	1048.96	708.26	1373.35	808.25	1810.38	731.55	948.21	917.75	1610.65
Cluster II		535.65	1070.48	875.62	1173.88	996.23	1095.76	2383.65	1017.61	1090.95
Cluster III			0	936.62	1800.62	2772.88	1396.25	864.1	677.01	1215.37
Cluster IV				0	2296.31	1883.58	1822.9	2166.42	476.01	1242.89
Cluster V					0	1090.35	826.57	2056.97	1561.49	2148.52
Cluster VI						0	1016.66	3896.92	2094.52	1464.71
Cluster VII							0	1529.27	1646.03	1455.28

Cluster VIII								0	1584.48	3096.12
Cluster IX									0	1351.3
Cluster X										0

**Table 3:** Cluster means for ten characters

	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches/plant	No. of capitula/plant	No. of seeds/capitulum	100 seed wt. (gm)	Volume wt. (gm/ 100 ml)	Oil content (%)	Seed yield/plant (gm)
Cluster I	80.42	113.52	58.33	8.82	20.41	24.7	3.44	42.13	26.16	39.99
Cluster II	88.69	123.52	57.67	7.98	10.79	20.79	2.99	37.76	29.7	24.21
Cluster III	70.38	106.38	57.32	9.1	17.14	11.48	3.01	36.4	24.74	30.35
Cluster IV	83.71	117.05	35.92	6.43	8.81	16.14	3.11	36.97	22.64	21.19
Cluster V	88.57	131.71	65.2	12.71	22.86	30.43	3.17	44.63	30.76	46.39
Cluster VI	104.05	132.05	56.92	8.76	10.81	39.48	2.55	31.83	36.08	27.75
Cluster VII	86.38	112.71	64.36	7.1	16.48	43.48	2.41	38.7	24.54	34.42
Cluster VIII	64.38	96.71	52.12	10.43	21.48	26.14	3.41	51.33	28.58	45.65
Cluster IX	78.71	120.05	40.72	5.43	27.81	15.14	3.61	36.97	24.84	28.39
Cluster X	82.71	119.05	56.62	5.43	10.81	23.14	3.11	10.17	26.64	25.79

**Table 4:** Contribution of each character towards genetic divergence

Source	Times rank first	% contribution
Days to 50% flowering	345	16.08
Days to maturity	395	18.41
Plant height (cm)	227	10.58
No. of branches/plant	10	0.47
No. of capitula/plant	142	6.62
No. of seeds/capitulum	275	12.82
100 seed weight (gm)	0	0
Volume weight (gm)	179	8.34
Oil content (%)	21	0.98
Seed yield/plant (gm)	551	25.69

**Table 5:** Genotype selected for different characters on the basis of cluster formed

Sr. No.	Character	Cluster	Genotypes selected from cluster formed
1	Early maturity (days)	I	GMU-7363(96.71), GMU-5135(104.71), GMU-5134(105.71)
		VIII	GMU-972(106.38)
2	Maximum plant height (cm)	II	GMU-7448(69.92)
		I	GMU-2757(68.76), GMU-1360 (67.79)
		IV	GMU-7569(67.12)
3	Maximum no. of branches	I	GMU-5136 (17.76), PKV Pink (12.71), GMU-2486(12.10)
4	Maximum no. of capitula/plant	I	GMU-2648(31.48), GMU-7351 (29.81), GMU-1360(27.81)
5	Maximum no. of seeds/ capitulum	I	GMU-2928(43.48), GMU-7359(40.48)
		II	GMU-7581 (39.48), GMU-1397(37.14)
6	Maximum 100 seed wt. (g)	I	GMU-667(4.51), GMU-1067(4.41), GMU-884(4.31)
		V	GMU-3438 (4.41)
		II	GMU-1894(4.41)
7	Maximum volume weight (g/100 ml)	I	GMU -1798(53.23), GMU-667 (52.20), GMU-7363(51.33)
8	High oil content (%)	II	GMU-2830(37.37), GMU-7591(36.78), GMU-7581(36.08)
9	Maximum seed yield (g)	I	GMU-7355(50.19), GMU-3266(49.12), GMU-1067 (48.95)

**Table 6:** Maximum intercluster distance and Cross combination suggested

Sr. No.	Cluster combination	Average intercluster distance	Cross combination suggested	Characters to be improved
1	VI x VIII	3896.92	GMU-7590 x GMU-972	High oil with earliness and high yield potential
2	X x VIII	3096.12	GMU- 4914 x GMU-972	Earliness with moderate volume weight and high yield potential
3	III x VI	2772.88	GMU-590 x GMU-7590	High plant height with high oil
4	II x VIII	2383.65	GMU2830 x GMU-972	High oil with earliness
5	V x IV	2296.31	GMU-3438 x GMU-7590	High 100 seed weight With high plant height
6	VIII x IV	2166.42	GMU-972 x GMU-7569	Earliness with plant height
7	V x X	2148.52	GMU-3438 x GMU-4914	High100 seed weight with earliness
8	VI x IX	2094.52	GMU-7590 x GMU-6852	High plant height and high oil with earliness
9	V x VIII	2056.97	GMU-3438 x GMU-972	High100 seed weight with earliness
10	VI x IV	1883.58	GMU-7590 x GMU-7569	High oil with High plant height

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