

## Research Article

# Genetic diversity analysis in selected germplasm lines of safflower (*Carthamus tinctorius* L.)

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### Abstract

In the present study, a total of 155 genotypes along with five checks 'A-1, PBNS-12, AKS-207, PKV Pink, Bhima' were assessed to study the genetic diversity among the genotypes. These genotypes were grouped into eleven clusters based on the measurements of genetic divergence obtained by means of Mahalanobis distance ( $D^2$ ) and in the grouping by Tocher optimization method. The average inter cluster distance was maximum between clusters VI and IX (7037.21) followed by clusters III and IX (6895.24), clusters IX and XI (6756.33), clusters IX and X (5760.02), clusters VII and IX (5724.53) which indicated that the genotypes included in these clusters may give high heterotic responses and thus better segregants. The present study projected the importance of GMU-4502, GMU-4934, GMU-4507 as parents for higher heterosis in  $F_1$  and potential transgressive segregants in subsequent generations as they have least mean values for days to 50% flowering, days to maturity whereas high mean values of GMU-4839, GMU-4934, GMU-40, GMU-5032, GMU-2969, GMU-5663 and GMU-3740 for characters viz. plant height, number of primary branch per plant, number of capitula per plant, volume weight, 100- seed weight, seed yield per plant and oil content respectively suggest their further improvement in respect to these yield attributing characters.

### Keywords

Safflower, Germplasm, Cluster analysis, Genetic divergence.

### Introduction

Safflower (*Carthamus tinctorius* L.), an oilseed crop is a member of the family compositae or asteraceae (Khan et al., 2009). Safflower is a multipurpose crop rich in vitamin A, iron, phosphorus and calcium. It has been grown form centuries in India for the orange-red dye (carthamin) extracted from its brilliantly coloured flowers (Koutroubas et al., 2009) and for its quality oil rich in polyunsaturated fatty acids oleic and linoleic acid, (78%) (Hamdan et al., 2009). The crop develops well under semi-arid conditions, in a diverse range of soil types and is grown in *rabi* season on residual soil moisture. The success of any crop breeding program depends on the nature and magnitude of genetic variability available in the germplasm collections. Collection and evaluation of genotype is a pre-requisite for a successful breeding programme. A quantitative assessment of the genetic divergence among the collection of germplasm and their relative contribution of different traits towards the genetic divergence provide essential and effective information to the breeder in his hybridization programme and thereby genetic improvement of yield. The genetic diversity analysis not only helps in selecting genetically diverse parents but also helps to produce high heterotic effects and desirable segregants. The present investigation was undertaken

to measure the genetic diversity among the germplasm accessions of safflower and to select diverse genotypes which will be further utilized for the further genetic improvement of safflower.

### Material and Methods

The present investigation was, therefore, planned to assess genetic diversity for yield, yield contributing traits and oil content in 155 germplasm lines of safflower along with five checks and these were evaluated in augmented design, in a single row plot of four meter length at the field of Oilseeds Research Unit, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola, during *rabi* season 2015-16. The experimental design consisted of five block design with each block containing 31 germplasm lines and five checks. Checks were common and all recommended cultural practices were followed to raise a good crop. The observations were recorded on five randomly selected plants for eleven quantitative traits viz., days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of capitula per plant, volume weight (g/100ml), 100 seed weight (g), seed yield per plant (g), oil content (%), plant spread (cm) and diameter of main capitula at maturity (cm). The data were subjected to  $D^2$  statistics as described by Rao (1952) and genotypes

were grouped into different clusters by following Tocher's method using Windstat statistical software.

### Results and Discussion

D2 analysis was carried out to analyze genetic divergence among these genotypes. The differences among the genotypes were significant for days to 50% flowering, plant height, number of capitula per plant, volume weight, 100 seed weight, oil content, plant spread and diameter of main capitula at maturity indicating the presence of wide genetic variability for these characters. Cluster analysis by the Tocher optimization method allowed the separation of 155 genotypes into eleven clusters (Table 1). The principle of this method is to maintain homogeneity within groups and also heterogeneity between groups. Cluster I comprised 60 genotypes. The next cluster was cluster II with 56 genotypes and cluster V with 16 genotypes each respectively. Cluster III had 12 genotypes, while cluster VIII contained 5 genotypes. The clusters IV, VI, VII, IX, X, XI involved only a single genotype in the cluster. In cluster II check AKS-207, PKV Pink, Bhima, PBNS-12 and in cluster V check A-1 were included.

Average intra and inter cluster distance values among eleven characters were calculated by Tocher's method and are presented in Table 2. Maximum intra cluster value was observed for cluster VIII (1188.50), hence selection within these clusters might be carried out on the basis of highest mean for the desirable traits. This genetic diversity among the genotypes may be due to genetic architecture of the populations, past history of selection in developmental traits, heterogeneity and degree of general combining ability while the minimum intra cluster value was for cluster I (307.43). These results are in agreement with the earlier reports of Murkute and Deshmukh, 2011. The average inter cluster distance was maximum between clusters VI and IX (7037.21), followed by clusters III and IX (6895.24), clusters IX and XI (6756.33), clusters IX and X (5760.02), clusters VII and IX (5724.53). 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 seed yield per plant, plant height, number of capitula per plant, plant spread, days to 50 percent flowering, days to maturity, volume weight, number of primary branch per plant and oil content contributed significantly towards genetic divergence. An overall study of cluster means for all eleven characters indicated that cluster IX showed maximum mean for characters viz., no. of capitula per plant, 100 seed weight and seed yield. The cluster VI exhibited highest cluster mean

for days to 50 per cent flowering and days to maturity indicating that these genotypes can be utilized for breeding for early duration to escape drought conditions while cluster VIII showed the highest cluster mean for number of primary branch per plant and oil content while cluster XI showed the highest cluster mean for plant height and diameter of main capitula at maturity. Similar results have been reported by Ghongade and Navale, 1995, Diwaker et al., 2006, Sreenivasa et al., 2010 and Shivani and Sreelakshmi, 2013. The contribution of each character towards genetic divergence has been presented in Table 3. The characters contributing to most of the divergence should be given more importance for the purpose of effective selection and the choice of parents for hybridization. The contribution to the total divergence was maximum by seed yield per plant (32.9%), plant height (22.75%), number of capitula per plant (20.68%), plant spread (13.07%), days to 50 per cent flowering (6.2%), days to maturity (2.19%), volume weight (2.14%), number of primary branches per plant (0.06%) and oil content (0.01%). While 100 seed weight and diameter of main capitula at maturity did not show any contribution towards genetic divergence in the present study.

The data on cluster distances and *per se* performance of genotypes were used to select genetically diverse and agronomically superior genotypes. On this basis of the maximum inter cluster values and *per se* performance for seed yield, plant height and oil content the genotypes GMU-4502, GMU-4934, GMU-4507, GMU-4839, GMU-40, GMU-5032, GMU-2969, GMU-5663, and GMU-3740 selected for crossing are expected to give rise to promising segregants for seed yield and hence may be used in future breeding programmes for improvement of yield in safflower.

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**Table1. Grouping of genotypes into different clusters in safflower**

Cluster	Number of genotypes	Genotypes
1	60	GMU-599,GMU-3047,GMU-707,GMU-593,GMU-2860,GMU-5841,GMU-6057,GMU-4972,GMU-4549,GMU-3607,GMU-3281,GMU-4558,GMU-4688,GMU-6851,GMU-2594,GMU-4693,GMU-1875,GMU-1603,GMU-5848,GMU-2413,GMU-2985,GMU-1047,GMU-1871,GMU-774,GMU-5361,GMU-1287,GMU-2987,GMU-3703,GMU-4400,GMU-1855,GMU-2437,GMU-1765,GMU-1315,GMU-2472,GMU-3639,GMU-2749,GMU-1185,GMU-1485,GMU-2969,GMU-671,GMU-4201,GMU-878,GMU-3189,GMU-2616,GMU-4234,GMU-3436,GMU-330,GMU-2944,GMU-864,GMU-4429,GMU-4812,GMU-1354,GMU-3707,GMU-4381,GMU-1339,GMU-1695,GMU-1409,GMU-1626,GMU-473,GMU-3822.
2	56	GMU-4507,AKS-207,PKVPink,GMU-4223,GMU-4627,GMU-5075,Bhima,GMU-3852,GMU-5923,GMU-4420,GMU-6663,GMU-638,GMU-3929,GMU-6424,GMU-6306,GMU-5825,GMU-95,GMU-1708,GMU-216,GMU-5046,GMU-5044,GMU-6506,GMU-5239,GMU-5081,GMU-5908,GMU-1748,GMU-2718,GMU-3084,GMU-224,GMU-6192,GMU-3386,GMU-6312,GMU-6548,GMU-2432,GMU-3537,GMU-1078,GMU-4966,GMU-6119,PBNS-12,GMU-2016,GMU-5163,GMU-1059,GMU-3629,GMU-5133,GMU-765,GMU-3617,GMU-3256,GMU-4305,GMU-4038,GMU-2136,GMU-6252,GMU-2198,GMU-1638,GMU-4696,GMU-3812,GMU-1824
3	12	GMU-3491,GMU-5935,GMU-2240,GMU-7191,GMU-1250,GMU-1137,GMU-4646,GMU-819,GMU-3177,GMU-4773,GMU-744,GMU-3740.
4	1	GMU-5701.
5	16	GMU-659, GMU-5170,GMU-5728,GMU-6026,GMU-3968,GMU-4623,A-1,GMU-4109,GMU-821,GMU-3095,GMU-4502,GMU-5295,GMU-4934,GMU-40,GMU-3208,GMU-5032.
6	1	GMU-4010
7	1	GMU-6556
8	5	GMU-3780, GMU-4066,GMU-2129,GMU-6869,GMU-5668.
9	1	GMU-5663
10	1	GMU-5335
11	1	GMU-4839



**Table 2. Average intra and inter cluster distances in safflower**

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X	Cluster XI
Cluster I	307.43	885.79	614.52	456.57	2907.74	509.32	561.27	1417.23	5591.33	1349.47	1739.91
Cluster II		424.86	1632.11	742.74	1329.47	1256.61	993.40	915.20	3169.78	1737.32	1753.83
Cluster III			613.42	1062.15	4100.42	1084.28	1015.47	2246.83	6895.24	2033.43	2787.42
Cluster IV				0.00	2714.65	274.22	134.74	1314.05	5390.83	610.55	637.78
Cluster V					890.17	3589.75	3130.20	1617.33	1552.18	3790.39	3671.74
Cluster VI						0.00	482.60	1690.03	7037.21	958.07	845.54
Cluster VII							0.00	1408.69	5724.53	570.34	897.52
Cluster VIII								1188.50	3348.17	1953.48	2127.33
Cluster IX									0.00	5760.02	6756.33
Cluster X										0.00	743.04
Cluster XI											0.00

**Table 3. Contribution of each character towards genetic divergence in safflower**

Sr. No	Source	Times rank first	% contribution
1	Days to 50 % Flowering	740	6.2
2	Days to Maturity	261	2.19
3	Plant height (cm)	2715	22.75
4	No.of pri.branch/Plant	7	0.06
5	No. of capitula/ plant	2468	20.68
6	Volume.wt (g/100ml)	256	2.14
7	100 seed wt (gm)	00	0.00
8	Seed yield /plant	3927	32.9
9	Oil content (%)	1	0.01
10	Plant spread (cm)	1560	13.07
11	Diameter of main capitula at maturity	00	0.00

**Table 4. Genotype selected for different characters on the basis of cluster formed in safflower**

Sr. No	Character	Cluster	Genotypes selected from cluster formed
1	Early maturity	V	GMU-4502(127), GMU-4934(131)
		II	GMU-4507(129) GMU-5044(131)
2	Late Maturity	II	GMU-1638(147)
		I	GMU-1875(147)
3	Maximum plant height	XI	GMU-4839(88.96)
		VIII	GMU-5668(87.28)
4	Maximum primary branch	V	GMU-4934(14.92), GMU-5295(13.28)
		II	GMU-6663(13.28)
5	No.of capitula/plant	V	GMU-40(73.88)
6	Maximum volume wt.	V	GMU-5032(64.79), GMU-4109(64.49)
		II	GMU-3256(64.37)
7	Maximum 100 seed weight	I	GMU-2969(7.88), GMU-4201(7.25)
		II	GMU-95(7.19), GMU-2198(7.19)
8	Maximum seed yield	IX	GMU-5663(78.73)
9	High oil	III	GMU-3740(31.28)
		II	PKV Pink (30.70)
		VIII	GMU-6869(30.12)
10	Plant spread	V	GMU-3208(73.87)
11	Diameter of main capitula	II	GMU-3617(3.1), GMU-3629(3.1)



**Table 5 . Cluster means for various characters in safflower**

	<b>Days to 50% flowering</b>	<b>Days to maturity</b>	<b>Plant height (cm)</b>	<b>No.of primary branch/Plant</b>	<b>No. of capitula/plant</b>	<b>Volume.wt (g/100ml)</b>	<b>100 seed wt (gm)</b>	<b>Seed yield /plant</b>	<b>Oil content (%)</b>	<b>Plant spread (cm)</b>	<b>Diameter of main capitula at maturity</b>
<b>Cluster I</b>	90.21	142.07	50.61	5.96	23.35	56.19	5.48	14.53	27.87	32.13	2.43
<b>Cluster II</b>	86.77	139.87	58.44	8.13	33.50	55.99	5.50	28.72	28.11	43.92	2.55
<b>Cluster III</b>	86.98	140.74	40.23	5.48	19.36	54.15	4.80	11.65	27.45	26.39	2.39
<b>Cluster IV</b>	85.60	140.76	65.69	5.09	18.42	60.02	4.96	17.43	26.21	34.15	2.50
<b>Cluster V</b>	89.74	139.98	62.07	10.16	50.44	55.87	5.41	45.59	28.08	54.20	2.55
<b>Cluster VI</b>	94.60	144.76	65.17	6.53	20.12	59.47	3.46	4.85	28.45	31.67	2.50
<b>Cluster VII</b>	79.60	141.76	64.69	5.09	19.22	59.22	5.66	18.73	28.42	24.75	2.30
<b>Cluster VIII</b>	90.72	141.20	63.09	10.26	42.48	54.14	4.47	30.03	28.66	33.91	2.25
<b>Cluster IX</b>	92.60	140.76	57.49	8.89	51.82	55.14	6.16	78.73	27.01	53.15	2.50
<b>Cluster X</b>	93.60	143.76	75.89	5.29	10.02	54.93	2.96	28.53	24.77	19.75	1.90
<b>Cluster XI</b>	88.40	136.96	88.97	5.93	16.84	53.17	3.15	14.27	23.26	35.31	2.78