Research Note

Assessment of genetic diversity in safflower germplasm lines (*Carthamus tinctorius* L.)

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Abstract
Twenty safflower germplasm lines were assessed for genetic divergence for seven characters using Mahalanobis D^2 statistic and principal component analysis. Test weight contributed maximum towards genetic divergence followed by oil content. All the germplasm lines were grouped into seven clusters. Clusters III and II were the best clusters based on seed yield and oil content. The first three principal components explained 83.16% variability. Maximum intercluster distance was observed between cluster IV and VII.

Keywords
Safflower, genetic divergence, Principal Component Analysis, D^2 analysis

Safflower (*Carthamus tinctorius* L.) is a drought tolerant and important oilseed crop grown during rabi *rabi* season on receding soil moisture. The crop is grown not only for oil but also for extraction of pigment from the flowers which is used for dyeing. Identification and utilization of diverse germplasm is the central issue in plant breeding. More accurate and complete descriptions of elite breeding materials and understanding the patterns of genetic diversity could help determine future breeding strategies and facilitate introgression of diverse germplasm into the current genetic base. Mahalonobis D^2 statistic is widely used for analysis of genetic diversity by many researchers in crop plants (Rao, 1952).

Twenty safflower germplasm lines obtained from Directorate of Oilseeds Research, Hyderabad were sown in Random Block Design at Agricultural Research Station, Tandur during *rabi* 2013-14. The entries were sown in 5m long four row plots with a spacing of 45 cm between the rows and 20 cm between the plants. The recommended agronomic practices have been followed to raise a good crop. Five plants were randomly selected for recording data on the following seven characters *viz*, days to 50% flowering, days to maturity, number of effective capitula per plant, number of seeds per capitula, test weight (g), seed yield (kg/ha) and oil content (%). Mahalonobis D^2 statistic and Principal Component Analysis (PCA) (Jackson, 1991) has been used to analyze genetic divergence among the selected set of safflower gemplasm lines.

The Mahalonobis D^2 values have grouped the twenty GMU lines (Table 1) to seven distinct clusters with cluster I comprising of 8 genotypes followed by cluster III with 5 genotypes, cluster II with 3 genotypes while the remaining clusters IV, V, VI and VII consisted of one genotype each (Table 2). The average intra and inter cluster distances are depicted in (Table 3). The intra D^2 values ranged from 0 (cluster IV, V, VI and VII) to 5.74 (cluster III). The maximum inter cluster distance was between cluster V and VII (10.83) followed by cluster III and IV (10.65). Cluster III recorded highest mean values for test weight (5.14g) and seed yield (1044.45kg/ha), cluster II recorded highest oil content of 31.92% while cluster IV had highest number of capitula per plant (35.40) indicating that neighboring clusters had high yielding genotypes (Table 4). The GMUs falling under these categories may be utilized in hybridization program for improvement of seed yield and oil content. Similar results have been reported by earlier researchers (Ghongade and Navale, 1995; Shivani and Sreelakshmi, 2013). Cluster IV recorded earliness for days to 50% flowering and days to maturity in addition to more number of capitula per plant indicating that these genotypes can be utilized for breeding for early duration to escape drought conditions. Contribution of various characters towards divergence was presented in (Table 5). Maximum contribution towards genetic divergence is by test weight (38.95) followed by oil content (27.89) and seed yield (17.89). These characters together recorded for more than 80% of the total divergence in the twenty germplasm lines studied. While earlier studies have reported maximum contribution by seed yield for genetic divergence (Shivani and Sreelakshmi, 2011, 2013). The first three principal components explained 83.16% variability with PC1 explaining maximum variability (44.81%).

The genotypes GMU-3876 (cluster IV), GMU-3708 (cluster V), GMU-3816 (cluster VI) and GMU-2551(cluster VII) are genetically divergent

and grouped into different clusters. The genotypes in cluster IV (GMU-3876) have earliness and more number of capitula per plant while in those in cluster VII (GMU-2551) has more number of seeds per capitula. The genotypes in cluster III have high mean seed yield and test weight and the genetic distance between genotypes in cluster III and those in cluster IV, V and VI are 10.65, 10.49 and 10.38 respectively indicating that these genotypes can be utilized in crossing program for the development of early varieties which can escape drought along with high seed yield.

References

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Table 1. Safflower genotypes used in the present study

S. No	Genotype
1	GMU-3876
2	PBNS-12
3	GMU-3856
4	GMU-3816
5	A1
6	MANJEERA
7	GMU-3796
8	GMU-3781
9	GMU-3719
10	GMU-3716
11	GMU-3708
12	GMU-3663
13	GMU-2366
14	GMU-3924
15	GMU-3963
16	GMU-2551
17	GMU-3638
18	GMU-3923
19	GMU-3438
20	GMU-3971

Table 2. Clustering of twenty safflower genotypes

Cluster No.	No. of Genotypes	Name of the Genotype
I	8	PBNS-12, GMU-2366, GMU-3856, GMU-3663, GMU-3638, GMU-3923, A1, GMU-3716
II	3	GMU-3781, GMU-3924, GMU-3796
III	5	GMU-3719, GMU-3963, GMU-3438, GMU-3971, MANJEERA
IV	1	GMU-3876
V	1	GMU-3708
VI	1	GMU-3816
VII	1	GMU-2551

Table 3. Average Inter and intra cluster distances (D^2) of seven clusters in safflower germplasm

	I	II	III	IV	V	VI	VII
I	4.56	6.24	7.31	6.25	5.97	6.89	8.01
II		3.94	9.08	6.54	8.51	7.00	6.03
III			5.74	10.65	10.49	10.38	7.52
IV				0.00	4.76	7.03	9.09
V					0.00	5.68	10.83
VI						0.00	8.26
VII							0.00

Table 4. Cluster means of seven clusters for seven characters in safflower germplasm

Cluster	Days to 50% flowering	Days to maturity	No. of effective capitula/plant	No. of seeds/capitula	Test weight (g)	Seed yield (kg/ha)	Oil content (%)
I	81.06	115.69	31.86	19.29	4.19	754.65	27.64
II	80.83	115.50	25.20	20.17	3.15	762.55	31.92
III	80.80	115.30	29.28	20.30	5.14	1044.45	28.81
IV	72.00	105.50	35.40	19.46	3.20	982.23	27.12
V	73.00	107.00	27.80	14.44	4.25	574.45	25.84
VI	73.50	107.50	16.90	17.98	4.10	240.00	29.95
VII	74.00	107.50	21.80	24.86	3.85	995.56	31.55

Table 5. Percent contribution of different characters towards genetic divergence in safflower

Character	% contribution	Times ranked first
Days to 50% Flowering	7.37	14
Days to Maturity	0.00	0
No. of Effective Capitula/Plant	0.53	1
No. of Seeds/Capitulum	6.32	12
Test Wight (g)	38.95	74
Seed Yield (Kg/ha)	17.89	34
Oil Content (%)	27.89	53

Table 6. Eigen values and proportion of total variance represented by three principal components of safflower gemplasm germplasm

	PC1	PC2	PC3
Eigen Value (root)	216.71	126.54	58.98
Percent Var. Exp	44.81	26.16	12.19
Cumulative Var. Exp	44.81	70.98	83.17
Days to 50% Flowering	0.10	0.03	0.63
Days to Maturity	0.01	0.01	0.10
No. of Effective Capitula/Plant	0.001	0.10	0.15
No. of Seeds/Capitulum	0.07	-0.20	-0.49
Test Wight (g)	0.73	0.60	-0.26
Seed Yield (Kg/ha)	0.47	-0.19	0.39
Oil Content (%)	0.46	-0.70	-0.10

*PC= Principal Component