Electronic Journal of Plant Breeding, 2(4):563-567 (Dec 2011)
ISSN 0975-928X

Research Note

Canonical variate analysis in safflower (*Carthamus tinctorius* L.)

D.Shivani*, Ch. Sreelakshmi and C.V. Sameer Kumar
Agricultural Research Station, ANGRAU , Tandur – 501 141,
*Email ID: rishith_sree@rediffmail.com

(Received: 09 Oct 2011; Accepted: 11 Nov 2011)

Abstract:
Seventy five genotypes of safflower representing the broad spectrum of variation were assessed for genetic divergence for eight characters using Mahalanobis D^2 statistic and principal component analysis. The seed yield contributed maximum towards the total genetic divergence followed by test weight and number of seeds per capitulam. On the basis of clustering method, twelve clusters were obtained for D^2 statistic. The best clusters with regard to seed yield and oil content were cluster XII and cluster II, respectively. Principal component analysis identified three principal components which explained 83.02% variability. Genotypes GMU 3470, GMU 3484, GMU 3499, A-1, JSF-1 and GMU 3475 (based on PCI axis) were divergent.

Key words: safflower, D^2 analysis, Principal Component Analysis

Safflower (*Carthamus tinctorius* L.) is an important oil seed crop and its oil constitutes an important source of PUFA in the oil based diets of many people in India. For improvement programme of existing safflower varieties, the selection of suitable diverse parents for hybridization is an important step for getting desired recombinations in the segregating generations. The D^2 classifies the genotypes into homogenous groups / clusters with little diversity within cluster while diversity between two clusters is usually high. Thus representative genotypes from diverse clusters can be earmarked for utilization in hybridization programme depending upon breeding objective. Since, the literature in respect of genetic divergence studies in safflower is meager, present investigation was undertaken to assess the presence of genetic diversity among safflower germplasm lines. Traditionally Mahalonobis D^2 statistic to measure genetic divergence as suggested by Rao (1952) has been used by different workers. The PCA technique has been applied in this study to identify divergent genotypes.

Seventy five safflower GMU lines obtained from Directorate of Oilseeds Research, Hyderabad were sown in Augumented Block Design at Agricultural Research Station, Tandur during rabi 2010-11. The entries were grown in 5 m long single row plots with a spacing of 20 cm between the plants and 45 cm between the rows. Recommended cultural practices were followed to raise a good crop. Five competitive plants from each line were randomly selected for recording observations for seven metric characters *viz.*, days to 50% flowering, days to maturity, number of capitula per plant, number of seeds per capitulum, test weight (g), seed yield (kg/ha) and oil content(%). Genetic divergence among 75 genotypes was analyzed by using Mahalanobis's D^2 statistic (Rao, 1952) and Principal Component Analysis (PCA) as described by Jackson (1991).

On the basis of D^2 values, the seventy five GMU lines (Table 1) were grouped into twelve clusters with cluster I possessing 26 genotypes followed by cluster III with 14 genotypes, cluster II with 11 genotypes, cluster VI with 9 genotypes, cluster V with 8 genotypes while the remaining clusters i.e., cluster IV, VII, VIII, IX, X, XI and XII consisted of single genotypes as shown in Table 2.

Based upon agglomerative cluster analysis, intra cluster D^2 values ranged from 0.00 (cluster IV, VII, VIII, IX, X, XI and XII) to 10.36 (cluster VI) whereas, maximum inter cluster distance was observed between cluster VI and XII (33.82) followed by cluster VII and XII (33.77) and cluster VI and XI (33.72) while the least D^2 values were recorded between cluster II and cluster IV (8.30) followed by cluster I and VI (9.46) and cluster I and VII (9.89) . D^2 statistic revealed (Table 4) that cluster XII recorded highest mean values for number of capitula per plant (23.00), number of seeds per capitulum (30.00) and seed yield (2009.50kg/ha) while cluster II recorded the highest mean values for test weight (5.05 g) and oil content (28.21%). The genotypes falling under these clusters may be tried for direct adoption and hybridization for improvement of yield. These results are in agreement with earlier findings of Diwakar *et al*., (2006). Cluster VII recorded the highest mean value for days to 50% flowering (88.50) and days to maturity (118.50), while cluster XI recorded for highest mean values for plant height (89.00). D2 statistic showed that the (Table 5) characters contributing towards divergence revealed that the maximum contribution towards divergence is by seed yield (42.52%) followed by test weight (27.89%), number of seeds per capitulum (12.61%) and number of capitula per plant (8.25%). These four characters altogether accounted for more than 80% of the total divergence in 75 GMU lines studied. Patil *et al*. (1991) and Patel (1990) reported similar findings in safflower.

The distribution of genotypes based on PCA values are shown in 3D plot where the genotypes (37 and 73) and (66 and 22) were away from other genotypes on the basis of PCA I and PCA II scores (Table 6). The first three principal components showed eigene values more than one and they altogether explained 83.78% of the variability. The first PC explained 55.28% of the total variability in the set of all variables and remaining ones accounted for progressively lesser amount of variation.

The above methods of grouping revealed a single concept of non-correspondence of genetic divergence and geographical diversity. The genotypes GMU 3470, GMU 3484, GMU 3499, A1, JSF 1 and GMU 3475 were found divergent. Arunachalam and Bandopadhyay (1984) have proved experimentally more number of heterotic combinations with higher level of heterosis from the parents grouped into moderate divergent groups. Hence, selection of varieties should be more dependent on genetic diversity than the geographical diversity. Similar findings were also reported by Pawar *et al*. (2006).

References

Arunachalam, V. and Bandopadhyay, V.A. 1984. Limits to genetic divergence for occurrence of heterosis-Experimental evidence from the crop plants. *Indian J. Genet.,* **44** (3): 548-554.

Diwakar, R. Sreedhar, N. and Mukta, N. 2006. Studies on genetic diversity in safflower, *Carthamus tinctorius* L. *J.Oilseeds Res.,* **23**:301-303.

Jackson, J. E. 1991. A User's Guide to Principal Component. John Wiley and sons, New York.

Patel, D. P. 1990. Genetic divergence in safflower (*Carthamus tinctorius* L.). *Indian J. Pl. Genet. Resources,* **3**: 13-20.

Patil, B. R., Dudhe, R. S., Ghorpade, P. B., Dhumale, D. B. and Deshmukh, M. P. 1991. Studies on genetic divergence in safflower. *J. Maharashtra Agrl. Univ.,* **16**:59-62.

Pawar, K.M., Joshi, B.M., Jagtap, P.K. and Jawanjal. 2006. Genetic divergence in safflower, *Carthamus tinctorius* L. *J. Oilseeds Res.,* **23**: 96-97.

Rao, C.R. 1952. *Advanced statistical methods in biometrical research*. John Wiley and Sons, Inc. New York.

Table 1 Genotypes of safflower selected for the study

S.No	Genotype	S.No	Genotype	S.No	Genotype
1	GMU 3431	26	GMU3460	51	GMU3493
2	GMU3432	27	GMU3462	52	GMU3494
3	GMU3433	28	GMU3463	53	GMU3495
4	GMU3434	29	GMU3465	54	GMU3496
5	GMU3435	30	GMU3467	55	GMU3499
6	GMU3436	31	GMU3468	56	GMU3501
7	GMU3438	32	GMU3469	57	GMU3502
8	GMU3439	33	GMU3470	58	GMU3503
9	GMU3441	34	GMU3472	59	GMU3504
10	GMU3442	35	GMU3473	60	GMU3505
11	GMU3443	36	GMU3474	61	GMU3506
12	GMU3444	37	GMU3475	62	GMU3507
13	GMU3445	38	GMU3476	63	GMU3508
14	GMU3446	39	GMU3477	64	GMU3509
15	GMU3447	40	GMU3478	65	GMU3510
16	GMU3448	41	GMU3480	66	GMU3511
17	GMU3449	42	GMU3481	67	GMU3512
18	GMU3450	43	GMU3482	68	GMU3513
19	GMU3451	44	GMU3484	69	GMU3514
20	GMU3452	45	GMU3485	70	GMU3515
21	GMU3454	46	GMU3486	71	A1
22	GMU3455	47	GMU3488	72	Manjira
23	GMU3456	48	GMU3490	73	JSF 1
24	GMU3458	49	GMU3491	74	HUS 305
25	GMU3459	50	GMU3492	75	Bhima

Table 2 Clustering pattern of 75 safflower GMU lines by Tocher's method

Cluster No.	No.of genotypes	Name of the genotype
I	26	GMU3446, GMU3465, GMU3434, GMU3490, GMU3456, GMU3435, GMU3459, GMU3449, GMU3447, GMU3474, GMU3488, GMU3441, GMU3510, Bhima, GMU3458, GMU3482, GMU3478, GMU3442, GMU3439, GMU3450, GMU3448, GMU3481, GMU3468, GMU3485, GMU3467, GMU3454.
II	11	GMU3491, GMU3492, GMU3452, GMU3451, GMU3493, GMU3432, GMU3515, GMU3444, GMU3443, GMU3438, GMU3455.
III	14	GMU 3431, GMU3445, GMU3463, GMU3469, GMU3495, GMU3480, HUS 305, Manjira, GMU3507, GMU3477, GMU3505, GMU3508, GMU3512, GMU3502.
IV	1	GMU3509
V	8	GMU3486, GMU3494, GMU3514, GMU3506, GMU3513, GMU3511, GMU3501, GMU3496
VI	9	GMU3460, GMU3462, GMU3476, GMU3472, GMU3503, GMU3504, GMU3436, GMU3433, GMU3473
VII	1	GMU3470
VIII	1	GMU3484
IX	1	GMU3499
X	1	A1
XI	1	JSF 1
XII	1	GMU3475

Table 3. Average intra and inter cluster distance (D2) values of twelve clusters in safflower

	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	6.71	10.18	10.14	8.30	16.40	9.46	9.89	11.68	21.72	14.62	30.99	31.21
II		7.27	11.85	12.64	14.20	10.81	15.52	15.97	22.36	18.16	30.70	31.51
III			8.77	11.96	12.35	13.50	14.41	10.30	15.91	13.56	24.83	26.06
IV				0.00	19.35	10.88	11.75	12.84	23.38	12.03	32.39	33.69
V					8.64	18.37	21.20	14.76	12.71	18.69	19.83	21.48
VI						10.36	12.11	14.76	24.77	17.33	33.72	33.82
VII							0.00	13.68	25.26	19.53	34.10	33.77
VIII								0.00	14.49	10.38	24.37	23.92
IX									0.00	18.16	10.36	14.68
X										0.00	27.37	28.99
XI											0.00	15.27
XII												0.00

Table 4. Cluster mean values of twelve clusters for eight characters in safflower

Cluster	**Days to 50% flowering**	**Days to maturity**	**Plant height (cm)**	**Number of capitula per plant**	**Number of seeds per capitulum**	**Test weight (g)**	**Seed yield (kg/ha)**	**Oil content (%)**
I	81.77	111.77	65.54	17.96	18.85	4.07	601.08	27.09
II	77.59	107.59	71.64	19.09	17.23	5.05	653.59	28.21
III	80.54	110.54	69.82	21.50	19.71	3.95	866.82	27.05
IV	76.00	106.00	82.50	17.50	22.50	3.63	479.50	26.50
V	80.13	109.50	70.69	21.00	20.00	4.80	1194.94	27.92
VI	83.28	113.22	67.78	12.78	20.56	4.58	544.67	27.69
VII	88.50	118.50	57.00	9.00	10.50	3.54	544.00	26.25
VIII	82.50	112.50	60.00	12.00	29.50	3.50	1001.50	26.65
IX	81.00	111.00	73.00	21.50	26.00	3.58	1521.50	26.75
X	82.00	112.00	82.50	22.00	40.50	3.24	820.00	26.85
XI	82.00	112.00	89.00	22.00	21.50	3.49	1905.50	26.50
XII	84.00	114.00	47.50	23.00	30.00	4.11	2009.50	24.50

Table 5 Contribution of different characters towards genetic divergence in safflower

Character	% contribution towards divergence	Times ranked first
Days to 50% flowering	0.86	24
Days to maturity	0.04	1
Plant height (cm)	7.21	200
Number of capitula per plant	8.25	229
Number of seeds per capitulum	12.61	350
Test weight (g)	27.89	774
Seed yield (kg/ha)	42.52	1180
Oil content (%)	0.61	17

Table 6. Eigene values, proportion of the total variance represented by first three principal components, cumulative percent variance and component loading of different characters in safflower

	PC1	PC2	PC3
Eigene value (root)	3663.71	1312.94	576.25
Percent Var. Exp	55.28	19.81	8.69
Cumulative variance explained	55.28	75.09	83.79
Days to 50% flowering	0.001	0.049	0.082
Days to maturity	0.006	0.026	0.022
Plant height (cm)	-0.042	0.018	-0.126
Number of capitula per plant	-0.139	-0.106	-0.215
Number of seeds per capitulum	-0.155	0.072	0.951
Test weight (g)	0.025	-0.961	0.105
Seed yield (kg/ha)	-0.967	0.009	-0.108
Oil content (%)	-0.129	-0.233	-0.035

* PC= Principal component