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GENETIC DIVERGENCE IN SAFFLOWER GERMPLASM (*Carthamus tinctorius* L.)

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ABSTRACT

One hundred fifty (*Carthamus tinctorius* L.) genotypes included five check varieties from Directorate of Oilseeds Research, Hyderabad were evaluated to study the genetic diversity existing among them by using Mahalanobis D^2 statistics. The genotypes were grouped into sixteen clusters. The pattern of distribution of genotypes into various clusters, maximum numbers of genotypes present in cluster IX (17) followed by cluster X (15). Maximum inter-cluster distance was observed between cluster I and cluster VI and minimum inter-cluster distance between cluster III and cluster IX. The maximum intra-cluster distance was obtained for cluster XI whereas minimum intra-cluster distance lowest was shown by cluster I. The inter-cluster distance was higher than the intra-cluster distance indicates that wide genetic diversity among the accessions of different groups. Genotypes of cluster XIV, VIII, III, I, XI, XII and VII showed highest mean value for days to 50% flowering, plant height, plant population, diameter of main capitulum, number of seeds per capitulum, hull content and seed yield, respectively. GMU- 3713, GMU- 3637, GMU- 3778, GMU-3777 and GMU- 3700 are the highest yielder in cluster VII. Based on present study these particular varieties could be used as parents in hybridization programmes.

Key words : *Safflower, genetic divergence, germplasm*

Safflower (*Carthamus tinctorius* L.) is one of the major oilseed crops after groundnut. It is especially grown for its good oil quality rich in vitamin E, linoleic acids and oleic acids. In India area under safflower crops are 2.95 lakh ha. and production1.89 lakh ton. Safflower is one of the important rabi oil seed crop in Chhattisgarh. It is grown as a sole crop as well as mixed crop/ inter- crop with gram and wheat. Area under safflower crop is 850 ha and productivity is 294 kg/ha. production is 0.250 ton (1). Careful selection of parents for hybridization programme will decide the extent of possible improvement in the genotypes under consideration. Improvement is primarily depends on the diversity of the parents. Hence an attempt was to make to classify the genotypes into different clusters by D^2 analysis. The existence of genetic divergence among the 150 safflower genotypes was examined by employing Mahalanobis's D^2 statistics.

MATERIALS AND METHODS

The experimental material comprised of 150 safflower germplasm accessions included 5 check varieties (A-1, Manjira, PBNS-12, PBNS-40 and JSF-1) received from the Germplasm Management Unit (GMU) of safflower, Directorate of Oilseeds Research, Hyderabad. The genotypes were evaluated in Randomized Complete Block Design at Research and Instructional farm, IGKV, Raipur (C.G.). The spacing was maintained at 45 cm x 20 cm. Recommended packages and practices. Data were recorded for 13 economic traits on an average 5 plants over two replications and mean values were used for analysis. Analysis for genetic divergence using Mahalanobis D^2 was carried out as described by (2). The genotypes were grouped into number of clusters by Tocher's method as described by (2).

RESULTS AND DISCUSSION

The 150 germplasm accession and 5 check varieties were grouped into sixteen clusters by using D^2 (Table 1). Maximum numbers of genotypes present in cluster IX (17) followed by cluster X (15) were the minimum number of genotypes present in cluster VI (5) followed by cluster I (4). As already reported by researchers on safflower (3, 4, 5, 6). The highest inter-cluster D^2 values was observed between cluster I and cluster VI (30.980) followed by cluster I and cluster XVI (28.206), cluster VI and cluster XI (27.541), cluster VI and cluster XII (26.512), cluster I and cluster XIV (24.700). The lowest inter cluster was found between cluster III and cluster IX (6.620) followed by cluster V and cluster VII (6.630), cluster IX and cluster X (6.653). The inter-cluster distance was higher than the intra-cluster distance indicates that wide genetic diversity among the accessions of different groups. The intra and inter

Table-1 : Clustering pattern 0f 150 Safflower genotypes.

Cluster No.	No. of Genotypes	Name of genotypes
I	4	GMU-3701, GMU-3727, GMU-3730, GMU-3735
II	14	GMU-3644, GMU-3654, GMU-3656, GMU- 3659, GMU-3670, GMU-3691, GMU-3692, GMU-3702, GMU-3744, GMU-3746, GMU-3768, GMU-3780, GMU-3798, A-1
III	10	GMU-3639, GMU-3673, GMU-3723,GMU-3725, GMU-3729, GMU-3733, GMU-3737, GMU-3745, GMU-3747, GMU-3756
IV	8	GMU-3652, GMU-3681, GMU-3690, GMU-3760, GMU-3762, GMU-3776, GMU-3791, GMU-3799
V	16	GMU-3625, GMU-3628, GMU-3635, GMU-3649, GMU-3660, GMU-3667, GMU-3678, GMU-3711, GMU-3715, GMU-3716, GMU-3719, GMU-3738, GMU-3750, GMU-3769, GMU-3792, GMU-3796
VI	5	GMU-3621, GMU-3642, GMU-3643, GMU-3671, JSF-1
VII	9	GMU-3637, GMU-3700, GMU-3704, GMU-3713, GMU-3753, GMU-3766, GMU-3777, GMU-3778, GMU-3794
VIII	11	GMU-3626,GMU-3658,GMU-3666,GMU-3684,GMU-3757,GMU-3765,GMU-3770,GMU-3772, GMU-3773,GMU-3782,GMU-3793
IX	17	GMU-3624, GMU-3631, GMU-3632, GMU-3653, GMU-3682, GMU-3683, GMU-3693, GMU-3694, GMU-3699, GMU-3703, GMU-3720, GMU-3722, GMU-3726, GMU-3749, GMU-3754, GMU-3781, Manjira
X	15	GMU-3641, GMU-3646, GMU-3647, GMU-3651, GMU-3661, GMU-3696, GMU-3706, GMU-3708, GMU-3734, GMU-3736, GMU-3743, GMU-3748, GMU-3764, GMU-3775, GMU-3800
XI	5	GMU-3636, GMU-3676, GMU-3718, GMU-3721, GMU-3750
XII	7	GMU-3634, GMU-3675, GMU-3677, GMU-3709, GMU-3761, GMU-3786, GMU-3789
XIII	7	GMU-3633, GMU-3638, GMU-3640, GMU-3679, GMU-3698, PBNS-12, PBNS-40
XIV	7	GMU-3662, GMU-3663, GMU-3664, GMU-3771, GMU-3774, GMU-3783, GMU-3790
XV	9	GMU-3623, GMU-3648, GMU-3668, GMU-3672, GMU-3674, GMU-3705, GMU-3731, GMU-3740, GMU-3741
XVI	6	GMU-3645, GMU-3680, GMU-3686, GMU-3687, GMU-3759, GMU-3787

cluster value (Table-2) Whereas minimum distance indicates that close relationship between this clusters and hybridization among the genotypes of these cluster would not provide provides good results. The greater distance between clusters, wider the genetic diversity between these genotypes. High divergent genotypes would produce for selection and improvement. The hybrids were produced from the selected genotypes and it is useful for desirable transgressive segregants and higher magnitude of heterosis. This would be useful in safflower breeding programmes.

The maximum intra-cluster distance was obtained for cluster XI (8.317) followed by cluster XIII (7.935), cluster XV (7.840), cluster VI (7.650). The lowest intra-cluster was shown by cluster I (6.315), cluster VII (6.553). The intra-cluster distance varied from 6.315 to 8.317. The data on cluster mean is presented (Table-3). Genotypes of cluster XIV, VIII, III, I, XI, XII and VII showed highest mean value for days to 50% flowering, plant height, plant population, diameter of main capitulum, number of seeds per capitulum, hull content and seed yield, respectively. GMU- 3713, GMU-3637, GMU-3778, GMU-3777 and GMU-3700 are the highest yielder in cluster VII. Based on present study these particular varieties could be used as parents in hybridization programmes. Similar findings were reported by (7) for high seed yield in GMU 3494, GMU 3482, GMU 3514 and GMU 3443.

Table-2 : Average intra (bold) and inter-cluster distance.

Cluster N0.	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI
I	6.315 (2.513)	14.077	13.778	16.974	11.916	30.980	22.353	18.447	13.410	20.016	19.123	18.096	18.147	24.700	24.039	28.206
II	3.752	6.895 (2.626)	11.431	8.856	8.231	12.131	11.628	7.252	7.728	11.710	22.924	15.031	15.233	12.766	11.943	11.235
III	3.712	3.381	6.943 (2.635)	14.025	8.497	15.968	7.382	10.407	6.620	8.242	15.405	14.258	15.944	15.936	12.489	16.451
IV	4.120	2.976	3.745	7.317 (2.705)	14.025	24.059	17.994	7.064	13.278	12.383	16.564	10.246	21.068	10.634	17.598	8.265
V	3.452	2.869	2.915	3.745	7.038 (2.653)	16.337	6.630	12.730	8.708	7.958	17.131	9.834	11.971	20.079	9.941	13.853
VI	5.566	3.483	3.996	4.905	4.042	7.650 (2.766)	15.069	16.548	9.535	11.397	27.541	26.512	14.561	20.793	17.313	21.622
VII	4.728	3.410	2.717	4.242	2.575	3.882	6.553 (2.560)	11.269	8.696	11.669	14.478	15.397	12.837	22.080	11.539	16.265
VIII	4.295	2.693	3.226	2.658	3.568	4.068	3.357	6.661 (2.581)	10.588	13.373	18.352	13.184	16.321	8.934	9.696	8.862
IX	3.662	2.780	2.573	3.644	2.951	3.088	2.949	3.254	6.775 (2.603)	6.563	14.348	10.233	8.538	13.905	10.426	17.808
X	4.474	3.422	2.871	3.519	2.821	3.376	3.416	3.657	2.562	6.744 (2.597)	22.335	11.764	16.719	16.499	12.623	12.027
XI	4.373	4.788	3.925	4.070	4.319	5.248	3.805	4.284	3.788	4.726	8.317 (2.884)	16.630	10.588	22.155	20.358	21.762
XII	4.254	3.877	3.776	3.201	3.136	5.149	3.924	3.631	3.199	3.430	4.078	7.349 (2.711)	15.000	9.535	8.988	11.648
XIII	4.260	3.903	3.993	4.590	3.460	3.816	3.583	4.040	2.922	4.089	3.254	3.873	7.935 (2.817)	18.593	15.108	17.330
XIV	4.970	3.573	3.992	3.261	4.481	4.560	4.699	2.989	3.729	4.062	4.707	3.088	4.312	7.144 (2.673)	12.531	9.229
XV	4.903	3.456	3.534	4.195	3.153	4.161	3.397	3.114	3.229	3.553	4.512	2.998	3.887	3.540	7.840 (2.800)	10.608
XVI	5.311	3.352	4.056	2.875	3.722	4.650	4.033	2.977	4.220	3.468	4.665	3.413	4.163	3.038	3.257	7.300 (2.702)

Table-3 : Cluster mean for 13 quantitative characters in Safflower.

Cluster No.	DF	PH	PB	LLB	WLB	PP	CP	DMC	NSP	HSW	HC (%)	OC (%)	SY
I	100.12	82.87	10.25	7.75	4.33	14.50	19.37	2.12	19.50	4.52	20.75	27.70	435.63
II	102.07	83.50	13.78	7.60	3.83	13.85	26.32	2.10	20.71	4.77	20.75	31.83	619.83
III	99.90	83.80	12.65	7.80	3.48	15.00	24.70	1.86	19.30	4.76	19.75	31.30	698.51
IV	102.56	91.31	10.06	7.00	3.28	12.87	22.06	1.70	19.62	4.10	20.25	31.94	485.13
V	101.40	83.43	15.93	7.12	3.52	12.03	18.71	1.94	19.31	4.97	20.03	31.12	768.28
VI	101.40	80.60	16.60	8.00	4.67	14.60	29.30	1.63	17.60	5.60	20.00	31.61	932.21
VII	100.50	89.05	14.44	8.05	3.48	13.27	23.66	1.98	19.00	4.59	17.50	31.64	959.46
VIII	102.72	94.45	13.40	7.50	3.80	14.27	23.31	1.98	19.72	4.74	20.22	31.03	673.91
IX	101.29	83.32	10.38	8.67	4.12	13.23	24.82	1.85	20.00	5.01	19.41	30.65	737.04
X	100.80	86.20	11.83	8.50	4.09	14.06	18.36	1.64	19.53	4.61	20.73	31.96	831.23
XI	100.40	79.90	14.00	8.20	3.95	12.00	23.40	1.69	21.60	4.31	15.50	28.81	470.38
XII	100.78	84.28	12.42	9.21	3.43	12.42	20.57	1.77	20.28	4.21	20.92	31.13	646.55
XIII	102.21	86.28	17.85	8.92	4.10	12.71	25.00	1.81	19.42	5.10	16.50	28.16	688.09
XIV	103.42	88.92	15.00	8.14	4.19	12.85	26.78	1.75	19.71	4.29	20.78	32.39	608.46
XV	100.16	86.05	18.55	10.00	4.00	12.27	22.94	1.96	19.22	4.71	20.61	32.57	687.86
XVI	102.66	86.91	17.41	8.00	3.29	14.41	21.83	1.80	18.50	4.13	20.25	32.18	576.22

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