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Research Note

Genetic Divergence for Seed Related Characters in Selected Germplasm of Safflower (*Carthamus tinctorius* L.).

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Abstract

A total of 150 genotypes along with five checks 'A-1, Bhima, Manjira, JSF-1 and HUS-305' were evaluated in an augemented block design with five blocks at the field of Oilseed Research Unit, Dr. PDKV, Akola during rabi 2012-2013. The data were recorded on the characters *viz*., days to 50% flowering, days to maturity, number of capitula per plant, number of seeds per capitulum, 100 seed weight (g), hull content (g), volume weight (g/100ml), seed yield per plant and oil content (%). The 150 genotypes were grouped into fourteen clusters. The average inter cluster distance was maximum between clusters IX and XII (3635.208), followed by clusters VI and XII (3615.87), clusters VIII and XII (3542.073), clusters I and XII (2924.360), clusters XII and XIII (2892.245). The seed yield per plant, number of capitula per plant, days to maturity, seeds per capitulum, days to 50% flowering, volume weight and oil content contributed significantly towards genetic divergence. The present study projected the importance of GMU-3439, GMU-3482, GMU-3475 as parents for higher heterosis in F_1 and potential transgrants in subsequent generations for further improvement in respect to these characters.

Keywords: Cluster analysis, Genetic divergence, Germplasm, Safflower.

Safflower (*Carthamus tinctorius* L.), is one of the important oilseed crops grown in winter season on residual soil moisture. The genetic diversity which is the basis of crop improvement is produced due to inherent genetic differences in plant species and hence, it is necessary to evaluate extent of genetic divergence in breeding lines. The selection of the parents for hybridization determines the success of breeding programme. There are many approaches for selection of parents for hybridization *viz*. multivariate analysis, ecographic diversity, regression analysis, selection of parents may also based on *per se* performance and combining ability analysis (Verma and Kumar, 1974). The importance of genetic diversity of crop improvement has long been appreciated by breeders but the basic difficulty was recognizing and estimating such diversity. The genetic diversity is the basis of plant breeding programme 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 F_1 and broad spectrum of variability in segregating generations. So, there is an urgent need of detailed genetic evaluation for variability and genetic diversity in safflower germplasm collections. 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 utilize for the further genetic improvement of safflower.

The experiment was conducted with 155 elite safflower genotypes including five released varieties (HUS-305, A-1, JSF-1, MANJIRA and Bhima) at the field of Oilseeds Research Unit Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola. The experiment was conducted during *rabi* season of 2012-13 in an augmented blocked design, in a single row plot of four meter length. The experimental design consisted of five block design with each block containing 30 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 nine quantitative traits *viz*., days to 50 % flowering, days to maturity, Number of capitula per plant, No. of seeds per capitulum, 100 seed weight, hull content %, volume weight (gm /100 ml), seed yield per plant and oil content. 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.

D^2 analysis was carried out to analyze genetic divergence among these genotypes. The differences among the genotypes were significant for days to 50% flowering, days to maturity, number of capitula per plant, number of seeds per capitulum, 100 seed weight, hull content ,volume weight, seed yield per plant and oil content indicating the presence of wide genetic variability for these characters.

The D^2 analysis resulted in the grouping of 150 genotypes and 5 checks into fourteen clusters by Tocher's method. Grouping pattern of different clusters is given in Table 2. Cluster IV was the largest involving 45 genotypes from different geographic origin. The next largest cluster was cluster V (44 genotypes) followed by cluster II (29 genotypes). Cluster I and III had 14 genotypes each. The clusters VI, VII, VIII, IX, X, XI, XII, and XIII involved only a single genotype.

Average intra and inter cluster distance values among 9 characters were calculated by Tocher's method and are presented in the Table 3. Maximum intra cluster value was observed for cluster V (308.713) and minimum for cluster I (61.179). The average inter cluster distance was maximum between clusters IX and XII (3635.208), followed by clusters VI and XII (3615.87), clusters VIII and XII (3542.073), clusters I and XII (2924.360), clusters XII and XIII (2892.245). 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, days to maturity, seeds per capitulum, days to 50% flowering, volume weight and oil content contributed significantly towards genetic divergence. Overall study of cluster mean for all nine characters indicated that cluster XII showed maximum mean for characters *viz.* seeds per capitulum, number of capitula per plant and seed yield. The cluster IX exhibited the highest cluster mean for oil content and hull content, while cluster VII showed highest cluster mean for days to maturity. The contribution of each character towards genetic divergence has been presented in the Table 4. The contribution to the total divergence was maximum by seed yield per plant (32.39 %) followed by number of capitula per plant (26.98 %), days to maturity (19.19 %), seeds per capitulum (10.83 %) and days to 50 per cent flowering (8.36 %).

The present study has helped to identify diverse parents for hybridization progaramme on the basis of mean performance and cluster formed. The genotypes identified for different characters for further breeding programme are given in Table 5. GMU-3439, GMU-3482 and GMU-3475 had low mean for days to 50% flowering, days to maturity and hull content. These genotypes can be utilized as parents for getting higher heterosis in F_1 and potential transgrants in subsequent. Similarly GMU-3590, GMU-3490, GMU-3433, A-1 and GMU-3522 had high mean for number of capitula and seed per capitilum, 100 seed weight, volume weight, seed yield per plant and oil content, respectively. These results are in conformity with that of Agarwal *et al*. (1982), Patil *et al*. (1991), Rao *et al.* (1980), Diwaker *et al* (2006), Murkute (2010) and Sirisha *et al*. (2012).

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Table1: Grouping of genotypes into different clusters

Cluster	No. of genotypes	Name of genotypes
I	14	GMU-3470, GMU-3444,GMU-3491, GMU-3436, GMU-3472, GMU-3475,GMU-3495, GMU-3522, GMU-3512, GMU-3517, GMU-3527, GMU-3589, GMU-3567, GMU-3573
II	29	GMU-3455, GMU-3448, GMU-3441, GMU-3450, GMU-3445, GMU-3488, GMU-3460, GMU-3509, GMU-3503, GMU-3502, GMU-3508, GMU-3524, GMU-3525, GMU-3523, GMU-3532, GMU-3514, GMU-3544, GMU-3507, GMU-3551, GMU-3552, GMU-3597, GMU-3561, GMU-3618, GMU-3616, GMU-3607, GMU-3585, GMU-3547, GMU-3620,JSF-1.
III	14	GMU-3469, GMU-3474, GMU-3442, GMU-3454, GMU-3499, GMU-3501, GMU-3504, GMU-3579, GMU-3614, GMU-3603, GMU-3594, GMU-3595, GMU-3600, GMU-3605.
IV	45	GMU-3478, GMU-3468, GMU-3481, GMU-3438, GMU-3452, GMU-3435, GMU-3447, GMU-3458, GMU-3467, GMU-3476, GMU-3462, GMU-3433, GMU-3548, GMU-3533, GMU-3541, GMU-3521, GMU-3516, GMU-3519, GMU-3505, GMU-3530, GMU-3492, GMU-3511, GMU-3518, GMU-3535, GMU-3549, GMU-3494, GMU-3539, GMU-3513, GMU-3558, , GMU-3562, GMU-3617, GMU-3583, GMU-3596, GMU-3577, GMU-3601, GMU-3586, GMU-3587, GMU-3598, GMU-3581, GMU-3593, GMU-3619, GMU-3571, GMU-3612, GMU-3599,HUS-305.
V	44	GMU-3451, GMU-3465, GMU-3446, GMU-3449, GMU-3473, GMU-3545, GMU-3490, GMU-3477, GMU-3432, GMU-3434, GMU-3443, GMU-3480, GMU-3485, GMU-3431, GMU-3459, GMU-3528, GMU-3537, GMU-3506, GMU-3510, GMU-3515, GMU-3526, GMU-3556, GMU-3553, GMU-3547, GMU-3531, GMU-3550, GMU-3496, GMU-3534, GMU-3543, GMU-3572, GMU-3575,MANJIRA, , GMU-3564,BHIMA, GMU-3557, GMU-3563, GMU-3578, GMU-3560, GMU-3610, GMU-3565, GMU-3568, GMU-3569, GMU-3602,A-1.
VI	1	3463
VII	1	3486
VIII	1	3493
IX	1	3615
X	1	3439
XI	1	3456
XII	1	3590
XIII	1	3482
XIV	1	3484

Table 2: Average Intra and Inter cluster distances

	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
I	61.179	471.682	859.416	211.842	1146.304	100.312	379.479	146.339	159.539	383.827	495.350	2924.360	529.682	1665.067
II		94.839	215.711	286.043	352.376	775.858	317.034	716.169	775.478	238.675	192.767	1261.576	710.517	618.495
III			152.704	558.858	441.246	1273.339	418.611	1072.276	1133.767	509.922	287.916	1078.193	1135.760	451.968
IV				212.678	781.428	353.318	359.036	380.316	418.844	350.152	373.988	2151.634	636.824	1241.423
V					308.713	1560.905	876.641	1552.793	1653.966	573.866	564.889	733.467	1185.858	607.969
VI						0.000	565.613	227.830	215.957	659.054	797.540	3615.870	560.791	2178.259
VII							0.000	523.237	485.477	325.654	149.505	2307.010	391.047	736.857
VIII								0.000	82.140	513.930	683.582	3542.073	858.254	2015.801
IX									0.000	640.192	659.954	3635.208	728.469	2058.607
X										0.000	210.249	1922.125	451.792	831.207
XI											0.000	1667.733	508.571	685.004
XII												0.000	2892.245	978.070
XIII													0.000	1276.098
XIV														0.000

Table 3: Contribution of each character towards genetic divergence

Sr. No	Source	Times rank first	% Contribution
1	Days to 50 % Flowering	998	8.36
2	Days to Maturity	2290	19.19
3	No. of Capitula Per Plant	3220	26.98
4	No.of Seeds/ Capitulum	1293	10.83
5	100 Seed Weight (g)	6	0.05
6	Hull content (%)	0	0.00
7	Volume wt (g/100ml)	215	1.80
8	Seed Yield/ Plant (g)	3866	32.39
9	Oil Content (%)	47	0.39

Table 4: Cluster means for nine characters

Character	Days to 50 % Flowering	Days to Maturity	No. of Capitula / Plant	No. of Seeds / Capitulum	100 Seed Weight (g)	Hull content (g)	Volume wt (g/lit)	Seed Yield / Plant (g)	Oil Content (%)
I	66.249	140.360	13.326	13.420	4.087	0.659	26.253	8.426	23.869
II	66.585	139.941	26.349	26.454	4.543	0.693	26.725	15.993	23.728
III	66.391	136.260	32.683	32.177	4.477	0.675	26.870	12.453	23.818
IV	68.060	141.228	18.901	19.415	4.658	0.784	27.249	10.865	22.811
V	67.412	143.640	31.605	31.798	4.805	0.809	27.481	25.185	23.511
VI	68.920	139.960	8.240	8.720	4.424	0.725	30.145	7.630	22.999
VII	63.920	126.360	21.840	21.320	4.944	0.831	29.143	10.798	23.781
VIII	59.920	140.360	12.840	12.320	4.744	0.581	21.713	1.398	21.421
IX	65.720	135.560	11.840	10.920	3.544	0.525	18.441	2.294	24.511
X	55.920	138.960	20.240	21.720	3.624	0.895	24.825	19.730	23.819
XI	63.920	130.960	20.240	29.720	2.624	0.965	24.055	15.670	24.229
XII	75.720	147.560	46.840	45.920	3.144	0.825	24.541	32.134	20.861
XIII	65.920	126.360	12.840	12.320	5.744	1.391	27.713	25.638	22.431
XIV	61.920	127.360	43.840	29.320	4.344	0.531	29.713	24.318	23.241