

EVALUATION OF THE THIRD CYCLE OF GMS BASED HALF-SIB'S IN SAFFLOWER (*Carthamustinctorius L.*)

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ABSTRACT

The present study was undertaken to evaluate the response to recurrent selection for seed yield and its components from half-sib selection in a safflower and to estimate the components of genetic variance, heritability and expected genetic advance in random mating population and to select the half-sib families significantly superior over the checks A-1, AKS-207, PKV Pink, Bhima and PBNS-12 for further yield testing. The 60 half-sib families were grown for evaluation in augmented block design with three blocks in *rabi* 2016-17 along with five check varieties i.e. A-1, AKS-207, PKV Pink, Bhima and PBNS-12. The expected genetic advance expressed as *per cent* of population mean at 5 and 10 *per cent* selection intensity was highest for number of seeds capitulum⁻¹ i.e. 61.59 and 52.62, respectively. The expected genetic advance over A-1 at 5 and 10 *per cent* selection intensity was 90.04 and 76.92 respectively. The narrow sense heritability on family means basis were high for oil content (0.968) followed by 100 seed weight (0.940). Thirteen half-sib families *viz.*, HS-4, HS-12, HS-18, HS-36, HS-38, HS-39, HS-40, HS-41, HS-43, HS-49, HS-50, HS-52 and HS-56 were significantly superior over all the checks which can be used for further recombination cycle in next season.

(Key words : Safflower, seed yield, GMS line, half-sibs, heritability, genetic advance)

INTRODUCTION

Safflower (*Carthamustinctorius L.*) is an important *rabi* oilseed crop of India. India is the largest producer of safflower in the world. Safflower is cultivated in more than 60 countries, but more than half is produced in India, mainly for vegetable oil market (Patil *et al.*, 1999). The largest hectareage of safflower is in the south-central India. In India, safflower is mainly grown as a rainfed crop. It has a long taproot system, which allows the plant to thrive well in lighter soils and can easily adapt with saline alkaline conditions. It gives better option to the farmers in dry land area for crop rotation and can give more yield under protective irrigated condition (Nimbkar, 2002).

In India 17 varieties and four safflower hybrids were released in last four decades *viz.*, DSH129, MKH11 and NARISH1. These varieties have the genetic potential to give yield of 15-20 q ha⁻¹ with oil content of about 30 % under optimal condition. However, attempts to further improve the yield and oil content were not successful for the last four decades. Similarly, there is no breakthrough in the improvement of oil content in the last seven decades. This is mainly due to the use of pedigree selection technique in population derived from two line crosses and negative

correlation between seed yield and oil content. The conventional breeding methods have been very useful only recombining simple inherited characters. Therefore, these conventional breeding methods have not been very efficient for improving quantitatively inherited characters like seed yield, oil content, tolerance to stresses and horizontal resistance to diseases and insects. Moreover, the crossing and record keeping procedure are often both money and time consuming for the rate of progress attained. Conventional method have several limitations such as limited use of available genetic variability resulting in the development of varieties with a narrow genetic base, successive loss of genes in the segregating generation with no chance of recombination for genes linked for yield and oil content (Jensen, 1970). Breeders are interested in applying more efficient breeding methods to self-pollinated crops to improve productivity potentials of these crops (Jennings, 1974). One such method utilized to accumulate desirable genes and facilitate breaking of linkages, is recurrent selection. Therefore, the present investigation was conducted to evaluate 3rd cycle half sib's families for recurrent selection of safflower developed by using GMS lines.

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MATERIALS AND METHODS

New random mating population using new GMS line i.e., HUS-MS-305, has been developed in collaboration with two safflower AICRP centers, viz., Akola and Solapur. The population was developed by crossing GMS line HUS-MS-305 with various male parents viz., NARI-SPS-34-46, NARI-SPS-50-1, AKS/S 41, GMU-2924, AKS-NS-1, PBNS-33, PBNS-58, GMU-148, GMU 2914-2, GMU 4811, PBNS-40, AKS-207, N-7, AKS-310, AKS 311, SSF 674, Bhima, A-1, JSI 99, GMU 3293, GMU 3420, PI-SPS-21-8, GMU 2724, C-2829-5-39-6, MMS, IVT 07-1, IVT 07-6, SSF 687, SSF 674, SSF 710, SSF 714, SSF 678, NARI 42, SSF 682, SSF 679, SSF 33, NARI 36, SSF 698, SSF 648, 99-1-1, 97-12—B, 11-17-2, 8-10-4-10, 6-9-2, 8-1-4, AV 98933, SSF 625, 24. The F_1 seeds of all these crosses were mixed together in equal quantity and sown for the first cycle recombination during 2010-11. Second cycle of recombination was conducted during 2012-13 and third recombination cycle during 2015-16. From which 60 male sterile plants were selected. All these 60 plants had sufficient seeds and their progenies were selected and sown in Augmented Block Design in three replications along with five checks (AKS-207, Bhima, A-1, PBNS-12 and PKV Pink) for third cycle evaluation keeping remnant seeds during *rabi* 2016-17 at Oilseeds Research Unit, Dr. PDKV, Akola. Each entry was of four meter length and 25 entries in each block along with checks. Sowing was done with dibbling method with spacing of 45 X 20 cm between rows and plants. All standard agronomical and plant protection practices were provided. Observations were recorded on days to 50% flowering, days to maturity on plot basis and plant height, number of primary branches plant⁻¹, number of capitula plant⁻¹, number of seeds capitulum⁻¹, 100 seed weight seed yield plant⁻¹ and oil content on plant basis. Data were subjected to analysis of variance as per the procedure given by Federer (1961), Estimation of family components, estimation of heritability in narrow sense, estimation of expected genetic advance was done as per the Hallauer and Miranda (1989).

RESULTS AND DISCUSSION

The analysis of variance for the half-sib families has been presented in table 1. The mean squares due to half-sib families were significant for all the characters except days to flowering, days to maturity, number of primary branches plant⁻¹, number of capitula plant⁻¹ and seed yield plant⁻¹ indicating substantial genetic variability existed among the half-sib families after third cycle of recurrent selection

The mean performance of 60 half-sib families (Table 2) recorded was 98.5 for days to 50 % flowering, 142.93 for days to maturity, 94.83 cm for plant height, 9.71 for number of primary branches plant⁻¹, 31.61 for number of capitula plant⁻¹, 34.59 for number of seed capitulum⁻¹, 33.44 g for seed yield plant⁻¹, 3.783 g for 100 seed weight, and 27.65 per cent for oil content in third cycle of recurrent selection.

The genetic variance among half-sib families ($s^2_{H.S.}$) and additive variance (s^2_A) (Table 3) were high and significant for seed yield plant⁻¹ (147.79 and 591.19, respectively) followed by number of seeds capitula⁻¹ (132.32 and 529.28, respectively), plant height (77.52 and 310.08, respectively), number of capitula plant⁻¹ (61.48 and 245.93, respectively), oil content (50.85 and 203.42, respectively), days to 50% flowering (30.04 and 120.18, respectively), days to maturity (9.56 and 38.24, respectively), number of primary branches plant⁻¹ (5.00 and 20.02, respectively) and 100 seed weight (1.10 and 4.42, respectively). The significant and high genetic variance among half-sib families was also reported by Tayade (2013), Garkal (2015) in random mating population of safflower as has been noticed in the present investigation.

The narrow sense heritability (Table 3) on family means basis was observed to be high for oil content (0.968) followed by 100 seed weight (0.940), number of seeds capitulum⁻¹ (0.808), plant height (0.793), days to 50% flowering (0.773), days to maturity (0.597), number of primary branches plant⁻¹ (0.557), seed yield plant⁻¹ (0.326) and number of capitula plant⁻¹ (0.279). High estimates of heritability have also been reported in random mating population of safflower for several agronomic traits by Tayade (2013), Garkal (2015), Patole *et al.* (2015) and Kurhade *et al.* (2016).

The expected genetic advance expressed as *per cent* of population mean at 5 and 10 per cent selection intensity (Table 4) was highest for number of seeds capitulum⁻¹ (61.59 and 52.62, respectively), followed by 100 seed weight (55.51 and 47.42, respectively) for mean of population, the genetic advance over A-1 at 5 and 10 *per cent* selection intensity was 90.04 and 76.92, respectively, over AKS-207 at 5 and 10 per cent selection intensity was 105.99 and 90.54, respectively, over PKV Pink at 5 and 10 per cent selection intensity was 69.96 and 59.8, respectively, over Bhima at 5 and 10 per cent selection intensity was 76.08 and 65.00, respectively, over PBNS-12 at 5 and 10 *per cent* selection intensity was 56.06 and 47.89, respectively. Similar to this results in safflower, Reddi (2002) reported 11.51, 9.48 and 7.82 per cent genetic advance in seed yield plant⁻¹ at 5, 10 and 20 per cent selection intensity, respectively, in random mating population of safflower after one cycle of recurrent selection and Patole *et al.* (2015) also reported 56.91, 38.24 and 111.96 per cent expected genetic advance at 10 per cent selection intensity over population mean, Bhima and PKV Pink, respectively for seed yield plant⁻¹.

In the present study, out of 60 half sib families, 13 half-sib families were significantly superior over check A-1, AKS-207, PKV Pink, Bhima and PBNS-12 for seed yield plant⁻¹, 12 half-sib families were significantly superior for oil content (%) over check A-1, AKS-207, PKV Pink, Bhima and PBNS-12 and have been represented in table 5. The remnant seeds of selected half-sib families can be used for further recombination cycle in next season in isolated field. Patole *et al.* (2015) also identified eight half sibs for forwarding to

Table 1. Analysis of variance for various characters in half-sib families of safflower

Sources of variation	d.f.	Days to flowering	Days to 50% flowering	Days to maturity	Plant height	No. of Primary branches plant ⁻¹	No. of capitulas plant ⁻¹	No. of seeds capitulum ⁻¹	100 seed weight	Oil content	Seed yield plant ⁻¹
Block (ignoring treatment)	2	33.653	68.813*	96.04*	111.409*	29.051*	364.499	249.351*	0.744**	39.318**	488.602
Entries (ignoring Block)	64	59.213	36.117*	13.314	92.086*	8.843	221.444	164.807**	1.293**	47.831**	417.066
Checks	4	27.9	9.733	7.233	15.124	1.172	77.926	240.691**	3.183**	7.313*	227.041
Checks + half sib vs. half-sib	60	61.301	37.876*	13.719	97.217*	9.354	231.012	159.749**	1.167**	50.532**	429.734
Error	8	33.601	8.783	6.433	20.198	3.968	158.376	31.381	0.070	1.642	304.907
Block eliminating (check+ half-sib)	2	74.594	40.866*	31.264*	5.06198	34.621*	698.129	91.027	0.050	0.320	15.314
Entries (ignoring Block)	64	57.934	36.990*	15.338	95.409*	8.669	211.018	169.755**	1.314**	49.049**	431.856
Checks	4	27.9	9.733	7.233	15.124	1.172	77.926	240.691**	3.183**	7.313*	227.041
Half-sib	59	60.857	38.830*	15.995	97.719*	8.975	219.860	163.701**	1.175**	52.498**	452.705
Checks vs. half-sib	1	5.603	37.453	9.013	280.256*	20.587	221.742	243.18*	2.078**	12.541*	20.988
Error	8	33.601	8.783	6.433	20.198	3.968	158.376	31.381	0.070	1.642	304.907

*, ** Significant at 5 and 1 per cent, respectively

Table 2. Mean performance of selected half-sib families for yield contributing characters

	Day to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches plant ⁻¹	No. of capitulum as plant ⁻¹	No. of Seeds capitula ⁻¹	100 seed weight (g)	Oil content (%)	Seed yield plant ⁻¹ (g)
Half-sibs									
MAX	112.00 (HS-51)	151.00 (HS-42, HS-51)	120.20 (HS-20)	16.80 (HS-39)	83.20 (HS-1)	65.00 (HS-51)	6.53 (HS-25)	32.24 (HS-2)	101.20 (HS-41)
MIN	88.00 (HS-12)	133.00 (HS-12)	68.00 (HS-23)	2.60 (HS-13)	3.80 (HS-13)	10.00 (HS-10, HS-11)	2.00 (HS-6, HS-8, HS-13, HS-24)	18.82 (HS-43)	2.33 (HS-28)
MEAN (HS)	98.50	142.93	94.83	9.71	31.61	34.59	3.78	27.65	33.44
Check varieties									
A-1	95.00	141.00	88.53	10.86	37.13	23.66	4.83	26.82	38.58
AKS-207	96.33	141.33	87.33	10.53	32.86	20.10	5.16	25.77	21.53
PKV Pink	95.66	140.66	90.93	10.40	29.13	40.71	3.00	29.72	31.70
Bhima	99.66	144.33	93.16	11.90	37.96	28.00	3.16	28.34	44.60
PBNS-12	97.00	143.00	90.06	11.40	42.46	38.00	4.83	26.69	37.40
GENERAL MEAN	98.14	142.76	93.87	9.97	32.47	33.69	3.86	27.62	33.70
SE(M)±	2.41	2.07	3.66	1.62	10.27	4.57	0.21	1.04	14.25

Table 3. Estimation of half-sib family component of variance and heritability in narrow sense

Half-sib family Component	Days to 50% flowering	Days to maturity	Plant height	No. of primary branches plant ⁻¹	No. of capitula plant ⁻¹	No. of seed capitulum ⁻¹	100 seed weight	Oil content	Seed yield plant ⁻¹
$\hat{\sigma}^2$ (H.S.) = $M_F - M_E$	30.047	9.562	77.521	5.007	61.484	132.32	1.105	50.856	147.79
$\hat{\sigma}^2 A = 4 \times \hat{\sigma}^2$ (H.S.)	120.188	38.248	310.084	20.028	245.930	529.280	4.420	203.420	591.190
$\hat{\sigma}^2 P$ (H.S.) = $\frac{1}{4} \hat{\sigma}^2 A + \hat{\sigma}^2 e$	38.830	15.995	97.719	8.975	219.860	163.701	1.175	52.498	452.700
h^2 (n.s.) = $\frac{\frac{1}{4} \hat{\sigma}^2 A}{\frac{1}{4} \hat{\sigma}^2 A + \hat{\sigma}^2 e}$	0.773	0.597	0.793	0.557	0.279	0.808	0.940	0.968	0.326

Where,

s^2 (H.S.) = Half sib family component of variance

M_F = Half sib family mean square

M_E = Error mean square

$s^2 A$ = Additive variance

$s^2 P$ = Phenotypic variance

h^2 (n.s.) = Heritability (narrow sense)

$s^2 e$ = Environmental variance or error variance

Table 4. Expected genetic advance in *per cent* per cycle using recurrent selection system in safflower

Unit of evaluation and Selection	Cycle	Selection intensity	Days to 50 % flowering	Days to maturity	Plant height	No. of primary branches plant ⁻¹	No. of capitula plant ⁻¹	No. of seed capitulum ⁻¹	100 seed weight	Oil content	Seed yield plant ⁻¹
Expected genetic advance over mean population											
Half-Sib	3	5%	10.08	3.44	17.03	35.45	27.02	61.59	55.51	52.29	42.78
		10%	8.61	2.94	14.55	30.29	23.08	52.62	47.42	44.67	36.55
Expected genetic advance over A-1											
Half-Sib	3	5%	10.45	3.49	18.24	31.69	23.00	90.04	43.45	53.90	37.08
		10%	8.93	2.98	15.59	27.08	19.65	76.92	37.14	46.05	31.68
Expected genetic advance over AKS-207											
Half-Sib	3	5%	10.31	3.48	18.49	32.68	25.99	105.99	40.67	56.10	66.45
		10%	8.80	2.97	15.80	27.92	22.20	90.54	34.76	47.93	56.78
Expected genetic advance over PKV Pink											
Half-Sib	3	5%	10.38	3.50	17.76	33.09	29.32	52.32	69.96	48.64	45.13
		10%	8.87	2.99	15.17	28.27	25.04	44.69	59.80	41.56	38.56
Expected genetic advance over Bhima											
Half-Sib	3	5%	9.96	3.41	17.33	28.92	22.50	76.08	66.29	51.01	32.08
		10%	8.51	2.91	14.81	24.71	19.22	65.00	56.66	43.58	27.41
Expected genetic advance over PBNS-12											
Half-Sib	3	5%	10.24	3.44	17.93	30.19	20.11	56.06	43.45	51.17	38.25
		10%	8.74	2.94	15.32	25.79	17.18	47.89	37.14	46.28	32.68

Table 5. Top ranking 13 half-sibs selected on the basis of seed yield plant⁻¹ (Superior over A-1, AKS-207, PKV-Pink, Bhima and PBNS-12)

Sr. No.	Half-sib families	Seed yield plant ⁻¹ (g)	Sr. No.	Half-sib families	Oil content (%)
1.	HS-4	63 ^{^\$*#@}	1.	HS-2	32.24 ^{^\$*#@}
2.	HS-12	45.4 ^{^\$*#@}	2.	HS-3	30.69 ^{^\$*#@}
3.	HS-18	58.4 ^{^\$*#@}	3.	HS-12	31.04 ^{^\$*#@}
4.	HS-36	48.6 ^{^\$*#@}	4.	HS-15	30.17 ^{^\$*#@}
5.	HS-38	45.8 ^{^\$*#@}	5.	HS-21	30.02 ^{^\$*#@}
6.	HS-39	61.8 ^{^\$*#@}	6.	HS-22	31.41 ^{^\$*#@}
7.	HS-40	74.2 ^{^\$*#@}	7.	HS-36	31.34 ^{^\$*#@}
8.	HS-41	101.2 ^{^\$*#@}	8.	HS-42	32.18 ^{^\$*#@}
9.	HS-43	61 ^{^\$*#@}	9.	HS-46	30.62 ^{^\$*#@}
10	HS-49	51.8 ^{^\$*#@}	10.	HS-56	30.39 ^{^\$*#@}
11	HS-50	56.8 ^{^\$*#@}	11.	HS-57	30 ^{^\$*#@}
12	HS-52	53.8 ^{^\$*#@}	12.	HS-59	30.58 ^{^\$*#@}
13	HS-56	77.2 ^{^\$*#@}	Checks	A-1	26.82
Checks	A-1	38.58	-	AKS-207	25.77
-	AKS-207	21.53	-	PKV-PINK	29.72
-	PKV-PINK	31.7	-	BHIMA	28.34
-	BHIMA	44.6	-	PBNS-12	26.69
-	PBNS-12	37.4	-	SE(m) ±	1.04
	SE(m)±	14.25		CD at 5 %	2.41
	CD at 5 %	32.86			

Where,

@ = Significantly superior over A-1

= Significantly superior over AKS-207

* = Significantly superior over PKV Pink

\$ = Significantly superior over Bhima

^ = Significantly superior over PBNS-12

next generation on the basis of evaluation of performance of half sibs for various traits and also reported that half sibs recurrent selection is effective in increasing population mean and extraction of superior recombination lines better than check varieties. Iqbal Ahmed *et al.* (2016) suggested that early generation segregates may be intermated to break the undesirable linkages and obtain desirable segregates for seed yield and other contributing traits in safflower. Hence, half sibs recurrent selection is very effective to intermate various genotypes with each other so that chances of breaking undesirable linkages can be accelerated and superior individuals can be identified and selected.

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