Electronic Journal of Plant Breeding, 5(2): 208-212 (June 2014)
ISSN 0975-928X

Research Article

Combining ability analysis in Safflower (*Carthamus tinctorious* L.)

Gopal Nai, Jogendra Singh*, S. P. Sharma and Chhagan Lal
Department of Plant Breeding and Genetics, Rajasthan College of Agriculture,
Maharana Pratap University of Agriculture and Technology, Udaipur-313001 (Rajasthan).
*Email: jschouhanpbg@gmail.com

(Received: 03 Feb 2014; Accepted:12 APR 2014)

Abstract

Ten parents and their 45 F_1 were evaluated for seed yield and its component characters over two environments *viz*, normal sown (E_1) and late sown (E_2) conditions. Highly significant variation was observed due to genotypes and environments for all the character studied. Both general combining ability and specific combining ability variances showed significant interactions. The genotypes GMU7359 and GMU5267 were found to be good general combiners and 15 crosses have been identified as good specific combiner for seed yield and other related traits. The cross GMU264 × GMU7359 were the best cross for seed yield and rest of the traits.

Keywords: Safflower, general combining ability, specific combining ability, gene action.

Introduction

Safflower (*Carthamus tinctorious* L; 2n=24), commonly known as "kusum", belongs to the family *Asteraceae.* Safflower (*Carthamus tinctorius* L.) is one of the important *rabi* oilseed crops of India, cultivated in vertisols under residual moisture in Maharastra, Karnataka, Andhra Pradesh, Chhattisgarh, Madhya Pradesh and Bihar. Safflower is known for its cultivation since time immemorial, either for orange red dye extracted from its florets and for its much valued oil. Latha and Prakash (1984) have reported that the seed contains 27.5 per cent oil, 15 per cent protein, 41 per cent crude fiber and 2.3 per cent ash. Safflower oil, which on average contains 75% linoleic acid, also contains tocopherols, known to have antioxidant effect and high vitamin E content. For this reason, safflower oil is used in the diets of patients with cardiovascular disease, and bears great importance for its anti-cholesterol effect. Safflower oil is flavourless. The oil is also used in manufacturing of paints as a substitute for linseed oil as it does not have the yellow tint which linseed oil posses. Safflower oil cake is a valuable animal feed (Weiss, 2000). In India, safflower is grown in 229 thousand hectares with a production of 143 thousand tonnes (2010-11) and ranked first in area and second in production accounting for 60 per cent and 45 per cent of global area and production respectively (Anonymous, 2010). Safflower is a predominantly self- pollinated crop; however, it may have some out crossing depending on genotype and insect activity (Weiss, 2000).

Combining ability analysis serves as very handy tool for selection of parents. Information on relative importance of general and specific combining abilities is helpful in analysis and interpretation of genetic basis of important traits. The relative amount of general and specific combining ability effects play vital role in planning the most appropriate breeding programme in safflower for seed yield and its related component traits. Therefore, present investigation was undertaken to study the combining ability for identification of good combiner and promising crosses for future better accomplishment in safflower.

Material and Methods

Ten promising germplasm accessions of safflower received from Directorate of Oilseed Research, Hyderabad namely GMU3806, GMU3955, GMU5267, GMU5394, GMU5712, GMU5815, GMU196, GMU217, GMU264 and GMU7359 of diverse genetic origin were crossed in half diallel fashion. This experiment was carried out at the Instructional Farm, Rajasthan College of Agriculture, Udaipur (Rajasthan). The parents along with 45 F_1s were grown in a randomized block design with three replications during *rabi*, 2009-10 under two distinct environments *viz*, normal sown on 24th November, 2009 (E_1) and late sown on 15th December, 2009 (E_2) condition. In each replication each cross and its parents were sown in a plot of 4×0.45 m^2 size accommodating one row of 4m length each. The plant to plant distance maintained was 25cm. Five competitive plants in each parent and 30 plants in each F_1 were selected randomly for recording observations under each environment. The statistical analysis for combining ability based on mean values was done as per method II model-I of Griffing (1956) and the pooled analysis over environment was carried out.

Results and Discussion

Pooled analysis of variance over environments revealed significant variation among parents for the traits, indicating adequate genetic variability among the parental lines used in the present study (Table-1 and 2). The genotype interacted significantly with the environments for all the traits except number of secondary branches per plant indicating that environment had significant influence on character expression.

Combining ability analysis revealed that *gca* and *sca* variances were highly significant for all the characters. Both *gca* and *sca* showed significant interaction with environments for all the traits. The significant *gca* × environment and *sca* × environment interactions indicated that the estimates of both additive and non additive gene effects are prone to change with the environment. Similar results were also reported by Patil *et al.* (2004), Singh *et al.* (2008) and Golkar *et al.* (2012) in safflower. Analysis also revealed higher magnitude of mean sum of squares for GCA than SCA for all characters except harvest index and oil content further indicates that additive gene actions were more important in these characters.

The parents GMU5267 and GMU7359 had good *per se* performance (51.10 and 59.73) and *gca* effect (6.50 and 10.31), respectively; which were show good general combiners for seed yield, biological yield, number of primary branches per plant, no. of secondary branches per plant and no. of effective capsules per plant (data not shown). The estimates of *gca* effects (Table 3) on the basis of pooled analysis revealed that no single parent was a good combiner for all the characters studied. Parents, GMU5267 and GMU7359 proved to be good general combiner for seed yield per plant, biological yield per plant, number of primary branches, number of secondary branches and number of effective capsules per plant. In addition to the above, GMU5267 was also a good combiner for plant height and days to maturity and GMU7359 for 100-seed weight. Besides these two parents, GMU3955, GMU5712 and GMU5815 were good general combiners for seed yield per plant, biological yield per plant. GMU3955 and GMU5815 were also good combiners for plant height, harvest index and oil content. In addition to above some of the other parents were good general combiners for trait like harvest index, days to 50% flowering and oil content (GMU3806); days to 50% flowering, days to maturity, harvest index, number of primary branches per plant and number of effective capsules per plant (GMU5394). Parents, GMU196, GMU217, and GMU264 were good combiners for 100-seed weight whereas, GMU217 and GMU264 were good combiners for days to maturity, plant height and harvest index.
The parent, GMU196 had shown highly significant positive *gca* effect for oil content. The good general combiners had fixable component of variance like additive and additive × additive epistasis component; therefore, parents *viz*., GMU7359 and GMU5267 offered the best possibilities of exploitation for development of improved high yielding lines in safflower.

Specific combining ability effects is an important parameter for judging and selecting superior cross combinations, which might be exploited through heterosis breeding programme. The crosses which showed highest significant positive *sca* effects for seed yield per plant presented in Table 4. The cross GMU264 × GMU7359 showed desirable negative significant *sca* effect for day to 50% flowering, days to maturity and plant height and exhibited positive significant *sca* effect for rest of the traits. The crosses, GMU3806 × GMU196, GMU3806 × GMU7359, GMU3955 × GMU5267, GMU3955 × GMU196, GMU3955 × GMU217, GMU3955 × GMU264, GMU5267 × GMU5394, GMU5712 × GMU7359, GMU5815 × GMU217 and GMU196 × GMU217 exhibited significant *sca* effect for primary branches per plant, secondary branches per plant and effective capsules per plant besides these eight crosses also show significant *sca* effect for biological yield per plant.

Cross, GMU3955 × GMU5712 showed significant *sca* effects for biological yield per plant, harvest index, 100-seed weight and oil content and desirable negative *sca* effect for days to 50% flowering and days to maturity. Crosses GMU3955 × GMU196 and GMU3955 × GMU217 exhibited significant *sca* effects for harvest index, 100-seed weight and oil content besides this cross also showed desirable negative *sca* effect for days to 50% flowering and plant height. Crosses GMU5267 × GMU5815 and GMU5394 × GMU264 exhibited significant *sca* effects for biological yield per plant and 100-seed weight and desirable negative *sca* effect for days to maturity. The cross, GMU5267 × GMU5815 also showed significant *sca* effect for oil content.

Crosses, GMU5712 × GMU7359 and GMU5815 × GMU217 exhibited significant *sca* effects for harvest index and desirable negative *sca* effect for days to maturity. In addition to these, cross GMU5815 × GMU217 also showed significant *sca* effect for 100-seed weight. Cross, GMU5815 × GMU264 exhibited significant *sca* effects for secondary branches per plant, effective capsules per plant, biological yield per plant and oil content and desirable negative *sca* effects for days to maturity. Crosses, GMU3806 × GMU7359, GMU5267 × GMU5394 and GMU196 × GMU217 also exhibited significant *sca* effect for oil content.

The crosses with significant positive *sca* effects for seed yield involved parents with low × low or low × high *gca* effects indicating the presence of non-allelic interactions. Both parent with high *gca* effects when crossed had probably low magnitude of non additive gene effect resulting in the small degree of *sca* effects. Therefore, recurrent selection for *sca* could be followed in the segregating generation of the crosses GMU3806 × GMU7359, GMU3955 × GMU5267, GMU5267 × GMU5394, GMU5267 × GMU5815, GMU5712 × GMU7359 and GMU264 × GMU7359, as this type of relation was proposed on the assumption that an important part of heterosis results from the non-linear interaction of gene at different loci, from interaction between alleles at the same locus or from both causes in combination. It is possible to obtain substantial improvement with regard to seed yield in a addition to other desirable traits like number of primary branches per plant, number of secondary branches per plant, number of effective capsules per plant and biological yield per plant.

References

Anonymous, 2010. Annual Progress Report. Directorate of Oilseed Research, Hyderabad.

Golkar, P., Arzani, A. and Rezaei, A. 2012. Genetic analysis of agronomic traits in safflower (*Carthamus tinctorious* L.). *Bot. Horti. Agrobo*., **40** (1): 276-281.

Griffing, B. 1956. Concept of general and specific combining ability in relation to diallel crossing system. *Australian J of biological Science*, **9**: 463-493.

Lutha, T. S. and Prakash, V. 1984. Studies on the proteins from safflower seed (*Carthamus tinctorius* L.). *J. Agriculture and Food Chemistry.* **32:** 1412-1416.

Patil, A. J., Kanade, B. C., Murumkar, D. R. and Kankal, V. Y. 2004. Combining ability and heterosis in seed yield of safflower (*Carthamus tinctorius* L.). *Journal of Oilseeds Research*, **21** (2): 349-350.

Singh, V., Kolekar, N. M. and Nimbkar, N. 2008. Breeding strategy for improvement of flower and seed yield in safflower. 7th International Safflower Conference, Wagga, New South Wales, Australia.

Weiss, E. A. 2000. Oilseed Crop, 2nd Addition, Blackwell Science Ltd, Oxford, p. 109.

Table 1. Analysis of variance giving mean sum of square for different characters in Environment I (E_1) and Environment II (E_2).

Source of variation	Env	d. f.	Days to 50% flowering	Days to Maturity	Plant height (cm)	Number of primary branches per plant	Number of secondary branches per plant	Number of effective capsules per plant	Biological yield per plant (g)	Seed yield per plant (g)	Harvest index (%)	100-seed weight (g)	Oil content (%)
Replication	E_1	2	0.84	0.38	1.56	49.48**	0.02	51.73**	0.52	0.03	0.01	0.003	0.27
	E_2	2	0.66	0.49	10.06**	0.04	0.05	0.18	1.06	0.40	0.18	0.003	1.20*
Genotype	E_1	54	5.47**	17.37**	87.21**	14.46**	12.91**	54.08**	8712.74**	719.22**	19.31**	0.67**	18.82**
	E_2	54	5.08**	29.07**	69.69**	6.37**	8.05**	28.34**	8699.95**	690.89**	18.26**	0.65**	14.05**
Parents	E_1	9	3.11**	12.20**	82.51**	19.92**	17.22**	73.27**	10231**	977.02**	25.18**	0.26**	8.23**
	E_2	9	10.74**	14.40**	68.37**	11.39**	15.09**	51.91**	10312.4**	934.02**	18.68**	0.29**	3.90**
Crosses	E_1	44	6.08**	15.03*	87.83**	10.75**	10.70**	42.50**	8235.19**	666.83**	16.11**	0.77**	20.81**
	E_2	44	3.82**	30.94**	71.32**	4.79**	5.28**	19.92**	8165.58**	641.02**	15.85**	0.74**	16.43**
Parent v/s Crosses	E_1	1	0.21	166.87**	87.83**	128.81**	71.25**	390.72**	16060.5**	704.30**	107.10**	0.07**	26.90**
	E_2	1	9.84**	78.54**	71.32**	30.79**	66.66**	186.84**	17700.3**	696.92**	120.43**	0.11**	0.67
Error	E_1	108	0.55	0.28	1.67	0.51	0.18	0.60	0.47	0.22	0.13	0.00	0.33
	E_2	108	0.56	0.81	0.51	0.12	0.06	0.16	0.83	0.30	0.19	0.00	0.36

* significant at $P = 0.05$, ** significant at $P = 0.01$

Table 2. Pooled analysis of variance for combining ability for various characters over two environments

Source	d. f.	Days to 50% flowering	Days to maturity	Plant height	Number of primary branches/plant	Number of secondary branches/plant	Number of effective capsules/plant	Biological yield per plant	Seed yield per plant	Harvest index	100 Seed weight	Oil content
Env.	1	39.38**	144.01**	65.77**	10.12**	0.00	10.17**	97.56**	52.66**	16.73**	0.009**	10.98**
GCA	9	4.79**	12.93**	58.83**	14.96**	16.45**	62.45**	12170.8**	978.39**	8.84**	0.55**	7.08**
SCA	45	2.30**	8.85**	48.75**	4.59**	4.57**	18.21**	4525.23**	367.98**	12.55**	0.41**	10.86**
GCA×E	9	0.37*	8.09**	1.22**	0.73**	0.28**	1.70**	9.40**	0.45**	1.37**	0.003**	0.66**
SCA×E	45	0.89**	5.52**	2.00**	0.59**	0.46**	1.92**	3.80**	0.29**	0.43**	0.002**	0.73**
Pooled Error	216	0.18	0.18	0.36	0.10	0.04	0.12	0.21	0.08	0.05	0.001	0.11

*Significant at $P = 0.05$; ** Significant at $P = 0.01$

Table 3. Pooled estimates of general combining ability effects for various characters over different environments

Parents	Days to 50% flowering	Days to maturity	Plant height	Number of primary branches/plant	Number of secondary branches/plant	Number of effective capsules per plant	Biological yield per plant	Seed yield per plant	Harvest index	100-seed weight	Oil content
GMU3806	-0.37*	0.42**	0.14	-1.15*	-1.29*	-2.44*	-40.65*	-11.21*	0.43**	-0.19*	0.21**
GMU3955	-0.75*	0.56**	-1.41*	0.07	0.15**	0.22**	10.21**	2.92**	-0.13*	-0.02*	0.74**
GMU5267	0.43**	-0.17*	-1.60*	1.13**	1.05**	2.18**	24.08**	6.50**	-0.22*	-0.08*	-0.45*
GMU5394	-0.56*	-0.72*	2.65**	0.16*	0.01	0.16*	-2.92*	-1.16*	0.39**	-0.19*	-0.40*
GMU5712	0.13	0.93**	1.28**	0.18**	0.30**	0.48**	1.84**	0.67**	-0.07	-0.16*	-0.43*
GMU5815	0.04	-1.10*	-0.75*	-0.04	0.01	-0.03	11.47**	3.65**	0.59**	0.10**	0.41**
GMU196	0.44**	0.07	-0.34*	-0.87*	-0.92*	-1.79*	-27.01*	-7.76*	-0.11*	0.04**	0.94**
GMU217	0.57**	0.82**	-2.30*	-0.37*	-0.46*	-0.83*	-4.61*	-2.74*	-1.34*	0.11**	-0.62*
GMU264	-0.14	-1.01*	0.91**	-0.47*	-0.30*	-0.77*	-8.04*	-1.17*	0.80**	0.14**	-0.28*
GMU7359	0.21*	0.21*	1.42**	1.36**	1.46**	2.82**	35.62**	10.31**	-0.35*	0.24**	-0.12
S.E. (Gi ±)	0.08	0.08	0.12	0.06	0.04	0.07	0.09	0.06	0.05	0.01	0.07

*Significant at P = 0.05 ; ** Significant at P = 0.01; Gi± standerd error of parental *gca*

Table 4. Estimates of specific combining ability effects of the best fifteen specific crosses over two environments

Parents	Days to 50% flowering	Days to maturity	Plant height	Number of primary branches/plant	Number of secondary branches/plant	Number of effective capsules/plant	Biological yield per plant	Harvest index	100-seed weight	Oil content	Seed yield per plant	*gca* status
GMU3806 × GMU196	1.98**	0.70*	-0.30	0.67**	0.80**	1.47**	-2.80**	4.23**	-0.45**	-4.21**	1.43**	L×L
GMU3806 × GMU7359	-0.29	2.39**	1.62**	3.24**	3.23**	6.48**	64.38**	-0.38*	-0.02	2.66**	17.35**	L×H
GMU3955 × GMU5267	1.03**	0.63*	-1.98**	1.00**	0.96**	1.96**	16.12**	0.15	-1.09**	-1.41**	4.69**	M×H
GMU3955 × GMU5712	-1.50**	-1.47**	2.67**	0.06	0.16	0.22	24.59**	2.12**	0.50**	1.60**	9.99**	M×L
GMU3955 × GMU196	-0.32	0.39	1.63**	1.01**	0.77**	1.78**	67.09**	1.47**	0.56**	0.48*	21.39**	M×L
GMU3955 × GMU217	-1.44**	0.47	-4.13**	0.65**	0.86**	1.51**	53.04**	1.89**	0.58**	0.44*	17.39**	M×L
GMU3955 × GMU264	-0.23	2.97**	6.58**	2.03**	1.71**	3.74**	76.34**	-1.08**	-0.08**	-2.43**	19.87**	M×L
GMU5267 × GMU5394	0.17	0.57*	2.29**	1.37**	1.41**	2.78**	60.15**	0.15	-0.10**	0.47*	18.53**	H×L
GMU5267 × GMU5815	-0.09	-0.55*	2.29**	-0.16	-0.34*	-0.51*	99.06**	-2.91**	0.30**	2.08**	21.66**	H×M
GMU5394 × GMU264	0.24	-0.58*	0.57	-0.38	-0.73**	-1.12**	29.05**	-0.67**	0.35**	-3.28**	8.38**	L×L
GMU5712 × GMU7359	-0.29	-3.96**	-1.24**	0.60**	0.98**	1.58**	30.05**	3.41**	-0.25**	-4.30**	13.92**	L×H
GMU5815 × GMU217	0.10	-3.04**	5.43**	1.05**	0.96**	2.01**	70.71**	1.88**	0.37**	-4.20**	23.50**	M×L
GMU5815 × GMU264	-0.02	-0.71*	0.07	0.30	0.31*	0.60*	5.13**	-0.69**	-0.06*	1.99**	1.05**	M×L
GMU196 × GMU217	1.20**	0.79**	2.90**	1.75**	1.83**	3.57**	13.16**	0.23	-0.01	1.52**	4.22**	L×L
GMU264 × GMU7359	-0.86**	-2.51**	-1.38**	3.02**	2.95**	5.97**	41.44**	2.10**	0.09**	1.50**	15.43**	L×H
SE (S_{ij})	0.28	0.28	0.39	0.21	0.13	0.23	0.45	0.22	0.02	0.22	0.19	

*Significant at *P* = 0.05 ; ** Significant at *P* = 0.01; M-medium, H- high and L- low and S_{ij} –standard error of cross *sca*.