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Genetic Analysis of Seed Yield, Oil Content and Their Components in Safflower (*Carthamus tinctorius* L.)

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Summary. The genetic architecture of seed yield, oil content and their components was studied in a diallel cross of F_1 and F_2: eleven parents, representing an adequate diversity for all considered characters in safflower were used. Combining ability analysis revealed the predominance of *gca* variance for plant height, total capitula, seed weight, seed number and seed yield in F_1 and F_2 generations and for days to flowering and oil content in F_1. The analysis of components of variance indicated that the nonadditive factor was the major influence on total capitula and seed yield in F_1s, and F_2s, and on plant height, seed weight and seed number in the F_2 alone. The heterogeneity of the dominance component over generations has been attributed to coupling phase linkage. All four Indian parents, namely S 144, A 1, MS 49 and 6 spl, together with G 1157 and US 104 in the exotic group, were the best combiners for seed yield and/or for one of its components while the remainder of the exotic parents were characterized by high *gca* effects for oil content. VFstp 1 and Frio were the only parents approximating both properties of oil content and seed yield. Breeding methods, such as biparental mating followed by reciprocal recurrent selection, were suggested for the simultaneous improvement of seed yield and oil content.

Key words: Safflower – Seed yield – Oil content – Combining ability – Components of variance

Introduction

Safflower is a potential oilseed crop. In spite of spectacular developments in modifying the quantity and quality of oil (Knowles 1969), very little is known about the inheritance of seed yield, oil content and their component characters. Ehdaie and Ghaderi (1978) have estimated the gene action for days to flowering, plant height, seed weight, seed number, embryo percent and seed yield in the cross, N10 × Arak 2811. Abel (1976) studied the inheritance of plant height and its components in three crosses. In both cases a simple additive-dominance model failed to explain the inheritance of all the characters. Similar results were also reported by Kotecha and Zimmerman (1978) for seed weight. In all these studies the information was obtained from limited material and was based on the comparison of means. Hence, a diallel cross of eleven parents representing a spectrum of variability for seed yield, oil content and their major components was selected to deduce the nature of gene action by a second order measure and to estimate the combining ability of the parents.

Materials and Methods

The experimental material comprised a 11 × 11 diallel set of F_1 and direct crosses of F_2. The parents included were S 144, A 1, MS 49 and 6 spl from local collections and US 104, G 1157, Frio, AC 1, VFstp 1, Th 5 and Oleicleed of exotic types. The experiment, consisting of 11 parents, 110 F_1 crosses and 55 direct crosses of F_2 arranged in two tiers with 10 (parents and F_1 s) and 150 (F_2 s) observation plants in each treatment of three replications, was laid out in a randomized block design during the 1978-79 crop season under rain-fed conditions at the Research Farm of the University of Agricultural Sciences, Dharwad, India. The spacing (45 cm × 30 cm), fertilizer dose (40, 30 and 20 kg per hectare of N, P and K, respectively) and other crop management practices were followed according to the recommended schedule. Observations on plant height (measured in centimeters from first node to the tip of the capitulum on the main axis), total capitula (per plant), seed weight (per 100 seeds in decigrams), seed number (per capitulum) and seed yield (per plant in grams) for F_1 s and F_2 s were recorded and days to flowering (sowing to the day of flowering of the capitulum on main axis) and oil content (per cent as estimated by NMR spectrophotometer and based on whole seed) were recorded for F_1 s alone. For the purpose of statistical analysis, full diallel sets of F_1 and direct crosses of F_2 were conceived as separate experiments. Combining ability analysis of Griffing (1956) and the analysis of components of variance as per Hayman (1954) were followed. Narrow sense heritability was estimated as per the formula of Mather and Jinks (1971).

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Results

The analysis of variance for plant height, total capitula, seed weight, seed number and seed yield in parental group, F_1 and F_2 (Table 1 and 2) and for days to flowering and oil content in the two first-mentioned categories revealed significant differences between parents, F_1s and parents vs F_1s. The final comparison for seed number in F_1 proved to be an exception. The *gca* variances were higher than the *sca* variances for all the characters, though the proportion of the *gca* variance to the *sca* variance varied from character to character (Table 3). The reciprocal differences in F_1 were also significant for all characters.

The *gca* effects as given in Table 4 were highest for US 104 and VFstp 1 with respect to days to flowering and plant height. The parents, MS 49, US 104 and S 144 were the best combiners for total capitula. The *gca* effects of G 1157 were worthy of note. The Indian parents, particularly 6 spl and A 1, and an exotic parent, US 104, expressed high *gca* effects for seed weight. Exotic parents such as G 1157, US 104, VFstp 1 and Frio were also considerably important with respect to *gca* effects for seed yield. The high oil lines, (Th5, AC1 and Oleicleed) with superior general combining ability for oil content were characterized by significantly negative *gca* effects for total capitula, seed weight and seed yield.

The estimates of genetic components of variance for total capitula and seed yield in F_1 and F_2 and for plant height, seed weight and seed number in F_2 alone (Table 5) differed distinctly from the results of the combining ability in that the dominance component (H_1) was higher than that of additive fraction (D). The overall degree of dominance varied accordingly for these characters (Table 6). The proportion of dominant genes was higher for all characters in the F_2 generation when compared to the F_1. Asymmetrical distribution of positive and negative genes was distinct for days to flowering, plant height, seed weight, seed number and oil content. The coefficient of correlation (r) between Wr + Vr and Yr was negative for seed weight and seed yield, indicating the dominance of positive genes. It was exactly reverse for the rest. The regression coefficient (b) of Wr on Vr was significantly different from unity for total capitula and seed yield in F_1 and F_2 and for seed weight in F_2 alone. Narrow sense heritability was lowest for seed yield and highest for oil content in F_1. It was also lower in the F_2 when compared to the F_1 for plant height, seed weight and seed number.

Discussion

The establishment of safflower as an important oilseed crop depends on the success of elevating oil content of

Table 1. Analysis of variance for oil content, seed yield and its major components in the F_1 generation of safflower

Source of variation	D.F.	Days to flowering	Plant height	Total capitula	Seed weight	Seed number	Seed yield	Oil content
Blocks	2	9.60**	1.70**	1.14	0.12	0.06	2.57**	0.06
Treatments	120	33.49**	198.10**	376.52**	253.50**	267.30**	672.93**	31.72**
Parents	10	115.70**	383.22**	368.24**	687.87**	910.02**	361.53**	105.23**
F_1s	109	24.84**	178.45**	330.37**	203.43**	210.76**	560.78**	25.17**
Parents vs. F_1s	1	154.47**	489.33**	5489.45**	1367.35**	0.56	16011.24**	10.22**
Error	240	0.19	0.16	0.40	0.22	0.16	0.62	0.13
CV		0.63	0.65	1.56	0.93	1.66	1.65	1.02

* Significant at $p < 0.05$
** Significant at $p < 0.01$

Table 2. Analysis of variance for seed yield and its major components in F_2 generation of safflower

Source of variation	D.F.	Plant height	Total capitula	Seed weight	Seed number	Seed yield
Blocks	2	1.21	0.56	0.71	0.34	0.59
Treatments	54	170.41**	224.71**	163.57**	137.28**	267.81**
Error	108	0.14	0.29	1.02	0.18	0.81
CV		0.60	1.49	2.08	1.78	2.20

** Significant at $p < 0.01$

Table 3. Analysis of variance for combining ability of different characters in the F_1 and F_2 generations of safflower

Source	DF	Days to flowering F_1	Plant height F_1	Plant height F_2	Total capitula F_1	Total capitula F_2	Seed weight F_1	Seed weight F_2	Seed number F_1	Seed number F_2	Seed yield F_1	Seed yield F_2	Oil content F_1
General combining ability	10	93.90**	619.21**	373.60**	852.05**	408.32**	842.81**	448.41**	888.18**	433.67**	1012.63**	332.05**	114.97**
Specific combining ability	55	6.37**	25.87**	13.96**	114.35**	31.86**	27.84**	16.14**	30.94**	21.26	298.04**	83.13**	1.77**
Reciprocal	55	0.91**	5.63**	–	4.57**	–	3.28**	–	1.97**	–	7.25**	–	0.39**
Error	240/ 130	0.19	0.16	0.06	0.40	0.12	0.22	0.29	0.16	0.06	0.62	0.26	0.13
GCA/SCA	–	14.74	23.93	26.76	7.45	12.82	30.27	27.78	28.71	20.40	3.40	3.99	64.95

** Significant at $p < 0.01$

Table 4. General combining ability effects of parents for different characters in F_1 and F_2 generations of safflower

Entry	Days to flowering F_1	Plant height F_1	Plant height F_2	Total capitula F_1	Total capitula F_2	Seed weight F_1	Seed weight F_2	Seed number F_1	Seed number F_2	Seed yield F_1	Seed yield F_2	Oil content F_1
S 144	1.22**	–2.67**	–2.36**	4.33**	6.82**	0.88**	0.83**	–4.27**	–3.09**	–1.65**	3.79**	–1.29**
A 1	0.96**	–0.37**	0.52**	3.60**	2.02**	8.47**	8.72**	–3.19**	–3.89**	6.51**	2.76**	–2.85**
MS 49	–1.40**	–6.37**	–5.68**	11.53**	10.08**	–4.80**	–3.10**	–4.16**	–4.98**	–1.82**	–0.57**	–1.07**
6 spl	–1.41**	0.91**	1.18**	–3.61**	–1.71**	12.08**	10.84**	–1.37**	–2.15**	4.87**	3.15**	–3.52**
US 104	3.09**	5.93**	8.14**	5.55**	4.14**	5.66**	4.68**	–4.16**	–3.25**	2.97**	2.27**	–1.45**
Frio	–1.78**	0.94**	0.75**	–1.25**	–1.31**	–0.47**	1.32**	0.43**	1.24**	0.45**	2.96**	2.12**
AC 1	–2.36**	–4.17**	–5.68**	0.04	–1.45**	–4.97**	–5.59**	–1.62**	0.30**	–5.54**	–4.22**	2.84**
G 1157	0.36**	4.88**	2.41**	–9.21**	–8.31**	–5.97**	–5.28**	18.02**	16.19**	9.41**	3.34**	–1.08**
Th 5	–2.33**	–6.72**	–6.57**	–8.96**	–7.72**	–6.19**	–5.82**	1.38**	–0.82**	–11.71**	–11.52**	1.97**
VFstp 1	3.52**	10.19**	9.69**	1.25**	0.48**	–2.21**	–2.09**	1.58**	1.67**	5.89**	0.80**	2.01**
Oleicleed	0.11	–2.52**	–2.41	–3.26**	–3.03**	–2.55**	–4.50**	–2.63**	–1.22**	–9.38**	–5.75	2.28**
SE (g_i)	± 0.09	± 0.08	± 0.06	± 0.13	± 0.09	± 0.10	± 0.14	± 0.08	± 0.07	± 0.16	± 0.13	± 0.07
CD (g_i–g_j) at 1%	0.34	0.31	0.25	0.49	0.34	0.37	0.55	0.31	0.26	0.62	0.51	0.28

** Significant at $p < 0.01$

Table 5. Estimates of genetic components of variance for different characters in the F_1 and F_2 generations of safflower

Component	Days to flowering	Plant height		Total capitula		Seed weight		Seed number		Seed yield		Oil content
	F_1	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1
D	38.37**	127.60**	127.60**	122.30**	122.40**	229.10**	228.40**	303.20**	303.20**	119.90**	119.70**	34.95**
	±1.01	±5.02	±4.14	±19.75	±6.16	±5.44	±6.72	±11.13	±10.14	±47.66	±21.78	±0.40
F	27.36**	39.97**	55.44**	−13.83	19.49	89.34**	266.90**	176.20**	501.30**	103.70	132.50	18.02**
	±2.31	±11.48	±18.94	±45.13	±28.14	±12.44	±30.71	±25.43	±46.37	±108.91	±99.58	±0.92
H_1	18.40**	76.36**	242.60**	246.60**	476.30**	68.72**	318.90**	95.98**	501.80**	669.30**	1225.00**	7.25**
	±2.08	±10.35	±34.14	±40.69	±50.73	±11.22	±55.37	±22.93	±83.61	±98.19	±179.54	±0.83
H_2	12.37**	51.42**	182.30**	227.90**	412.60**	55.25**	194.30**	61.56**	265.60**	594.90**	1010.00**	3.29**
	±1.75	±8.70	±28.70	±34.20	±42.65	±9.43	±46.55	±19.27	±70.29	±82.54	±150.93	±0.69
h^2	16.98**	53.92**	57.31**	604.78**	202.98**	150.61**	48.25**	0.01	0.23	1764.11**	672.94**	1.10*
	±1.17	±5.82	±4.80	±22.88	±7.13	±6.31	±7.78	±12.89	±11.75	±55.21	±25.24	±0.46
E	0.19	0.16	0.18	0.40	0.35	0.22	0.88	0.16	0.19	0.61	0.77	0.13
	±0.29	±1.45	±1.20	±5.70	±1.78	±1.57	±1.93	±3.21	±2.93	±13.76	±6.29	±0.12

* Significant at $p < 0.05$

** Significant at $p < 0.01$

Table 6. Derived parameters of genetic components from the F_1 and F_2 analysis for different characters in safflower

Derived parameter	Days to flowering	Plant height		Total capitula		Seed weight		Seed number		Seed yield		Oil content
	F_1	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1
$(H_1/D)^{1/2}$	0.69	0.77	1.38	1.42	1.97	0.55	1.18	0.56	1.29	2.36	3.20	0.45
$H_2/4H_1$	0.17	0.17	0.19	0.23	0.22	0.20	0.15	0.16	0.13	0.22	0.21	0.11
KD/KR	3.12	1.51	1.37	0.92	1.08	2.11	2.96	3.13	4.60	1.04	1.42	3.61
H_1-H_2	6.03	24.94	60.30	18.70	63.70	13.47	124.60	34.42	236.20	74.40	215.00	3.96
h^2/H_2	1.37	1.05	0.31	2.65	0.49	2.72	0.25	0.00	0.00	2.96	0.67	0.33
Heritability	0.72	0.81	0.59	0.57	0.45	0.82	0.47	0.84	0.22	0.23	0.28	0.92
Correlation (Yr, Wr + Vr)	0.87	0.83	0.48	0.04	0.26	−0.40	−0.16	0.60	0.89	−0.45	−0.54	0.82
b(Vr, Wr)	1.00	0.80	0.76	0.53	0.73	0.97	1.49	0.91	1.05	0.21	0.36	1.03
	±0.05	±0.67	±0.09	±0.14	±0.08	±0.13	±0.17	±0.11	±0.10	±0.18	±0.19	±0.07

seed and seed yield. The latter is a genetically complex character. This is observable by the low heritability estimates of the F_1 and F_2 generations (Table 6). There was high heterogeneity for the estimates of genetic components over generations. As an example, partial dominance in F_1 and overdominance in F_2 for plant height, seed weight and seed number suggested additive and non-additive gene action, respectively. Such differences may be attributed to coupling phase linkage which may cause bias in the estimates derived from early generations. According to Robinson et al. (1960) if there is repulsion phase linkage, additive genetic variance increases as the generations are advanced and if the linkage phase is mostly coupling, additive genetic variance decreases. Thus the overdominance in F_2 may not be an index of real overdominance, since particular combinations of positive and negative genes or a complementary type of epistasis or simply correlated gene distribution may seriously inflate the mean degree of dominance and convert partial into overdominance (Hayman 1954).

The overall picture is that gene action is predominantly additive for oil content, seed weight, seed number, days to flowering and plant height, and predominantly, non-additive for total capitula and seed yield. The improvement of such characters should be based on simultaneous exploitation of both additive and nonadditive components of genetic variance. Hanson (1959) showed linkage to be a tremendously conservative force inhibiting the frequency of genetic recombination. Breeding methods such as biparental mating followed by reciprocal recurrent selection may increase the frequency of genetic recombination and hasten the rate of genetic improvement.

All the Indian parents (S 144, A1, MS 49 and 6 spl) and two of the exotics, US 104 and G 1157, were the best general combiners for one or more components of seed yield. Other exotic parents, particularly VFstp 1 and Frio, exhibited in addition to being the best general combiners for oil content, high general combining ability for seed yield and its major components. Thus, the present studies suggest that all the Indian parents along with such exotic parents as VFstp 1, Frio and G 1157 may be used as potential sources in a hybridization programme. An intermating population involving all possible crosses between these parents and subjected to biparental progeny selection as described by Murty (1979) is expected to offer the maximum potential in breeding for high oil and high seed yield.

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