

Genetic analysis of seed yield and oil content in safflower using F₁ and F₂ progenies of diallel crosses

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Abstract

Improvement of seed yield and oil content in safflower (*Carthamus tinctorius* L.) as an oilseed crop is the main objective of its breeding programs. However, little genetic information is available for these traits. The main objective of this study was to estimate genetic parameters for seed yield and oil content. Six safflower lines each derived from different Iranian local populations and Saffire as a foreign cultivar were crossed in all combination as a diallel set without their reciprocals. Crosses were selfed to obtain seeds of F₂ progenies. F₁ and F₂ progenies along with their parents were evaluated in two separate experiments to do F₁ and F₂ diallel analysis. The GCA mean squares were significant for all traits including seed yield per plant, heads per plant, seeds per head, 100-seed weight, days to flowering, plant height and oil content. In both analyses, positive GCA effects for seed yield were found for parental lines IUTE₁₄₄₉ and IUTH₁₃, indicates that progeny with those genotypes as parents showed seed yields that were greater than the average of all crosses. The parental line IUTKH₂₁₁ was the best combiner for developing genotypes with high oil content. For achieving genotypes with short time to flowering and plant height, Saffire was the best parent. GCA/SCA ratio indicated there were large additive effects for all the traits, except for seed yield per plant. Narrow-sense heritability for seed yield per plant and oil content was 9.3 and 23.5%, respectively. However, seeds per head, 100-seed weight, days to flowering and plant height had moderate to high narrow-sense heritability (79.8, 55.4, 65.6 and 89.4%, respectively). There was reasonable consistency for estimating genetic parameters from analysis of F₁ and F₂ progenies.

Keywords: Safflower; Diallel; Combining ability; Heritability.

Introduction

Safflower (*Carthamus tinctorius* L.) is an oilseed crop grown commercially in Iran, as one of the centers of culture in the old world (Knowels, 1969). Cultivars with high seed yield and oil content are necessary for safflower production to compete with other oilseed crops growing in the country. Thus, breeding efforts in safflower should emphasize

improvement of seed yield and oil content. Safflower is a highly self pollinated crop. However, it may have some out crossing depending on genotype and insect activity (Weiss, 2000; Knowles, 1969). Therefore, the breeding methods of self-pollinated crops are used in breeding of safflower (Dajue and Mundel, 1996). Safflower cultivars are basically highly homogenous populations, but production of hybrid cultivars is also considered in breeding programs. Genetic variation and information regarding genetic control for different traits is needed to produce improved cultivars. Genetic variation for different traits including seed yield and oil content has been previously reported in safflower germplasms (Pascual-Villalobos and Albuquerque, 1996; Ashri et al., 1974) but little genetic information is available.

The importance of additive and non-additive genetic effects is well established in controlling many traits in safflower. It was shown that the dominance effects of the genes played a major role in the variation of seed yield per plant in safflower (Ehdaie and Ghaderi, 1978) and number of heads per plant (Kotecha, 1981). Also, the influence of both additive and non-additive effects of genes on the number of heads per plant has been reported (Sahu and Tewari, 1993). However, for some traits such as height (Abel, 1976a), days to 50% flowering, number of seeds per head and 100-seed weight (Sahu and Tewari, 1993), additive genetic effects explained considerable amount of variation.

Abel (1976b) reported that broad sense heritability of seed yield in safflower was very low. Kotecha and Zimmerman (1978) found that narrow sense heritability for seed weight in safflower was high and varied from 66.0 to 85.5%. Heterosis for oil content and a wide range of heterosis for seed yield has been reported (Patil and Narkhede, 1996; Yazdi-Samadi et al., 1975).

Diallel analysis can provide the necessary genetic information for breeding programs (Hill et al., 2001), and has been frequently used to obtain the genetic information regarding various traits in different crops (Bolanos et al., 2001; Stoddard and Herath, 2001; Guines *et al.*, 2002). Diallel analysis is usually conducted according to the Griffing method (1956) which partitions the total variation of the trait in F_1 progenies into General Combining Ability (GCA) of their parents and Specific Combining Ability (SCA) of the crosses. However, in many hermaphrodite plants in which it is difficult to produce F_1 seeds, it is easier to use F_2 progenies in diallel analysis (Mather and Jinks, 1982). Genetic analysis based upon F_1 progenies in diallel crosses has been previously used in safflower (Mandal and Banerjee, 1997), but it seems that using F_2 progenies in diallel analysis has not been established so far.

Since there is not enough genetic information regarding seed yield, yield components and oil content of the seed in safflower, the objectives of this study were: (i) to estimate GCA, SCA and other genetic parameters by using F_1 and F_2 progenies in two sets of diallel crosses, (ii) to compare the results from F_1 and F_2 diallel analysis, and (iii) to determine phenotypic and genetic correlations between these traits.

Material and methods

Seven safflower genotypes including six lines (IUTKH₂₁₁, IUTC₁₂₉, IUTH₁₃, IUTK₁₁₅, IUTM₁₂ and IUTE₁₄₄₉) which were obtained by single plant selection from various Iranian local populations and then selfing for one generation, along with Saffire which was a

registered Canadian cultivar (Mundel et al., 1985) were used for this study. The parental lines, which had high homogeneity, were chosen based on their genetic variation for traits such as seed yield and oil content. These genotypes were crossed in a half-diallel mating design to provide 21 F₁ hybrids. The F₂ seeds of these crosses were produced in a greenhouse by bagging F₁ plants during flowering period.

The experiments were conducted in summer of 2002 at the Research Farm of Isfahan University of Technology located at Isfahan, Iran, which has an altitude of 1626 m above sea level, annual precipitation of 375 mm, and a soil pH of 5.7. Two separate but adjacent experiments were conducted as Randomized Complete Block Designs with two replications. In one experiment (Exp.1) the parental lines along with their F₁ progenies were evaluated and in the second experiment (Exp.2) evaluation of F₂ progenies and their parental lines were followed. For Exp.1 each experimental unit consisted of three 2.5-m rows spaced 50 cm apart and for Exp.2 consisted of three 3.5-m rows spaced 50 cm apart. Enough seeds were planted, and then plants thinned to have 10 plants per meter of row for measuring and harvesting.

In both experiments, number of days to flowering and days to 50% flowering were recorded for each experimental unit. Also, the means of plant height, seed yield per plant, number of heads per plant, number of seeds per head and 100-seed weight for each plot were calculated based on measurements of 5 in Exp.1 and 25 in Exp.2 randomly chosen plants. The oil content of the seed for genotypes was determined only in experiment 1 (F₁ diallel) by Soxhlet method in which n-hexane was used as solvent. Samples for each plot were analyzed in triplicate, and their means were considered in statistical analysis.

Since parental genotypes were selected from different sources, the data were analyzed as a fixed model (Baker, 1978). For calculation of combining ability, the diallel design was analyzed according to Griffing's method 2, model I (Griffing, 1956). For statistical analysis in both experiments, the below model was considered.

$$g_{ijk} = m + g_i + g_j + s_{ij} + e_{ijk}$$

In this model, m is mean of the experiment, g_i is GCA effects for the i th parent, g_j is the GCA effects for j th parent, s_{ij} is the SCA effects for the ij th F₁ or F₂ progenies and e_{ijk} is the residual. Narrow-sense heritability was calculated as $h^2_n = \sigma^2_A / (\sigma^2_A + \sigma^2_D + \sigma^2_e)$; where σ^2_A , σ^2_D and σ^2_e were estimated for each of F₁ and F₂ diallel analysis (Kearsy and Pooni, 1996).

The collected data were subjected to analysis of variance using General Linear Model (GLM) of the Statistical Analysis System program (SAS Institute, 1996). The Least Significant Difference (LSD) test was used to determine the statistical difference between means when the F value was significant. Phenotypic and genetic Pearson's correlations among the traits were calculated using Statistical Analysis System program (SAS Institute, 1996).

Results

The effects of genotypes including parental lines and their crosses in both F_1 and F_2 diallel analysis were significant for all of the traits (Table 1). Means of parents for all traits were shown in Table 2. Means of seed yield per plant for parental lines, averaged over two experiments varied between 20.17 (IUTC₁₂₉) to 35.57 g (IUTE₁₄₄₉). Lines IUTKH₂₁₁ and IUTH₁₃ had the highest (33.42%) and the lowest (27.12%) oil content among all parents, respectively. Saffire had the lowest mean of days to flowering, days to 50% flowering and plant height (Table 2).

The mean squares of GCA in F_1 and F_2 diallel experiments were highly significant for all traits (Table 1). In F_1 diallel analysis, SCA mean squares were significant for all traits except for days to flowering, 50% flowering and plant height. However, in analysis of F_2 progenies, mean square of SCA was significant for all of the traits (Table 1). The GCA/SCA ratio of mean squares ranged from 0.4 (for seed yield per plant) to 39.1 (for plant height) in F_1 diallel analysis. In F_2 diallel, the lowest and the highest ratios of GCA/SCA were for heads per plant (0.9) and plant height (19.4), respectively (Table 1).

In F_1 diallel analysis, narrow sense heritability (h^2_n) was relatively low to moderate for all of the traits, except for number of seeds per head and plant height (Table 1). The lowest narrow sense heritability in F_1 diallel was observed for the number of heads per plant and oil content (Table 1). A moderate to high narrow sense heritability was found for all traits in F_2 diallel analysis (Table 1). All the traits (except for the number of seeds per head and days to flowering) were almost consistent in terms of their narrow sense heritability in F_1 and F_2 analysis (Table 1).

The number of seeds per head showed a high (79.8%) and a moderate (46.4%) narrow sense heritability in F_1 and F_2 diallels, respectively. The narrow sense heritability for days to flowering was 36.1% in F_1 and 65.6% in F_2 progenies. For 100-seed weight, days to 50% flowering and plant height, the narrow sense heritability increased a little from F_1 to F_2 diallels analysis, but in terms of broad sense, all the traits had a relatively high heritability in both analyses (Table 1).

General combining ability (GCA) effects in F_1 and F_2 diallels for all of the traits are presented in Table 3. For seed yield per plant, the estimates of GCA effects varied between 3.40 (IUTE₁₄₄₉) to -2.68 (IUTC₁₂₉) in F_1 , and between 3.11 (IUTE₁₄₄₉) to -4.69 (Saffire) in F_2 diallel analysis. GCA for number of heads per plant had a variation of 6.32 (Saffire) to -5.34 (IUTC₁₂₉) in F_1 diallel and between 3.42 (Saffire) to -2.49 (IUTH₁₃) when estimated by F_2 progenies (Table 3). The minimum and maximum GCA for seeds per head belonged to the parental lines Saffire and IUTE₁₄₄₉ in both F_1 and F_2 analysis, respectively (Table 3). However, IUTE₁₄₄₉ and Saffire had the lowest and highest GCA effects for seed weight in both F_1 and F_2 diallels, respectively (Table 3).

Saffire had the lowest GCA effects for days to flowering and days to 50% flowering in both analyses of F_1 and F_2 progenies. The minimum and maximum GCA for plant height in F_1 and F_2 diallels was for Saffire (-10.46 and -11.07) and IUTC₁₂₉ (13.46 and 12.54), respectively. Among parental lines, only IUTKH₂₁₁ had significant and positive GCA effects for oil content (Table 3).

The GCA estimates of the parental lines for some traits varied over the two diallel analyses (Table 3). There was more instability for estimating GCA effects for seed yield per plant, head per plant and seeds per head when estimated by F_1 than when estimated by F_2

Table 1. Mean squares for the diallel analyses and estimates of important genetic parameters by F_1 (1) and F_2 (2) progenies.

Source of variation	Experiment	df	Yield per plant (g)	Heads per plant	Seeds per Head	100-Seed weight (g)	Days to flowering	Days to 50% flowering	Plant height (cm)	Oil (%)
Block	1	1	4.6*	4.2*	3.3*	0.02*	28.5**	30.0**	0.6	2.6*
	2	1	596.7**	844.7**	15.4**	0.01	11.1**	62.1**	39.75**	—†
Crosses	1	27	156.5**	166.0**	90.1**	0.42**	22.3**	28.0**	322.0**	8.13**
	2	27	79.4**	68.2**	125.2**	0.20**	24.4**	24.4**	264.8**	—
GCA	1	6	85.0**	221.8**	341.4**	1.16**	50.4**	57.6**	1329.4**	14.8**
	2	6	108.8**	65.8**	350.2**	0.58**	65.2**	76.4**	1029.2**	—
SCA	1	21	177.0**	150.0**	18.2**	0.22**	14.2	19.4	34.0	6.2*
	2	21	71.0**	68.8**	60.8**	0.08*	5.4**	9.4**	52.8**	—
Error	1	27	1.1	1.12	0.9	0.01	10.0	10.6	29.1	2.0
	2	27	22.5	25.5	11.6	0.03	0.4	1.8	13.0	—
GCA/SCA	1	—	0.4	1.4	18.7	5.27	3.54	2.96	39.1	2.38
	2	—	1.5	0.9	5.75	7.25	12.07	8.12	19.49	—
h^2_n	1	—	—‡	9.6	79.8	48.7	36.1	30.4	89.4	23.5
	2	—	—‡	—‡	46.4	55.4	65.6	56.4	77.5	—
h^2_b	1	—	99.3	99.3	99.0	97.6	55.0	61.1	90.1	75.3
	2	—	81.2	75.1	95.7	88.7	98.5	94.9	96.5	—

GCA, general combining ability; SCA, specific combining ability.

*and **: significant at 0.05 and 0.01 of probability levels, respectively.

†: Data for oil content was obtained only for F_1 progenies.‡: In these cases SCA mean squares were greater than GCA mean squares, thus h^2_n could not be calculated.

Table 2. Mean of characteristics for seven safflower genotypes as parental lines.

Character	IUTKH ₂₁₁	IUTC ₁₂₉	IUTH ₁₃	IUTK ₁₁₅	IUTM ₁₂	IUTE ₁₄₄₉	Saffire	LSD(0.01)
Yield per plant (g)	22.87	20.17	24.90	26.42	24.05	35.57	23.05	12.36
Heads per plant	23.37	21.00	25.03	28.37	23.85	32.50	39.62	12.54
Seeds per Head	28.03	30.67	28.53	30.36	29.43	40.76	15.87	10.23
100-Seed weight(g)	3.77	3.28	3.45	2.76	3.29	2.68	3.61	0.69
Days to flowering	99.00	105.00	102.25	101.25	105.50	107.75	97.75	6.75
Days to 50% flowering	107.25	113.00	109.25	108.25	110.25	109.00	100.00	8.17
Plant height(cm)	104.32	136.22	102.05	98.85	116.00	115.82	84.40	17.45
Oil (%)	33.42	29.41	27.12	32.62	30.42	32.67	30.20	3.95

†: Data for oil percent was obtained only for F₁ progenies.

progenies. However, relatively consistent estimates of GCA effects for different traits over F_1 and F_2 diallels were observed in parental lines Saffire and IUTE₁₄₄₉ (Table 3).

The GCA effects estimates had significant positive correlations with parental values for all of the traits in both experiments, except for days to flowering in F_1 and heads per plant in F_2 diallel (Table 4).

Seed yield per plant showed a positive and considerable genetic correlation with number of heads per plant and oil content in F_1 , and with the number of seeds per head and days to 50% flowering in F_2 progenies (Table 5). However, seed yield per plant had a considerable genetic correlation with days to flowering and 50% flowering (-0.45** and -0.47**, respectively) in F_1 and with seed weight (-0.40) in F_2 generation. Number of heads per plant had a negative and relatively high genetic correlation with days to flowering, days to 50% flowering and plant height in F_1 and with seeds per head in F_2 generation (Table 5).

Number of seeds per head showed consistency in terms of direction and magnitude of genetic correlation with other traits over two types of progenies, except with plant height (Table 5). The genetic correlation coefficients of days to flowering with plant height were 0.72** and 0.77** in F_1 and F_2 , respectively. Also, a significant negative correlation was found between days to flowering and oil content (-0.59**) using F_1 diallel analysis (Table 5).

Discussion

There was considerable genetic variability among the parents for all evaluated traits (Table 2) and this was not surprising since these genotypes originated from different genetic backgrounds. The existence of genetic variation for different traits in safflower has been previously reported by Ashri et al. (1974). This genetic variation can be used in breeding programs to improve cultivars of safflower.

In both F_1 and F_2 diallels, it was found that GCA had contributions in genetic variation of the traits. Therefore, the additive effects of the genes were important in genetic variation of these traits and selection programs can improve them. For almost all of the traits, GCA variation among the parents had an acceptable consistency in two types of diallel analyses. Therefore, it seems that F_1 or F_2 diallel analysis can provide almost the same results for estimating genetic parameters such as GCA. This conclusion is in agreement with the findings of Abdel-Sabour et al. (1996) and Hassan et al. (1996) indicating that using F_1 and F_2 progenies provided similar results in bread wheat (*Triticum aestivum*).

Significant SCA mean squares were observed for seed yield per plant, heads per plant, seeds per head, 100-seed weight and oil content in F_1 crosses and for all of the traits in F_2 progenies (Table 1). This considerable genetic variation among crosses indicates that it is possible to find suitable combinations of the parental lines for hybrid cultivar production. Significant SCA mean squares for different traits were also reported in other crops (Sharma et al., 1991; Le Gouis et al., 2002).

The mean squares of SCA for the traits such as days to flowering, days to 50% flowering and plant height were not significant in F_1 diallel, although their values were considerable (Table 1). The inconsistency in statistically being significant of SCA in two diallel analyses was observed in another study as well (Meredith, 1990). For seed yield per plant and number of heads per plant, the mean squares of GCA and SCA were the same in terms of magnitude. This indicates that both selection and hybridization programs can be used for producing high yielding cultivars of safflower. The same results regarding equality

Table 3. General combining ability (GCA) effects for seven parents in F₁ and F₂ diallel analyses.

Parent	Experiment	Yield per plant	Heads per plant	Seeds per Head	Seed weight	Days to flowering	Days to 50% flowering	Plant height	Oil (%)
IUTKH ₂₁₁	F ₁	1.25**	0.09	-1.70**	0.30**	-2.33*	-1.41	-3.76*	0.87*
	F ₂	-0.79	-1.47	0.32	0.08	-0.81**	0.03	-2.88*	— [†]
IUTC ₁₂₉	F ₁	-2.68**	-5.34**	2.35**	-0.05	1.72	2.36*	13.46**	0.39
	F ₂	-0.15	-1.28	-0.43	0.04	1.85**	1.97**	12.54**	—
IUTH ₁₃	F ₁	1.76**	1.12**	0.45	0.01	0.50	-0.24	-6.91**	-1.86**
	F ₂	1.91	-2.49	3.65**	0.04	1.85**	0.53	-3.61**	—
IUTK ₁₁₅	F ₁	-1.43**	-1.78**	1.25**	-0.19**	0.11	0.69	-4.06*	0.20
	F ₂	0.497	-0.03	2.04*	-0.21**	0.07	0.42	-2.70*	—
IUTM ₁₂	F ₁	-1.38**	-0.83*	-0.31	-0.06*	1.27	0.53	7.41**	0.20
	F ₂	0.11	0.99	-0.61	0.04	0.74**	0.92	5.33**	—
IUTE ₁₄₉	F ₁	3.40**	0.42	6.10**	-0.35**	1.05	1.14	4.34*	0.66
	F ₂	3.11*	0.62	4.07**	-0.26**	1.30**	0.58	2.40*	—
Saffire	F ₁	-0.93**	6.32**	-8.14**	0.35**	-2.33*	-3.07**	-10.46**	-0.39
	F ₂	-4.69**	3.42*	-9.05**	0.262**	-3.86**	-4.46**	-11.07**	—

*and **: significant at 0.05 and 0.01 of probability levels, respectively.

†: Data for oil percent was obtained only for F₁ progenies.

of GCA and SCA mean squares have been reported for some seed yield components in alfalfa (Peterson, 1983).

The ratio of GCA/SCA mean squares indicates the ratios of $V_A/(V_A+V_D)$ in F_1 and $V_A/(V_A+1/2V_D)$ in F_2 generation, respectively and these ratios express the relative importance of additive and dominance effects (Baker, 1978). The GCA/SCA ratio for all traits in F_1 and F_2 diallels were higher than unity except for seed yield per plant in F_1 (0.4) and number of head per plant in F_2 (0.9) analysis. Therefore, additive effects of genes had considerable contribution in variation of the number of seeds per head, 100-seed weight, days to flowering and 50% flowering; plant height and oil content and selection can be effective in their improvement. The same results were obtained in wheat indicated that GCA effects were larger than SCA for different traits (Morgan et al., 1989; Perenzin et al., 1998; Oury et al., 2000).

High estimates of narrow sense heritability for plant height and number of seeds per head indicated that additive genetic variances for these traits were relatively large (Table 1) and this was in agreement with findings of Kotecha (1979). However, estimation of very low narrow sense heritability for seed yield per plant and number of heads per plant in this study contradicts the findings of Kotecha (1981). The low heritability of seed yield and its components also were reported in other crops (Bonlanos et al., 2001, Dahanayake and Galwey, 1999). On the other hand, high estimates of broad sense heritability for seed yield and its components in this study indicated that other types of genetic effects such as dominance or epistasis might be involved in their variation (Mather and Jinks, 1982).

As mentioned by Kearsy and Pooni (1996), GCA effects provide a measure of the general potential of genetic material. Based on GCA of parental lines (Table 3), it can be concluded that for improvement of seed yield per plant the genotypes IUTE₁₄₄₉ and IUTH₁₃ have good genetic potential. However, the highest mean of seed yield per plant in F_1 and F_2 diallels was obtained for crosses IUTKH₂₁₁ × IUTK₁₁₅ and IUTH₁₃ × IUTK₁₁₅, respectively (data not shown). This result indicates that for achieving cultivars with high seed yield, both GCA and SCA effects should be considered. Saffire and IUTE₁₄₄₉ were the best combiner parents in terms of the number of heads per plant and seed per head, respectively. Also, the highest positive and significant GCA effects for seed weight in both F_1 and F_2 diallels were observed in Saffire. In addition, the greater mean seed weight in F_1 and F_2 diallels was obtained for Saffire × IUTM₁₂ and Saffire × IUTK₁₁₅, respectively (data not shown). Accordingly, to improve seed weight in safflower, parents like Saffire can be used in breeding programs as a source of desirable genes. Guines et al., (2002) used the GCA effects to select appropriate parental lines for improvement of protein content in alfalfa.

Production cultivars with shorter time to 50% flowering and maturity could be obtained by utilizing Saffire as a parent, since it was the only line with negative and significant GCA for this trait (Table 3). Selection of parental lines for reduction of neutral detergent fiber and acid detergent fiber as undesirable components in alfalfa has been conducted based on negative GCA effects for these traits (Guines et al., 2002). The highest and positive GCA effect for plant height was for IUTC₁₂₉ (Table 3) which was the tallest genotype among the parents (Table 2). Also, among the F_1 and F_2 progenies, the tallest genotype (data not shown) was obtained from a cross of this parent with IUTM₁₂ which had the second highest GCA for this trait. But, Saffire as an important foreign cultivar (Mundel et al., 1985), had the lowest GCA for plant height and the lowest plant height among the parents. Therefore, for producing short cultivars of safflower, Saffire can be used in breeding programs.

Table 4. Correlation Coefficients between mean of parental lines and their GCA effects in F₁ and F₂ diallel.

GC A	Yield per plant (g)	Heads per plant	Seeds per Head	100-Seed weight (g)	Days to flowering	Days to 50% flowering	Plant height (cm)	Oil (%)
F ₁	0.84*	0.85*	0.97**	0.91**	0.60	0.91**	0.98**	0.84*
F ₂	0.78*	0.09	0.86*	0.96**	0.91**	0.94**	0.95**	—†

* and **: significant at 0.05 and 0.01 of probability levels, respectively.

†: Data for oil content was obtained only for F₁ progenies.Table 5. Phenotypic and genetic (in Italics) correlations among the traits in F₁ and F₂ progenies (n=28).

Character	Heads per plant		Seeds per head		Seed weight		Days to flowering		Days to 50% flowering		Plant height		Oil (%)
	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂	
Yield per plant (g)	0.75**	0.45**	0.26	0.58**	0.12	-0.37*	-0.17	0.24	-0.21	0.24	-0.11	0.09	0.32*
	<i>0.75**</i>	<i>-0.14</i>	<i>0.27</i>	<i>0.84**</i>	<i>0.13</i>	<i>-0.40*</i>	<i>-0.45**</i>	<i>0.24</i>	<i>-0.47**</i>	<i>0.32*</i>	<i>-0.13</i>	<i>0.13</i>	<i>0.40*</i>
Heads per plant			-0.30	-0.35*	0.22	-0.10	-0.32*	-0.06	-0.39*	0.01	-0.39*	-0.09	0.14
			<i>-0.30</i>	<i>-0.56**</i>	<i>0.23</i>	<i>0.09</i>	<i>-0.69**</i>	<i>-0.30</i>	<i>-0.72**</i>	<i>-0.28</i>	<i>-0.43**</i>	<i>-0.17</i>	<i>0.16</i>
Seeds per head			-0.61**	-0.59**	0.39*	0.35*	0.41**	0.27	0.49**	-0.59**	0.24	-0.59**	0.24
			<i>-0.61**</i>	<i>-0.61**</i>	<i>0.59**</i>	<i>0.45**</i>	<i>0.67**</i>	<i>0.47**</i>	<i>0.55**</i>	<i>0.17</i>	<i>0.31*</i>	<i>0.31*</i>	<i>0.31*</i>
Seed weight (g)			-0.54**	-0.45**	-0.50**	-0.34*	-0.37*	-0.12	-0.00	-0.00	-0.00	-0.00	-0.00
			<i>-0.54**</i>	<i>-0.45**</i>	<i>-0.50**</i>	<i>-0.34*</i>	<i>-0.37*</i>	<i>-0.12</i>	<i>-0.00</i>	<i>-0.00</i>	<i>-0.00</i>	<i>-0.00</i>	<i>-0.00</i>
Days to flowering			0.93**	0.90**	0.45**	0.73**	0.73**	0.15	0.48**	0.66**	0.73**	0.15	0.48**
			<i>0.93**</i>	<i>0.90**</i>	<i>0.45**</i>	<i>0.73**</i>	<i>0.73**</i>	<i>0.15</i>	<i>0.48**</i>	<i>0.66**</i>	<i>0.73**</i>	<i>0.15</i>	<i>0.48**</i>
Days to 50% flowering			0.84**	0.97**	0.72**	0.77**	0.77**	-0.13	0.48**	0.66**	0.73**	-0.13	0.48**
			<i>0.84**</i>	<i>0.97**</i>	<i>0.72**</i>	<i>0.77**</i>	<i>0.77**</i>	<i>-0.13</i>	<i>0.48**</i>	<i>0.66**</i>	<i>0.73**</i>	<i>-0.13</i>	<i>0.48**</i>
Plant height (cm)			0.30	0.30	0.73**	0.74**	0.74**	0.30	0.73**	0.74**	0.74**	0.30	0.30
			<i>0.30</i>	<i>0.30</i>	<i>0.73**</i>	<i>0.74**</i>	<i>0.74**</i>	<i>0.30</i>	<i>0.73**</i>	<i>0.74**</i>	<i>0.74**</i>	<i>0.30</i>	<i>0.30</i>

* and **: significant at 0.05 and 0.01 of probability levels, respectively.

Genotype IUTKH₂₁₁ had the highest mean of oil content among parental lines and also the highest positive GCA effects (0.87*) for this trait. This genotype was a line selected from a local population and it has a good genetic potential for oil content improvement. However, among the progenies, the highest oil content belonged to the cross Saffire × IUTC₁₂₉ with a high SCA effect (data not shown). This indicates that both GCA and SCA effects should be considered in choosing the parental lines in breeding programs of safflower. As mentioned by Sharma (1998), even crosses of parents with relatively low GCA effects could lead to high performance progenies.

Considerable association between GCA effects and mean traits of parental lines (Table 4) imply that the value can be used to choose parents with better combining ability instead of using the GCA effects. The positive correlation coefficients implied that parental lines with high values of the traits can have superior combining ability.

A positive and considerable phenotypic and genetic correlation between seed yield per plant with each of heads per plant and seeds per head (Table 5) were in agreement with findings of Abel (1976b). These correlations indicate that the number of heads per plant and seeds per head could be used as selection criteria in improving seed yield. In this study a positive and considerable correlation was found between plant height and days to flowering (Table 5) which agreed with the results of Kotecha (1979). The positive and considerable correlation of oil content with seed yield per plant (Table 5) implies that selection for increased seed yield should have no deleterious impact on oil content.

There was reasonable consistency between genetic and phenotypic correlations among the traits, which indicates limited effects of environmental factors (Guines *et al.*, 2002). However, reduction of genetic or phenotypic coefficients of correlation from F₁ to F₂ progenies for some traits such as seed yield per plant and days to 50% flowering could be related to the larger plots used in evaluation of F₂ progenies (Sharma *et al.*, 1991).

In general, there was considerable consistency for the results obtained from analysis of F₁ and F₂ progenies in terms of GCA, SCA, h^2_n and phenotypic and genetic correlation. It is expected that the results of analysis for F₁ and F₂ progenies in a diallel set of crosses should not be different in terms of theoretical aspects (Mather and Jinks, 1982). The results of this study and the others in bread wheat (Abdel-Sabour *et al.*, 1996, Hassan *et al.*, 1996) and cotton (Meredith, 1990) indicated that there are some consistencies between results of F₁ and F₂ diallel analyses. Therefore, it seems that F₂ diallels may provide similar results as F₁ diallels in other crops. One of the most important advantages of the F₂ diallel is to have sufficient seeds to overcome the difficulties regarding artificial crossing and F₁ seed production in many hermaphroditic plants such as safflower. Also, sufficient F₂ seeds provide the opportunity to have more replication or environments in the experiments.

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