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Genetic analysis of harvest index in safflower (*Carthamus tinctorius* L.) via diallel crosses

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The F_1 and F_2 progenies of the eight-parent diallel crosses were used to investigate the mode of inheritance of harvest index (HI) (%) in safflower (*Carthamus tinctorius* L.) seeds. The results indicated significant differences among the parents for general (GCA) in two evaluated generations. Specific combining ability (SCA) was significant in F_1 generation. Furthermore, the estimates of genetic variance components and predictability factor (PF) proposed the more importance of additive genetic effects that contribute to genetic variation in harvest index. The overall results indicated that C_{4110} was the best parental genotype for increasing HI (%). Also, superior crosses of $K_{21}\times$ 22-191 (F_1 generation) and 22-191×C_{4110} (F_2 generation) could be employed for the production of high seed yielding safflower lines in breeding programs.

Key words: diallel, effect, harvest index, safflower

Safflower (*Carthamus tinctorious* L.) is an oilseed crop that improvement of yield is being emphasized for this crop. Safflower plant is tolerant to severe drought and salinity (Gecgel et al., 2007; Singh, 2007). It is an important alternative oil sources (Cosge et al. 2007; Weiss, 2000). Thus, breeding efforts in safflower should emphasize on the improvement of seed yield and oil content (Cosge et al. 2007). One of the most important physiologic indexes in improvement of seed yield is harvest index. The term 'harvest index' (HI) was first introduced by Donald (1962) who defined it as the ratio of economic yield to total biomass yield. Studies were conducted to examine the use of HI as an indirect selection criterion for improving seed yield of crop (Sharma et al. 1991). Estimation the genetic control of HI has been studied in some species of oilseed crops such as flax (Mohammadi et al. 2010), rapeseed (Sabaghnia et al. 2010) and sunflower (Tavade et al. 2009) but literature review shoed that there is no any report about the genetic control and combining ability of harvest index in safflower.

In view point of HI importance for safflower improvement, identification and selection of suitable parents could be including in crossing plants could be effective breeding method for improving HI. Evaluation the genetic variation among parent could distinguished the superior parents. Improving seed yield in safflower needs suitable information regarding the nature of general combining ability (GCA) and specific combining ability (SCA) of the parents available in a broad array of genetic material to be used in the hybridization programs. Diallel analysis provides a unique opportunity to test a number of lines in all possible combinations (Griffing, 1956; Mather and Jinks, 1982).

The first objective of this study was to determine the range of HI in eight diverse safflower genotypes and estimate their GCA for this trait. The second objective was to identify superior hybrid combination of HI based on mean HI and SCA estimates.

Material and Methods

Eight genotypes representing a diverse range for plant yield, plant type and genetic background were selected for this study). Six native lines (C_{111}, C_{4110}, ISF_{14}, A_2, K_{21} and IL.111) which were selected from various Iranian local populations and two exotic genotypes [one from Mexico (22-191) and one from Germany (GE_{62918})] were used in this study. These parental genotypes were crossed manually in a full diallel mating design to produce 56 F_1 hybrid populations. All of the F_1 hybrids were selfed by bagging to produce 28 F_2 progenies with out reciprocals. An experiment including 64 genotypes of F_1 (56 F_1 hybrids and 8 parental genotypes) with 36 genotypes of F_2 were laid out in a complete randomized block design with 3 replications at Agricultural Research Farm of Yazd of Iran (54^o 21´ longitude and 31^{o}52´ latitude and, 1200 asl). Each plot of parents and F_1 had two row of 2m length while each plot of F_2 consisted of 3 rows of 3m in length. At maturity, each individual plant was harvested separately with total of the head. In F_1 and F_2 generations, 15 and 30 single plant was selected randomly, respectively. After that, total of the heads per plant was weighted to estimate biological yield for each plant. Individual samples were threshed and total grain of each plant was weighted to estimate grain yield (economical yield). Analysis of variance (ANOVA) was conducted for two generation. Combining ability analyses was carried out using Griffing s Method 1 and 2 (1956), fixed model. The diallel analysis was carried out with Ukai program (1989).

Results and discussion

Analysis of variance revealed significant differences among genotypes (Table 1). This analysis showed that GCA mean squares were significant in two generation while the SCA mean squares were significant only in F_1 populations, indicating that GCA effects were more important than SCA effects in explaining variability for HI in these crosses. This implies that additive gene action was more important than non-additive gene action for HI in safflower. Other studies in oilseed crops demonstrated on predominance of additive gene effects for genetic control of harvest index in flax (Mohammadi et al. 2010) and rapeseed (Sabaghnia et al. 2010). Tavade et al. (2009) reported the importance of both additive and non-additive gene effects in genetic control of HI in sunflower. Reciprocal effects were significant in F_1 generation (Table 1). This result showed the importance of cytoplasmic effects in genetic control of HI. Mohammadi et al. (2010) reported the significant of reciprocal effects in genetic control of HI (%) in flax.

Table 1 Results of analysis of variance for combining ability and variance components in a diallel cross of safflower genotypes

Population		F_1	F_2
Source	df	Mean squares	
Replication	2	107.77**	69.25**
Genotype	63	30.09**	7.80**
GCA	7	34.55**	28.66**
SCA	28	17.8**	2.58^{ns}
REC	28	33.77**	-
Error	126	3.25	1.96
	Components of variance		
P.F.¥.	79		95
GCA/SCA	1.94*		11.10**

* and ** significant at P<0.01 and P< 0.05, respectively
¥: Predictability factor

The increased ration of GCA/SCA mean squares in F_2 generation and PF factor, implied the predominance role of additive gene effects in F_2 generation (Table 1). The relative importance of variances due to GCA and SCA were compared by the predictability factor $[2\sigma^2_{GCA}/(2\sigma^2_{GCA}+\sigma^2_{SCA})]$ (Baker, 1978). Also, predictability factor (PF) was increased in F_2 generation rather than F_1 generation (Table 1). This result showed that GCA effects had more magnitude rather than SCA effects in F_2 generation. The GCA /SCA mean squares were significant in two generation but it had more magnitude in F_2 generation than F_1 generation that showed the more importance of additive gene effects in F_2 generation. Parental means and their GCA effects are presented in Table 2. The highest mean and GCA effect for HI among parents was denoted to 22-191 and C_{4110} in F_1 and F_2 generations, respectively (Table 2). The lowest mean and highest negative GCA effect was denoted to K_{21} in two generation (Table 2). In F_1 generation, 22-191 had the only positive significant GCA effect, but in F_2 generation C_{111}, C_{4110}, IL.111 and 22-191 had positive significant GCA effect (Table 2). There were slight changes in relative rankings of the parents in two generation. The correlation between mean of HI (%) and GCA estimates over generations indicating that GCA of the parents for HI could be predicted to a certain extent on the basis of their mean HI (%) value.

Positive and significant association between GCA effects and means of the parents in both evaluated generations (Table 2). According to Banerjee and Kole (2009) this result suggested that performance of it parent could be a good indicator of its potential to transmit suitable traits to its progenies.

Cross mean and estimates of specific combining ability (SCA) for HI in F_1 and F_2 generations in presented in Table 3. The highest mean for HI in F_1 and F_2 generation was denoted to IL.111× 22-191 (55.36) and C_{4110} × IL.111 (55.96), respectively.

In F_1 generation the crosses with mostly high HI (%) were ISF_{14} ×IL.111 (53.98), K_{21} ×22-191 (55.28) and C_{111} ×22-191 were in the superior crosses. Also, C_{111} ×C_{4110} (56.26), GE_{62918} ×C_{4110} (55.66) and IL.111 × 22-191 (55.36) were the most high crosses for HI in F_2 generation (Table 3).

Table2. Means of the parental genotypes s and their GCA effects in F_1 and F_2 generation in a diallel cross of safflower genotypes

	F_1		F_2	
	Mean	GCA	Mean	GCA
GE_{62918}	52.76	0.51	52.76	0.30
C_{111}	55.1	0.41	55.46	1.01**
C_{4110}	57.16	0.60	56.76	1.95**
ISF_{14}	53.2	0.11	53.30	-0.45
A_2	49.66	0.02-	49.50	-1.40**
K_{21}	46.83	-1.93**	46.83	-3.14**
IL.111	55.01	0.16	55.06	0.74
22-191	55.36	0.81**	55.57	1.26**
r(GCA, mean)¥	0.85**		0.98**	

¥:Calculated correlation (r) between the mean value for trait and the value for GCA of eight genotypes

There was a moderate consistency between crosses mean in two generation. Among 28 crosses in F_1 generation, 7 crosses showed positive significant SCA effect (Table 3). The highest SCA effect was denoted to GE_{62918} × K_{21} (3.6) (Table 3). In F_2 generation, there was not a positive significant SCA effect (Table 3). This result is in agreement with non-significant of SCA effects in this generation. The highest and positive SCA effect was observed in GE_{62918}×A_2 (1.09) (Table 3). This result might be due to the diminishing of dominant gene effects in F_2 generation because of selfing F_1 progenies. On the other hand, the high SCA effects in F_1 generation could have arises from high dominant effects in F_1 hybrids and heterosis effects. There was consistency between SCA effects of crosses in two generation. It appears that environmental conditions might have influenced the SCA component in a more unpredictable manner compared to the environmental influence on the GCA component.

Table 3. Cross mean and estimates of specific combining ability (SCA) and reciprocal effects for harvest index in F_1 and F_2 generations in safflower genotypes

	F_1			F_2	
	Mean	SCA	Reciprocal	Mean	SCA
GE_{62918}×C_{111}	51.26	-1.33*	1.83*	54.63	0.72
GE_{62918}×C_{4110}	53.05	0.92	5.45**	55.66	0.79
GE_{62918}×ISF_{14}	52.76	0.46	0.30	52.30	-0.14
GE_{62918}×A_2	53.80	1.63*	0.93	52.6	1.09
GE_{62918} ×K_{21}	53.85	3.6**	-2.71**	50.46	0.70
GE_{62918}×IL111	49.98	-2.36**	-2.51**	51.56	-2.08*
GE_{62918}×22-191	50	-2.99**	-2.46**	53.43	-0.73
C_{111}×C_{4110}	50.46	-1.55*	-2.43**	56.26	0.43
C_{111} × ISF_{14}	50.47	-1.73**	-5.00**	51.96	-1.44
C_{111}×A_2	50.55	-1.51*	0.08	51.23	-1.24
C_{111}×K_{21}	49.58	-0.56	-0.98	50.10	-0.63
C_{111} ×IL. 111	54.84	2.60**	0.0	55.26	0.63
C_{111}× 22-191	54.40	1.5*	-0.16	55.48	0.34
C_{04110} × ISF_{14}	50.05	-1.67**	1.51*	54.23	-0.14
C_{4110}×A_2	53.83	2.24**	0.03	54.03	0.59
C_{4110}×K_{21}	48.96	-0.70	0.86	49.56	-2.12**
C_{4110}×IL.111	50.45	-2.88**	3.41**	55.96	0.38
C_{4110}×22-191	52.26	-1.97**	2.31**	56.20	0.10
ISF_{14}× A_2	51.06	0.50	-0.43	51.60	0.58
ISF_{14}×K_{21}	50.45	1.22	4.6**	49.56	0.29
ISF_{14}×IL.111	53.98	-1.49*	0.35	51.83	-1.33
ISF_{14}×22-191	50.01	1.38*	4.05**	53.17	-0.50
A_2×K_{21}	51.31	0.30	2.35**	48.76	0.43
A_2×IL.111	51.71	-0.49	-1.21	52.36	0.14
A_2×22-191	48.88	-0.74	-0.68	52.26	-0.47
K_{21}×IL.111	48.66	-1.01	-0.01	50.86	0.38
K_{21}×22-191	55.28	-1.88**	2.10**	51.43	0.43
IL.111×22-191	55.36	2.63**	1.41	55.36	0.48
LSD(1%)	3.27	2.43	11.36	1.42	0.26

A novel finding of this study involves the identifying genetic inheritance of harvest index in safflower. In both F_1 and F_2 generation, it was found that the variance due to GCA was higher than those of SCA. Therefore, the additive-dominance genetic model was adequate for HI (%) in safflower. Also, the significance ratio of GCA/SCA mean squares, and the predictability factor for HI (%) (close to unity) indicate the predominance of additive gene effects in the genetic control of HI (%) in this study. Therefore, breeding procedures based on selection among lines derived from the hybridization program/recurrent selection would obtain high efficiency for improvement of harvest index in safflower.

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