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Full Length Research Paper

Genetic analysis of earliness and its components in safflower (*Carthamus tinctorious* L.)

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In this research, F_1 and F_2 progenies of diallel crosses with eight-parental genotypes were used to investigate the mode of inheritance for earliness in safflower (*Carthamus tinctorius* L.). Days to emergence, days to budding, days to bolling, days to flowering and days to maturity were estimated in 64 and 28 genotypes in F_1 and F_2 generation, respectively. The results indicated that there was enough genetic variation among genotypes for diallel analysis. Also, the results indicated significant differences for general combining ability (GCA) and specific combining ability (SCA) for all evaluated traits in two generations. Except for days to maturity, reciprocal effects were significant for studied traits. Additive gene action had more importance for days to budding and days to maturity in F_1 and F_2 generation, respectively. For days to budding additive gene effects had more importance for genetic control of it. For days to emergence and days to flowering additive and dominance gene effects were important. The highest narrow-sense and broad-sense heritability were denoted to days to budding in two generations. Among parental genotypes, IL.111 and GE_{62918} were the best negative combiners for earliness. There was a moderate consistency in estimation of genetic parameters in two generations.

Key words: Analysis, earliness, effect, genetic, heritability, safflower.

INTRODUCTION

Safflower (*Carthamus tinctorious* L.), an oilseed crop belongs to the family Asteraceae (Knowles, 1969; Weiss, 2000) is an annual, bushy, herbaceous possessing several branches (Dajue and Mundel, 1996; Li and Mundel, 1996). Days to emergence, days to budding, days to bolling, days to flowering and days to maturity are sequentially developmental stages in safflower ripening (Singh, 2007). The development of productive acceptable early maturing cultivars is a priority objective in many plant breeding programs. Earliness reduces the duration of trop risk, allows greater flexibility in planting time within growing seasons, facilitates irrigation water conservation and reduces irrigation expense and is important in areas with short rainy seasons and subsistence farming. The capability of a variety to produce a reasonable quantity of seed during the short seasons in some areas becomes even more important than good yield performance in favorable condition. One of the major aims in safflower breeding is development of early-maturing genotypes. Therefore, production of early maturing genotypes could be an effective breeding strategy for improving seed yield of safflower. Advancement in producing early maturing genotypes via genetic designs requires certain information regarding the nature of combining ability of parents used in the hybridization programs and also the nature of gene action involved in the expression of phonological traits.

Early maturity enables safflower to escape from environmental stresses. Two types of environmental stresses including biotic stresses (disease and insects) and abiotic stresses (heat and drought) could diminish the seed yields, significantly at the late stages of safflower ripening (Mundel et al., 1992). Earliness is an effective strategy for escaping of plants from insects and diseases infections at the beginning of reproductive stage in safflower, with considering that significant genetic erosion has also been occurred in safflower genotypes over the years due to diseases, insects, and environmental stresses. Safflower has diverse agro-ecological regions for its cultivation (Mundel et al., 1992). Safflower could be able to well adapt to short growing season if they are categorized to early maturity groups. Also, cultivation of early maturing genotypes enables the cultivation of a second crop on the same land

Table 1. Plant materials used for diallel cross-design in safflower.

Entry		Parents	Origin
1	P_1	GE_{62918}	Germany
2	P_2	C_{111}	Selected from Kouseh landrace
3	P_3	C_{4110}	Selected from Kouseh landrace
4	P_4	ISF_{14}	Selected from Isfahan landrace
5	P_5	A_2	Selected from Azarbayejan landrace
6	P_6	K_{21}	Selected from Kordestan landrace
7	P_7	IL111	Selected from Auroumieh landrace
8	P_8	Mex.22-191	Mexico

(Hatamzade et al., 2007). It seems that cultivation of early maturing genotypes of safflower is necessary for its cultivation in hot and dry climates. Breeders could employ available means to develop early maturing varieties, but success in breeding programs depends upon our knowledge of the genetic bases of earliness and its components (Kidambi et al., 1988; Sahu and Tewari, 1993). Genetic information can be used to formulate the most efficient breeding strategy for developing early maturing genotypes (Upadhyaya and Nigam, 1994). Information on general combining ability (GCA) and specific combining ability (SCA) is very important to organize a successful breeding program (Kearsey and Pooni, 1996; Huang et al., 2010). Estimation of GCA and SCA effects in F_1 and F_2 generation could be a suitable way for perfect-fit estimates of genetic components (Hayman, 1954; Joshi et al., 2004). Some phonologic stages, including flowering and maturity are the most critical stage influencing the yield of safflower (Weiss, 2000). Combination of early maturity and high seed yield genotypes in safflower is the most promising type in its breeding (Weiss, 2000). Estimation of heritability of phonological traits and the magnitude of environmental effects of growth stages could be an effective criterion for selection of suitable genotypes (Hatamzade et al., 2007).

Different genetic studies have been done for genetic analysis of phonological traits in oilseed crops such as peanuts (Gibori et al., 1978), brassica (Amiri-Oghan et al., 2009), mustard (Teklewold and Becker, 2005) and flax (Mohammadi et al., 2010). Also, various genetic studies on safflower genotypes has been carried out for determination of genetic control of phonological traits in safflower including emergence (Kotecha, 1979), flowering (Gupta and Singh, 1988; Kotecha, 1979; Patil et al., 1992; Ramachandram and Goud, 1981,) and maturity (Kotecha, 1979) in safflower. Hatamzade et al. (2007) reported the importance of both GCA and SCA effects in genetic control of earliness in safflower via diallel analysis. Previous investigations have not shown any result about genetic control of some phonological traits including days to emergence, days to budding and days to bolling. It is evident from this review that several researchers have studied earliness but maybe no effective criterion for screening large populations of safflower lines for earliness has been defined.

The main objective of the present study was designed to determine gene actions, combining ability and genetic parameters in earliness-related traits in safflower. Therefore, the genetic control determining the number of days to the beginning of flowering, and days to maturity needs to be determined to allow the efficient breeding of early maturing lines and varieties.

MATERIALS AND METHODS

The experimental material was composed of the following eight genotypes of safflower from different geographical regions of Iran including C_{4110}, C_{111}, ISF_{14}, A_2, K_{21}, IL.111 along two exotic genotypes provided from Germany (GE_{62918}) and Mexico (Mex.22-191) (Table 1). These genotypes were crossed manually in a full diallel fashion including direct crosses and their reciprocals during spring of 2007. In order to produce F_2 seeds, 28 genotypes of directed crosses from F_1 hybrids were selfed by bagging them in the summer of 2007. Thus, a small portion of F_1 seeds were sown (1 row of 2 m length for each F_1) and allowed to self pollinate to produce 28 F_2 genotypes. The selfing process was ensured by protecting plants with insect proof net to prevent out-crossing through insect pollination.

Total of the F_1 and F_2 progenies along with 8 parental genotypes, were grown in a randomized complete block design with three replications during the spring of 2008 at the research farm of Isfahan University of Technology, Iran (51° 32'E and 32° 32'N, 1630 m asl). The soil at this site is silty clay loam, typic Haplargids of the arid tropic with pH= 7.5 and organic mater content of 1%. The fertilizers were applied at 100 kg N/ha and 100 kg P/ha prior to sowing and 75 kg N/ha top dressed at shooting stage. Each plot comprised two 1.5 m rows spaced 50 cm apart and two 3 m rows spaced 50 cm apart for F_1 and F_2 generations, respectively. Standard agronomic package of practices and suitable plant protection measures were taken to raise a healthy crop. All phonological traits including days to emergence (DE), days to budding (DBu), days to bolling (DBo), days to flowering (DF) and days to maturity (DM) were recorded on plot basis mean.

Statistical analysis

Analysis of variance (ANOVA) of data was performed using SAS statistical program to estimate variance components (SAS Institute, 1997). Analysis of combining ability for F_1 hybrids was performed using Method I, fixed model, according to Griffing's (1956) method,

Table 2. Analysis of variance for combining ability of different traits in the F_1 and F_2 generations of safflower.

Source of variation	Mean squares (MS)					
	df	DE	DBu	DBo	DF	DM
F_1 hybrids						
Replication	2	64.31**	31.73**	37.38**	259.90**	326.44**
Genotypes	63	10.41**	16.51**	22.84**	10.95**	5.74**
Residual	126	0.40	5.66	7.13	4.09	2.33
F_2 populations						
Replication	2	7.03	75.02**	78.92**	63.86**	47.33**
Genotypes	35	8.66**	24.76**	26.75**	10.93**	9.50**
Residual	70	2.48	11.59	11.28	3.66	2.68

DE: days to emergence; DBu: days to budding; DBo: days to bolling; DF: days to flowering; DM: days to maturity.

using SAS program (Zhang and Kang, 1997). In F_2 generation combining ability analysis was performed using Griffing's method II (Griffing, 1956), fixed model. To test the assumptions of Hayman's (1954) model for fulfillment of additive-dominance model, the values of Wr (array parent-offspring covariance) were regressed on Vr (array variance) values.

If the regression coefficient (b) between Wr and Vr are not differed significantly from unity (1-b) it indicated the absence of non-allelic interaction (Mather and Jinkd, 1982). Therefore, the genetic components for two generations were estimated according to Jinks-Haman (1953) analysis. Broad-sense (h^2_b) and narrow-sense (h^2_n) heritability estimates were obtained from different genetic parameters including D, H_1, H_2 and F, according to Mather and Jinks (1982), where D is additive effects; H_1 and H_2 values are dominance effects and F value is the sum of the cross product of the additive and dominance effects (Mather and Jinks, 1982).

Genetic parameters were estimated by Diall program (Ukai, 1989). Predictability factor (PF) calculated from GCA and SCA variances reflect the degree to which additive and dominance gene effects of the trait are transmitted to the progeny (Banerjee and Kole, 2009). Therefore, the predictability of progeny performance based on the GCA-effect will be reliable for earliness in safflower.

RESULTS AND DISCUSSION

The analysis of variance for phonological evaluated traits revealed highly significant differences among genotypes in two generations (P<0.01) (Table 2). The mean squares due to GCA and SCA effects were significant for DE (Table 3). This result implied the importance of both additive and non-additive gene effects in genetic control of it. Inconsistent with our results, Kotecha and Zimmerman (1978) reported that non-additive genetic effects had a significant role in genetic control of DE. These dissimilarities could be because of different genetic materials in different experiments. Significance ratio for GCA/SCA was observed for DE. According to Table 3, GCA effects were significant for DBo and DBu, but the SCA effects were not significant, in F_1 generation. This result showed more importance of additive gene effects in genetic control of these two traits. In F_1 generation, for DF and DM, both GCA and SCA effects were significant, that implies the importance of both additive and non-additive gene effects in genetic control of these traits (Table 3). Sahu and Tewari (1993) declared that DF was influenced by genetic additive effects and DM was influenced by additive and non additive genetic effects.

In F_2 generation, GCA effects were significant for all studied traits, but SCA was significant for DE, DBo and DF. This result showed more importance of additive gene actions for genetic control of DBu and DM (Table 3) Also, Patil et al. (1992) reported a significant GCA for DM in safflower. But, Gupta and Singh (1988) reported that additive, dominance and epitasis gene effects were important for DF. Also, Kotecha (1979) reported that gene action was non additive for flowering time, maturity time and flowering to maturity time. The mean squares of reciprocal effects was significant (P<0.01) for all evaluated traits in F_1, except DM (Table 3). Therefore, cytoplasmic inheritance could have an important role in genetic control of these traits in F_1 generation (Table 3). Ramachandram and Goud (1981) reported the significant effect for reciprocal effects for DF. According to Table 3, predictability factor (PF) showed that for DBu and DBo, this ratio was close to unity that represented more importance of additive gene action in F_1 generation. In F_2 generation, the most ratio was observed for DM that implied the predominance of additive gene effects in genetic control of DM in F_2 generation (Table 3). The positive correlation between GCA effects and parental means suggested the possibility of further selection of parents for these traits on the basis of their performance (Banerjee and Kole, 2009). With considering that early maturity is an important aim in safflower breeding, the least mean for each trait and the highest negative GCA was considered for this study. The comparison of parental means showed that IL.111 (9.06) had the least mean for DE among parental genotypes in two generation (Table 4). For DBu, IL.111 (55.15) had the least mean among parents in two generations. For DBo, IL.111 (67.11) had the least mean among parents in two

Table 3. Components of analysis of variance for different traits in safflower.

Parameter	Mean squares (MS)					
	df	DE	DBu	DBo	DF	DM
F_1 hybrids						
GCA	7	38.54**	75.74**	105.88**	45.42**	19.04**
SCA	28	6.64**	7.51	10.25	6.98**	4.72**
Reciprocal	28	7.24**	10.75**	14.68**	6.31**	3.43
GCA/SCA		5.17*	34.6**	21.23**	3.87**	3.27**
P.F. ¥.		0.53	0.90	0.87	0.75	0.57
h^2_b†		0.62	0.93	0.92	0.86	0.76
h^2_n ††		0.35	0.86	0.81	0.65	0.62
F_2 populations						
GCA	7	27.72**	54.13**	50.43**	27.23**	32.00**
SCA	28	3.90**	17.42	20.83**	6.85**	3.86
GCA/SCA		3.27**	11.39**	10.82**	9.88**	0.82**
P.F.¥.		0.77	0.55	0.38	0.55	0.72
h^2_b†		0.76	0.95	0.93	0.92	0.84
h^2_n††		0.39	0.82	0.73	0.58	0.59

*and ** significant at P<0.05 and P<0.01 respectively. DE: days to emergence; DBu: days to budding; DBo: days to bolling; DF: days to flowering; DM: days to maturity; ¥ PF: prediction factor; h^2_b†: broad-sense heritability; h^2_n††: narrow-sense heritability.

Table 4. Means of phenological traits for eight safflower genotypes used as parental lines in diallel mating design.

Trait	GE_{62918}	C_{111}	C_{4110}	ISF_{14}	A_2	K_{21}	IL.111	Mex.22-191	$LSD_{5\%}$
DE	13.78	12.41	10.05	14.79	15.26	14.18	9.09	9.96	1.34
DBu	58.33	61.10	61.74	60.19	64.08	62.69	55.15	64.33	5.08
DBo	69.10	71.23	70.81	70.32	70.28	70.24	67.11	69.53	4.34
DF	76.5	79.49	79.35	79.01	81.02	79.66	75.32	80.85	3.27
DM	107.46	107.47	107.48	108.85	112.89	109.83	103.83	109.32	3.22

DE: Days to emergence; DBu: days to budding; DBo: days to bolling; DF: days to flowering; DM: days to maturity.

generation. For DF, the early flowering genotypes were GE_{62918} and IL.111 in two evaluated generations. Table 4 showed that IL.111 (103.83) had the least mean for DM in two generations.

In comparison for GCA effects, C_{4110}, Mex. 22-191, C_{111} and IL.111 had negative GCA effect in two generations for DE (Table 5) but C_{4110} and IL.111had the most negative and significant GCA effect in F_1 and F_2 generations, respectively. For DBu and DBo, IL.111 had the highest negative GCA effect in two generations. The highest negative GCA effect for DF was denoted to GE_{62918} and IL.111 in F_1 and F_2 generations, respectively. For DM, IL.111 had the highest negative GCA in two generations and had the shortest time for maturity among parental genotypes. The means of the crosses for DE varied from 9.56 (C_{4110}× IL.111) to 14.98 (ISF_{14}×K_{21}) and from 9.33 (C_{4110}× IL.111) to 15.3 (A_2 ×IL.111) in F_1 and F_2 generations, respectively (Table 6). In comparison among genotypes (GE_{62918}× Mex.22-191) (55.67) and A_2×IL.111 (57.66) had the least means in F_1 and F_2 generations, respectively, for DBu (Table 6). Also, A_2×Mex.22-191 (F_1) and IL.111× Mex.22-191 were in the group of superior means for reducing in DBu. Mean of the crosses for DBo varied from 65.50 (GE_{62918}×Mex.22-191) to 73.06 (C_{4110}×ISF_{14}) in F_1 generation (Table 6). In F_2 generation, the mean of the crosses for DBo were ranged from 64.66 in A_2 × IL.111 to 75.33 (C_{111} ×ISF_{14}). Mean of the crosses for DF in F_1 generation varied from 75.33 (K_{21}×IL.111) to 81.66 (C_{111}×K_{21}) (Table 6). Also in F_2 generation, the means varied from 76 (IL.111×Mex.22-191) to 82.33 (C_{111}×ISF_{14}) for DF (Table 6). These superior means could be applied in safflower breeding for reduction of DF. According to Table 6, the mean of the crosses for DM varied from 103.33 (C_{4110}× IL.111) to 109 (C_{111}×A_2) in F_1 generation. Therefore, C_{4110}× IL.111 and GE_{62918}×K_{21} were the best crosses for DM in F_1 generation. Also, in F_2

Table 5. General combining ability (GCA) effects for eight parents in F_1 and F_2 generations.

Parent	Generation	DE	DBu	DBo	DF	DM
GE_{62918}	F_1	0.15	-1.25**	-1.53**	-1.42**	-0.65**
	F_2	0.06	-0.34	-0.27	-0.83*	-0.62*
C_{111}	F_1	-0.35**	1.14**	1.31**	1.24**	0.42*
	F_2	-0.29	1.12	1.19*	1.23**	-0.38
C_{4110}	F_1	-1.14**	1.13**	1.33**	0.60*	0.21
	F_2	-0.46	0.49	0.55	0.63*	-0.28
ISF_{14}	F_1	1.25**	1.08**	1.32**	0.24	0.62**
	F_2	0.79**	-0.80	-0.7	0.63*	-0.08
A_2	F_1	0.57**	0.39	0.49	0.90**	0.82**
	F_2	0.66**	1.02	1.02	0.43**	1.58*
K_{21}	F_1	1.01**	0.33	0.39	-0.13	-0.29
	F_2	1.42**	0.49	0.55	0.10	1.340**
IL.111	F_1	-0.99**	-2.24**	-2.62**	-1.32**	-0.94**
	F_2	-1.67**	-2.87**	-2.80**	-1.70**	-1.58**
Mex.22-191	F_1	-0.49**	-0.59	-0.70*	-0.10	0.20
	F_2	-0.40	0.89	0.45	-0.50	-0.14
r(GCA, Mean)	F_1	0.91**	0.74*	0.71*	0.64	0.82*
	F_2	0.90**	0.85**	0.72*	0.80*	0.95**

* and ** significant at P<0.05 and P<0.01 respectively. DE: days to emergence; DBu: days to budding; DBo: days to bolling; DF: days to flowering; DM: days to maturity; r (GCA, Mean): Correlation between the mean value for trait and the value for GCA of eight genotypes in F_1 and F_2 generation.

generation, IL.111×Mex.22-191 (106.33) and GE_{62918} ×ISF_{14} (107) were the best crosses for DM (Table 6). The positive correlation between GCA estimates and their performance, except for DF in F_1 generation was observed (Table 5).

Genetic components and gene action

Estimates of the various components of genetic variances for studied traits based on Jinks-Hayman's (1953) method given in Table 7 confirmed the results obtained by Griffing's (1956) method. The regression coefficient (b) did not differ significantly from unity (1-b) in both generations for DBu, DBo and DM, that indicated the absence of non-allelic interaction for genetic control of these traits. Therefore, genetic parameters of Jinks-Hayman were estimated for all studied traits, except for DF (in F_1 generation) and DE (in F_2 generation). The estimate of additive component (D) was significant for studied traits in both generations. The estimates of dominance components (H_1 and H_2) were significant for studied traits, except for DBu. Also, H_1 component was non-significant for DM in F_1 generation. These results indicated the importance of additive and dominance gene action in genetic control of these traits. The significant positive values of F components for all studied traits showed that dominant alleles were frequent than recessive alleles in the parental lines.

The estimates of $H_2/4H_1$ were smaller than 0.25 (the theoretical maximum) for all studied traits in two generations, indicating that alleles for these phonological traits were not equal in proportion in the parents. Such an allelic distribution may be the result of selection forces for these traits, causing differential distribution of dominant and recessive alleles in these parental lines. In all studied traits, the positive F value in two generations, revealed the excess of dominant alleles rather than recessive alleles in genetic control of these traits. The ratio of $(H_1/D)^{0.50}$ was less than unity for all studied traits, except for day to flowering in F_2 generation. This result suggests the partial dominance for genetic control of DE, DBu,

Table 6. Mean values of F1 and F2 generations for phenological traits in 8×8 diallel cross of safflower.

Crosses	DE		DBu		DBo		DF		DM	
	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
C_{111}× GE_{62918}	12.9	13	59.52	68	69.83	75	77.66	80	107	107.93
C_{4110}× GE_{62918}	11.5	12.33	59.50	66.33	70	73.33	77.65	78	106.5	107.66
ISF_{14}× GE_{62918}	14.38	12.66	57.80	60.10	68	67	76.66	76.63	107	107
A_2× GE_{62918}	11.51	11	59.07	62.33	69.50	69.33	78.66	78	108.5	107.33
K_{21} ×GE_{62918}	14.01	14.66	56.38	63	66.33	70.00	75.50	76.66	105.33	109.66
IL.111× GE_{62918}	12	10	56.24	63.66	66.16	70.66	76.66	77	107	107.66
Mex.22-191× GE_{62918}	12.58	10.66	55.67	64.66	65.50	71.66	76.33	79	105.83	108.13
C_{4110}× C_{111}	11.35	12.66	61.18	61.66	71.98	68.66	80.50	77.66	107.16	107
ISF_{14} × C_{111}	12.28	12	61.34	68.33	72.16	75.33	79.36	82.33	108.5	108.33
A_2× C_{111}	13.03	10.66	60.49	64.66	71.16	71.66	80.50	79.66	109	109.66
K_{21}× C_{111}	14.10	12.66	62.05	65.66	73	72.66	81.66	81	107.75	109
IL. 111 ×C_{111}	10.63	10.33	58.05	65	68.33	72.00	79.50	80.33	108.33	108
Mex.22-191× . C_{111}	12.28	11.33	58.53	62.66	68.66	69.66	79	77.66	107.33	109
ISF_{14} × C_{4110}	14.13	11.66	62.11	63.33	73.06	70.33	79.75	80.66	108.83	109.05
A_2× C_{4110}	10.94	11.33	61.22	65	72.03	72	79.83	80.66	107.16	109.66
K_{21}× C_{4110}	12.10	13.66	60.41	65	70.8	72	79.66	81.02	107.16	110.33
IL.111× C_{4110}	9.56	9.33	57.46	66	67.60	68	77	77.66	103.33	108.33
Mex.22-191× C_{4110}	13.71	13.33	58.70	66	69.15	73	78.38	78.33	107.16	108
A_2× ISF_{14}	14.95	14.63	59.81	65.33	70.36	72.33	80.33	80.33	107.836	110.66
K_{21}× ISF_{14}	14.98	14.60	59.22	64.33	69.66	71.33	78.50	80.33	107.10	110.33
IL.111× ISF_{14}	13.66	12	57.37	59.66	67.50	66.66	77.83	77	106.83	109
Mex.22-191× ISF_{14}	12.26	12.01	60.50	64.33	71.46	71.66	77.43	78	108.50	109.33
K_{21}× A_2	13.36	12	59.90	64.33	70.66	71.33	78.33	77	107.16	112.33
IL.111× A_2	13.68	15.30	57.37	57.66	67.50	64.66	76.33	76.66	106.33	107.66
Mex.22-191× A_2	12.98	11	56	66.33	67	68	79.48	76.06	107.66	108.66
IL.111× K_{21}	14.06	12.33	57.79	60.33	68	67.33	75.33	76.66	106.33	107.33
Mex.22-191× K_{21}	13.05	13.33	58.08	62.33	68.33	69.33	76.5	76.33	107.5	109.93
IL.111× Mex.22-191	10.61	11.66	55.95	60	65.83	67.01	77.30	76	106.66	106.33
LSD (5%)	1.01	2.56	3.84	5.54	4.38	5.47	0.26	2.05	2.43	2.57

E: Days to emergence; DBu: days to budding; DBo: days to bolling; DF: days to flowering; DM: days to maturity.

DBu and DM in two evaluated generations. The mean degree of dominance $(H_1/D)^{0.5}$ was more than unity in F_2 generations, for DF indicating the presence over-dominance for DF in F_2 generations. Gupta and Singh (1988) reported partial dominance and over dominance for genetic control of DF and DM, respectively. The dominance effect, that is, sum of total over all loci at heterozygous state (h) was significant only for DF in F_2 generation. The ratio of total dominant and recessive alleles pooled over all parents, that is $\left(\frac{(DH_1)^{0.5}+F}{(DH_1)^{0.5}-F}\right)$ was more than unity, indicating prevalence of dominant over recessive genes for all studied traits.

Heritability of studied traits

All of the studied traits, except for DE, had medium broad-sense heritability that ranges from 30 to 70% in two generations. Also h^2_b was high (>70%) for DM in F_2 generation (Table 6). This result showed that environmental effect had a medium influence on the phenotypic variation of these traits. Narrow-sense heritability for studied traits ranged in medium values ($30<h^2_n<70$) that implied a moderate progress will be achieved through selection for these traits. In F_1 generation, the narrow-sense heritability ranged from 57% for DE to 36% in DM (Table 6). Also, in F_2 generation, h^2_n ranged from 54% for DM to 24% in DF. In consistence with our report, Patil et al. (1992) reported high heritability for DF and DM. This study manifested important knowledge about genetic control of earliness and its components in safflower. With considering the contribution of different genetic components in genetic control of a trait, appropriate strategy for improvement of each desirable trait, could be achieved.

Genetic control determining the traits involved in earliness, allows the efficient breeding of early maturing

Table 7. Estimation of the derived parameters of genetic variance components and regression coefficients between Wr/Vr in F_1 and F_2 progenies from diallel crosses of safflower genotypes.

Genetic components	Generation	DE	DBu	DBo	DF	DM
D	F_1	6.61**	6.56*	9.22*	-	5.62**
	F_2	-	7.58**	14.72*	3.08*	7.56*
H_1	F_1	5.51**	3.76	5.09*	-	3.51*
	F_2	-	2.94	11.48**	6.63**	3.83*
H_2	F_1	4.16**	1.28	2.03*	-	1.61
	F_2	-	1.54	15.09**	5.67**	2.75*
F	F_1	4.78**	3.25	4.14	-	2.15
	F_2	-	3.6	8.97	2.56	3.55
h	F1	0.55*	-0.27	-0.17	-	-0.23
	F_2	-	-0.31	0.67	0.71**-	1.26-
$H_2/4H_1$	F_1	0.18	0.086	0.1	-	0.11
	F_2	-	0.13	0.15	0.21	0.17
$(H_1/D)^{0.50}$	F_1	0.91	0.75	0.74	-	0.79
	F_2	-	0.62	0.87	1.46	0.71
b (Wr,Vr)	F_1	0.82±0.2	1.27±0.43	1.33±0.43	0.36±0.1	0.86±0.1
	F_2	0.31±0.14	0.87±0.23	0.97±0.4	0.68±0.3	0.95±0.15

DE: Days to emergence; DBu: days to budding; DBo: days to bolling; DF: days to flowering; DM: days to maturity.

lines and varieties. The use of parental genotypes with high negative GCA effects for earliness and its components in recombination breeding programs may accumulate the suitable genes for improving earliness in the recombinant inbred lines. The results showed that parents IL.111 and GE_{62918} were better than other parents for earliness traits. There were suitable genes in two parents for earlier days to the beginning of flowering, earlier days to the end of flowering and earlier DM, as indicated by these having the highest negative GCA effects for the aforementioned traits. Joint analysis of two sequential traits including F_1 and F_2 showed some dissimilarities in the estimation of different genetic parameters. This result could be the result of sampling variation in two different generations and environmental effects.

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