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Genetic Analysis of Agronomic Traits in Safflower (*Carthamus tinctorious* L.)

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Abstract

Genetics of agronomic traits in safflower was determined using 6×6 full diallel population. Data were recorded on days to flowering, days to maturity, plant height, primary branches per plant, head diameter, number of heads per plant, number of seeds per head, 1000-seed weight and seed yield per plant. Variance components showed that days to maturity and heads per plant were largely controlled by dominance gene effects, whereas 1000-seed weight, plant height and seeds per head were governed by additive type of gene action. The results also revealed both additive and non-additive types of gene actions for remaining traits. The significant mean squares of reciprocal crosses for days to flowering, head diameter, number of seeds per head, 1000-seed weight and seed yield per plant suggested that maternal inheritance also played an important role in the inheritance of these traits. Significant general combining ability for yield revealed that genetic improvement through accumulation of desirable alleles from parents in the target genotype using appropriate selection methods would be desirable in safflower.

Keywords: combining ability, heritability, inheritance, maternal effect, variance components

Introduction

Safflower (*Carthamus tinctorious* L.) is an important oilseed crop that has long been cultivated for different purposes, such as oil, fabric dyes, food coloring, medicinal and industrial needs (Dajue and Mundel, 1996). Iran is regarded as one of the centers of diversity for safflower in the world (Dajue and Mundel, 1996). Local safflower cultivars and landraces are grown commercially in different geographical regions of Iran. Safflower plant is tolerant to heat, drought and salinity, which are among the most important factors limiting plant production (Singh, 2007). The knowledge of inheritance of agronomic traits helps in planning an efficient strategy for further improvement of yield potential and its stability in safflower.

There is growing interest in developing hybrid cultivars in self-pollinated crops in recent years. Specific combining ability (SCA) of agronomic traits is an important indicator of the potential of inbred lines in generating successful hybrid combinations (Huang *et al.*, 2010). General combining ability (GCA) is a measure of additive gene action, whereas SCA is related to dominance (Huang *et al.*, 2010; Wang *et al.*, 2010). The diallel genetic design provides an opportunity to test a number of lines in all possible combinations (Singh and Pawar, 2005).

Reports on combining ability and inheritance, in general, of some agronomic traits in safflower are available (Gupta and Singh, 1988b; Mandal and Banerjee, 1997; Singh *et al.*, 2008), while genetic parameters of some agronomic traits are still lacking in the literature. Therefore, the objective of present study was to determine inheritance and combining abilities for the agronomic traits in safflower using a diallel design.

Materials and methods

Plant materials and growth conditions

Eight safflower genotypes, including six native ('C_{111}' 'C_{4110}', 'ISF_{14}', 'A_2', 'K_{21}' and 'IL.111') and two exotic genotypes [one from Mexico ('Mex.22-191') and one from Germany ('GE_{62918}')] were crossed in all possible combinations. Seeds of 56 F_1 hybrids were produced by hand-emasculation and pollination in 2007. The seeds of 64 genotypes (8 parents and 56 F_1 hybrids, including reciprocals) were sown in the field using a randomized complete-block design with three replications. The experiment was conducted at the research farm of Isfahan University of Technology located at Lavark-Isfahan (51º32´ E and 32º32´ N, 1630 m a.s.l.) in 2008. Each plot consisted of 2 rows of 1.5 m length each.

Data were recorded on nine agronomic traits comprising days to flower (DF), days to maturity (DM), plant height (cm) (PH), primary branches per plant (BP), head diameter (cm) (HD), number of heads per plant (HP), number of seeds per head (SH), 1000-seed weight (g) (SW) and seed yield per plant (g) (YP). Two phenological traits DF and DM, were recorded on a plot basis. Fifteen randomly chosen plants from each plot were used for recording data on other agronomic traits, PH, BP, HD, YP, HP, SH and SW.

Statistical analysis

The data were subjected to an analysis of variance (ANOVA) using PROC GLM of SAS (SAS Institute 2002). Least significant difference (LSD) test was used for mean separation. Combining abilities (general and specific) were estimated following Method 1, Model 1 of Griffing (1956) by using SAS program (Zhang *et al.*, 2005). Genetic parameters were estimated by DIALL computer program (Ukai, 1989). To fulfill the assumption of genetic analysis of Hayman (1954), data were subjected to regression, as described by Mather and Jinks (1982). The regression coefficient (b) represented the relationship between Vr (the variance of the rth array) and Wr (the covariance of the rth array values with the non-recurring parents) in in graphical approach (Jinks and Hayman, 1953) Genetic components for F_1 generation were estimated according to Singh and Pawar (2005).

Total genotypic variance was partitioned into variance components, including GCA, SCA and reciprocal (REC). Reciprocal mean squares were partitioned into maternal and non-maternal components using Griffing's Methods 1 and 3 (Griffing, 1956).

The relative importance of variances due to GCA and SCA were compared via the predictability factor (PF) $[2s^2_{GCA}/(2s^2_{GCA}+s^2_{SCA})]$. The closer this ratio is to unity, the greater the predictability based on general combining ability alone. The estimates of genetic components were obtained based on the expectations of the mean squares.

Results and discussion

There were highly significant differences among genotypes ($p<0.01$) for all agronomic traits (Tab. 1), which implied genetic variation existed for these traits.

Days to flowering (DF)

Analysis of variance for combining ability revealed significant effects of both GCA and SCA for days to flowering (Tab. 1). Result indicates the importance of both additive and non-additive gene actions for the genetic control of DF. The proportion of GCA variance (σ^2g) to SCA variance (σ^2_S), represented by the PF factor suggests the

importance of both additive and dominance gene action in the genetic control of this trait (Tab. 1). Likewise, Singh *et al.* (2008) reported the importance of both additive and dominance gene action in genetic control of days to flowering. On the other hand, present findings were inconsistent with those of Gupta and Singh (1988a), who reported partial dominance for the genetic control of days to flowering in safflower. The inconsistency could be due to different genotypes and different environmental conditions of these experiments. But with considering this difference, selection of superior genotypes for hybrid production in advanced generations could be suggested for improvement of days to flowering in safflower.

The mean square for reciprocal effects (REC) was significant for DF (Tab. 1). This result implies that selection of desirable female parents would be important in hybridization programs for improvement of this trait.

Days to maturity (DM)

The deviation of the predictability factor (PF) from unity (0.57) suggested that the relative predominance of dominance over additive effects plays an important role in the genetic control of days to maturity. Gupta and Singh (1988a) reported that overdominance controlled days to maturity in safflower. The reciprocal effect was not significant for days to maturity (Tab. 1) indicating non-significant influence of maternal effects on DM.

Plant height (PH)

The relatively small deviation of PF factor from unity (0.89) revealed the prime importance of additive gene action for the genetic control of plant height, which suggested that cyclic selection should be effective for improving PH (Tab. 1). REC effect for plant height was not significant which is in agreement with the observations of Mandal and Banerjee (1997). Therefore, it has been firmly established that extra-nuclear genes do not play role in governing PH.

Among the parents, 'IL.111' and 'A$_2$' had the lowest and the highest PH, respectively (Tab. 2). In safflower breeding programs, reducing plant height is one of the major objectives. The parental genotypes 'IL.111' and 'GE$_{62918}$'

Tab.1. Analysis of variance for nine agronomic traits in safflower

Source of variation	df	Mean square (MS)								
		DF	DM	PH	BP	HD	HP	SH	SW	YP
Replication	2	259.9**	326.4**	792.3**	4.7**	0.02	208.1**	80.5**	16.1	500.8**
Genotype	63	10.9**	5.7**	271.4**	2.3**	0.08**	13.5**	134.7**	44.7*	124.6**
GCA	7	45.4**	19.0**	1948.6**	11.1**	0.22**	45.4**	1015**	232.1*	758.3**
SCA	28	6.9**	4.7**	97.3**	1.6**	0.06**	18.6**	35.1**	20.1**	57.2**
Reciprocal	28	6.3**	3.4	26.2	0.9	0.05**	1.4	14.1**	22.6**	33.9**
Residual	126	4.0	2.3	49.3	0.7	0.028	6.8	2.0	8.09	21.8
PF¥		0.75	0.57	0.89	0.70	0.46	0.33	0.86	0.79	0.74

** and * significant at $p<0.01$ and $p<0.05$, respectively; PF¥: Predictability factor; DF: days to flowering; DM: days to maturity; PH: plant height; BP: Primary branches per plant; HD: Head diameter; HP: Heads per plant; SH: Seeds per head; SW: 1000-Seed weight; YP: Yield per plant

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could be used as the sources of favorable genes for reducing PH. The relative importance of variances due to GCA and SCA was assessed by calculating the PF ratio for PH (0.89), and indicated that additive gene action was more important in governing this trait.

Branches per plant (BP)

The general combining ability and specific combining ability variances for branches per plant were significant, indicated that both additive and non-additive genetic effects were important in the inheritance of branches per plant. The PF factor of 0.70 suggested that additive effects were relatively more important than dominance effects for BP (Tab. 1). Gupta and Singh (1988b) reported that additive gene effects play an important role in genetic control of BP. Narkhede and Patil (1987) reported that epistasis effects had a significant role in controlling BP, whereas the results of present study indicated a non-significant effect of epistasis in controlling BP. Nevertheless, the practical utilization of information regarding epistasis in breeding is a challenging issue that needs to be fully addressed by the scientists in the field of biometrics.

Head diameter (HD)

The estimated mean squares of GCA, SCA and REC were highly significant for head diameter (Tab. 1). The relatively large deviation of PF from unity (0.46) suggested a greater influence of dominance gene action than additive gene action in governing this trait (Tab. 1). This is the first report on the genetic variance components for head diameter. Camas and Esendal (2006) reported a low broad-sense heritability for HD in safflower.

Seed yield and its components

Mean squares due to GCA and SCA were significant for all the seed yield-related traits including heads per plant, seeds per head, seed weight and seed yield per plant (Tab. 1). Mean squares due to reciprocal effect (REC) were significant for seeds per head, seed weight and yield per plant (Tab. 1), which implied the influence of the cytoplasmic factors on their inheritance. Results obtained from Hayman's analysis showed significant effects of maternal inheritance in governing seed weight and seeds per head (data not shown). These results suggested that selection of desirable female parents would be important in hybridization programs for improvement of these traits.

The calculated PF for yield per plant indicated that additive gene effects were more important than dominance gene effect in governing yield per plant in safflower. These findings are inconsistence with those of Rajab and Fried (1992). Singh *et al.* (2008) and Mandal and Banerjee (1997), who observed that predominantly dominance controlled yield per plant.

Among parental genotypes, 'K$_{21}$' (44.67) and 'A$_2$' (25), had the maximum and minimum values of yield per plant, respectively (Tab. 2). The PF for seeds per head was 0.86, which suggested additive genetic effects were more important than non-additive effects in controlling seeds per head. This result suggests a greater effectiveness of the selection-based breeding programs than hybrid developing method.

General combining ability effect for seed weight was greater than SCA effect (Tab. 1). Additive genetic effects were more important than non-additive effects in controlling seed weight in safflower, which is in contrast to the finding of Camas and Esendal (2006).

Tab. 2. General combining ability effects and mean values for eight safflower parents estimated by diallel analyses

Traits parents		DF	DM	PH	BP	HD	HP	SH	SW	YP
'GE$_{62918}$'	GCA	-1.42**	-0.65**	-5.17**	0.52**	-0.048*	-0.01	-8.70**	1.05**	-2.2*
	Mean	76.66	108.93	82.35	9.90	2.63	27.01	26.56	30.40	27.32
'C$_{111}$'	GCA	1.24**	0.42*	2.97**	-0.09	-0.057**	0.18	2.08**	-1.30**	0.06
	Mean	77.63	108.31	102.45	7.56	2.41	23.98	45.91	28.18	31.37
'C$_{4110}$'	GCA	0.60*	0.21	5.35**	-0.42**	-0.05	-0.90**	4.95**	-1.67**	-0.16
	Mean	79.04	108.63	103.50	7.48	2.36	24.60	52.66	28.57	32.88
'ISF$_{14}$'	GCA	0.24	0.62**	7.32**	-0.29**	-0.02	-0.47**	1.84**	-0.66	-0.11
	Mean	79.04	108.70	106.35	7.75	2.68	23.59	47.82	29.01	32.87
'A$_2$'	GCA	0.90**	0.82**	6.47**	-0.60**	0.02	-1.51**	-3.5**	-2.85**	-6.64**
	Mean	80.66	114.66	112.33	7.05	2.58	21.60	31.29	26.53	25.01
'K$_{21}$'	GCA	-0.13	-0.29	-2.37**	0.71**	-0.02	1.19**	3.45**	-0.23	5.35**
	Mean	80	112	95.93	10.30	2.73	30.33	50.80	29.16	44.67
'IL.111'	GCA	-1.32**	-0.94**	-9.76**	-0.20	0.14**	0.17	-5.44**	4.25**	-1.11
	Mean	76.33	104.66	72.33	8.92	3.10	24.68	32.02	39.10	30.97
'Mex.22-191'	GCA	-0.10	0.20	-4.82**	0.39**	0.03	1.34	5.30**	1.31**	7.26**
	Mean	81.36	109.32	85.22	8.63	2.83	28.20	49.33	29.85	37.25
r(GCA, Mean)		0.64	0.82*	0.96**	0.89**	0.87**	0.90**	0.97**	0.91**	0.88**

** and * significant at *p*<0.01 and *p*<0.05 respectively. DF: days to flowering; DM: days to maturity; PH: plant height; BP: Primary branches per plant; HD: Head diameter; HP: Heads per plant; SH: Seeds per head; SW: 1000-Seed weight; YP: Yield per plant

The SCA effects for seed weight ranged from 2.31 'GE$_{62918}$'×'ISF$_{14}$' to -1.65 'GE$_{62918}$'×'Mex.22-191', where some of the SCA effects were not statistically significant. This result suggests that hybrid breeding program can not be used to improve seed weight.

The GCA, SCA and REC mean squares for heads per plant were significant (Tab. 1). The low PF (0.33) indicated the predominant role of non-additive gene action in the genetic control of heads per plant. There were some discrepancies between the results of present study and those of previous workers, which could be explained by the difference between genetic background of genotypes used in this study and used by others, non-equal distribution of positive and negative alleles controlling each quantitative trait in the parental genotypes, sampling variation, and the confounding effects of linkage and epitasis.

Parental GCA and SCA of crosses

Selecting parents based on their genetic merit is a vital component of utilization of genetic resources (Banerjee and Kole, 2009). Although, use of parameters relevant to gene action is a preferred strategy, a more rational approach is to select parents based on their combining ability rather than based on their genetic distance.

The GCA effects between parental genotypes varied from -1.42 ('GE$_{62918}$') to 1.4 ('C$_{111}$') for days to flowering (Tab. 2). Half of the parents displayed negative GCA effects for days to flowering. 'K$_{21}$'×'IL.111 and 'GE$_{62918}$' ×'K$_{21}$' had the lowest DF among the F$_1$ hybrids (Tab. 3). Because of the contributions of σ^2$_{gca}$ and σ^2$_{sca}$ to genetic variability of DF, it seems that hybrid development could be successfully employed to breed for early flowering genotypes. Hence, 'IL.111' line could be suggested as a source of favorable genes for reducing days to maturity in a safflower breeding program.

Reducing days to maturity is one of the main objectives in safflower breeding. Thus, negative GCA effects for days to maturity will be desirable to produce early maturing genotypes in safflower breeding projects. In this study, three of the eight parental genotypes showed negative GCA effects for days to maturity. 'IL.111' had the lowest GCA effect and 'A$_2$' had the highest GCA effect for DM. Therefore, in safflower breeding for early maturity,

Tab. 3. Mean performance of agronomic traits of F$_1$ generation in 8×8 diallel cross of safflower

Crosses/Traits	DF	DM	PH	BP	HD	HP	SH	SW	YP
'C$_{111}$'×'GE$_{62918}$'	77.66	107	84.78	9.41	2.64	23.96	31.83	33.32	25.73
'C$_{4110}$'×'GE$_{62918}$'	77.63	106.5	92.37	8.92	2.80	20.71	37.06	32.14	27.74
'ISF$_{14}$'×'GE$_{62918}$'	76.66	107	96.52	8.61	2.62	20.52	25.06	35.1	27.74
'A$_2$'×'GE$_{62918}$'	78.66	108.5	89.74	8.13	2.83	22.71	34.59	32.54	25.3
'K$_{21}$'×'GE$_{62918}$'	75.50	105.33	86.12	10.18	2.54	21.52	31.55	32.85	45.07
'IL111'×'GE$_{62918}$'	76.66	107	77.14	8.28	2.81	23.62	28.54	36.47	24.74
'22-191'×'GE$_{62918}$'	76.33	105.83	83.14	9.28	2.66	25.69	42.90	32.83	44.87
'C$_{4110}$'×'C$_{111}$'	80.50	107.16	103.05	8.23	2.70	24.28	48.13	27.89	30.75
'ISF$_{14}$'×'C$_{111}$'	79.36	108.5	101.29	8.15	2.75	22.93	46.80	30.66	33.23
'A$_2$'×'C$_{111}$'	80.50	109	97.90	7.75	2.64	20.45	38.90	28.54	24.99
'K$_{21}$'×'C$_{111}$'	81.66	107.75	90.99	9.53	2.65	33.2	45.20	32.09	36.52
'IL.111'×'C$_{111}$'	79.50	108.33	89.26	7.72	3.04	23.76	41.86	34.06	33.04
'22-191'×'C$_{111}$'	79.01	107.33	87.62	9.42	2.63	24.72	48.00	32.66	44.85
'ISF$_{14}$'×'C$_{41100}$'	79.75	108.83	104.17	7.22	2.59	21.20	48.49	28.57	32.90
'A$_2$'×'C$_{4110}$'	79.83	107.16	98.70	7.13	2.65	19.15	39.66	28.99	22.54
'K$_{21}$'×'C$_{4110}$'	79.66	107.15	94.91	9.11	2.77	35.4	50.30	30.22	35.57
'IL.111'×'C$_{4110}$'	77.01	103.33	91.28	8.19	2.74	24.66	41.23	33.39	33.08
'22-191'×'C$_{4110}$'	78.38	107.16	88.45	8.85	2.89	21.20	52.09	34.8	38.30
'A$_2$'×'ISF$_{14}$'	80.33	107.83	111.99	8.62	2.86	23.95	43.85	29.10	32.40
'K$_{21}$'×'ISF$_{14}$'	78.50	107.10	92.66	8.69	2.76	28.7	49.03	30.04	32.60
'IL.111'×'ISF$_{14}$'	77.83	106.83	79.3	8.31	2.76	23.30	32.90	36.45	31.71
'22-191'×'ISF$_{14}$'	77.43	108.50	99.84	8.84	2.71	23.81	51.1	33.03	44.8
'K$_{21}$'×'A$_2$'	78.33	107.16	93.48	7.97	2.80	23.49	42.63	29.25	30.07
'IL.111'×'A$_2$'	76.33	106.33	91.26	8.89	2.90	19.65	31.86	35.34	22.21
'22-191'×'A$_2$'	79.48	107.66	89.98	8.14	2.84	22.73	42.60	30.85	30.20
'IL.111'×'K$_{21}$'	75.33	106.33	77.35	8.25	2.80	26.30	34.83	36.46	33.85
'22-191'×'K$_{21}$'	76.5	107.50	83.12	10.20	2.70	34.96	52.86	34.7	55.21
'22-191'×'IL.111'	77.30	106.66	77.54	8.31	2.94	23.30	41.96	32.52	48.21
LSD (1%)	3.27	2.43	11.36	1.42	0.26	4.21	1.62	4.6	7.55

DF: days to flowering; DM: days to maturity; PH: plant height; BP: Primary branches per plant; HD: Head diameter; HP: Heads per plant; SH: Seeds per head; SW: 1000-Seed weight; YP: Yield per plant

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'IL.111' could be used as a source of favorable genes for reducing days to maturity in safflower breeding programs.

'GE$_{62918}$'×'IL.111' and 'ISF$_{14}$'×'IL.111' were two of the lowest value crosses as far as plant height is concerned. This suggested that 'GE$_{62918}$' and 'IL.111' would be superior parents with negative GCA for plant height (Tab. 3).

The GCA effects for branches per plant varied from -0.6 (A$_2$) to 0.71 (K$_{21}$) (Tab. 2). Therefore, 'K$_{21}$' and 'Mex.22-191' could be used as good parental combiners for improving BP in safflower breeding programs. Among all F$_1$ hybrids, 'K$_{21}$'×'Mex.22-191' and 'GE$_{62918}$'×'K$_{21}$' were two of the topmost hybrids for branches per plant (Tab. 3). These two superior crosses could be exploited in safflower breeding programs.

'IL.111' line had the highest head diameter value among the eight parents and 'C$_{111}$'×'IL.111' had the highest HD value among the hybrids (Tab. 3). This indicated that HD, which is an important trait for either ornamental or seed production purposes, has been improved when 'IL.111' contributed as a parent.

'K$_{21}$' and 'Mex.22-191' had two of the highest GCA effects for yield per plant among all parental genotypes (Tab. 2). It is also interesting to note that, 'K$_{21}$'×'Mes.22-191' also produced the highest yield among the hybrids. Thus, these two genotypes were the best combiners for increasing yield per plant. Although some F$_1$ hybrids possessed greater yield per plant than their parents due to the positive GCA effects of their parents (Tab. 3), both GCA and SCA effects are important in identifying the superior crosses,.

Considering the positive correlation between parental yield per plant and their GCA effects, the performance of single-cross hybrids may be adequately predicted on the basis of GCA effects (Huang *et al.*, 2010). In most of the genotypes, the cross with the highest SCA originated from a cross between a high GCA parent and an average GCA parent (data not shown). But this object is not a clear reason for obtaining the highest yield among evaluated crosses.

A positive and significant relationship between GCA effects and mean performance of the parents was observed for the studied traits with the exception of days to flowering (Tab. 2). Therefore, parental genotypes with both high GCA effects and mean performance could be suggested as a good general combiner parents in the hybridization programs of safflower.

Five of the eight parental genotypes showed positive GCA effects for number of seeds per head. 'Mex.22-191' had the largest positive GCA effect and thus it could be used to improve seeds per head (Tab. 2). The means for seeds per head among F$_1$ hybrids varied from 25.06 ('GE$_{62918}$'×'ISF$_{14}$') to 52.9 ('K$_{21}$'×'Mex.22-191'). The F$_1$ hybrids 'K$_{21}$'×'Mex.22-191', 'ISF$_{14}$'×'Mex.22-191' and 'C$_{4110}$'×'K$_{21}$' possessed the top three highest seeds per head values among 28 F$_1$ hybrids. Therefore, these hybrids could be used for improving SH in safflower.

'GE$_{62918}$', 'IL.111' and 'Mex.22-191' possessed positive GCA effects for seed weight, indicating that they could be used as good combiners for production of recombinant lines in safflower breeding programs (Tab. 2). 'GE$_{62918}$'×'IL.111' (36.47) had the highest mean for SW (Tab. 3). F$_1$ genotypes with superior means had at least one parent with a significant positive GCA effect. The highest GCA effects for number of heads per plant belonged to 'K$_{21}$' and 'Mex.22-191' (Tab. 2). 'K$_{21}$'×'Mex.22-191' and 'C$_{4110}$'×'K$_{21}$' crosses possessed two of the highest means for heads per plant among F$_1$ hybrids (Tab. 3).

Genetic parameters

The regression coefficient (b) differed significantly from zero (b-0) but not from the unity (1-b) for the studied traits with the exception of days to maturity. The absence of non-allelic interaction (epistasis) for the majority of traits could be inferred from this finding.

Estimation of genetic parameters in diallel analysis is important for estimating allelic distribution and degree of dominance among the parents. The estimates of additive component (D) and two measures of dominance components (H$_1$ and H$_2$) were significant for the studied traits (Tab. 4). The magnitude of H$_1$ was larger than that of D for DF and HP, which implied that dominance effects were more important than additive effects in genetic control of these two traits.

Tab. 4. The derived parameters of genetic variance components and regression coefficients between Wr/Vr in F$_1$ progenies from diallel crosses of safflower genotypes

Traits Components	DF	PH	BP	HD	HP	SH	SW	YP
D	2.98*	173.12**	1.6**	0.046**	5.65**	70.4**	25.12*	38.47*
H$_1$	3.43**	32.8*	0.55*	0.028*	8.45*	30.94**	10.71*	35.03*
H$_2$	1.96**	32.5*	0.47	0.023*	7.96**	22.92**	8.07*	33.03*
F	0.05	14.46	0.32	0.03*	3.01	5.96	9.17	-18.41*
h	-1.10	-6.70	0.20	0.14*	-4.51**	-0.03	5.78**	-2.04
H$_2$/4H$_1$	0.21	0.25	0.21	0.20	0.23	0.21	0.18	0.23
(H$_1$/D)$^{0.50}$	1.46	0.43	0.69	0.8	1.22	0.66	0.65	0.94
b (Wr,Vr)	0.36±0.12	0.78±0.04	0.7±0.15	1.1±0.16	0.74±0.2	0.85±0.15	1.01±0.15	0.86±0.17

** and * significant at *p*<0.01 and *p*<0.05, respectively. DF: days to flowering; DM: days to maturity; PH: plant height; BP: Primary branches per plant; HD: Head diameter; HP: Heads per plant; SH: Seeds per head SW: 1000-Seed weight; YP: Yield per plant

The value of $H_2/4H_1$ provides an estimate of the mean value of uv, where u is the proportion of positive alleles and v is the proportion of negative alleles (Mather and Jinks, 1982). Therefore in allelic equilibrium (u=v=0.5) this ratio (uv) is not significantly different from 0.25. The estimated value of uv deviated from 0.25 for all studied traits with the exception of plant height, indicating non-equal distribution of the dominant and recessive alleles among the eight parents analyzed for most of the traits. (F is the covariance of additive and dominance effects in a single array in diallel) (Mather and Jinks, 1982). Positive F value for all traits with the exception of yield per plant, suggested that dominance alleles were more abundant than recessive ones in the parents (Tab. 4). Genetic parameters (D, H_1 and H_2) estimated by Jinks-Hayman's method revealed the relative importance of additive and dominance effects in controlling most of the traits.

Conclusions

For improving safflower yield, the most important prerequisite is the selection of suitable parents, with good combining ability. Parental lines 'K$_{21}$' and 'Mex.22-191' with positive GCA effects for yield and yield components, along with 'IL.111' for seeds per head, could be used as good combiners for a selection scheme to produce superior genotypes. Moreover, the preponderance of additive gene action in explaining genetic variations for yield per plant supports the statement that genetic improvement through accumulating favorable alleles from parents with high GCA values in the target genotype using appropriate methods such as recurrent selection can be suggested.

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