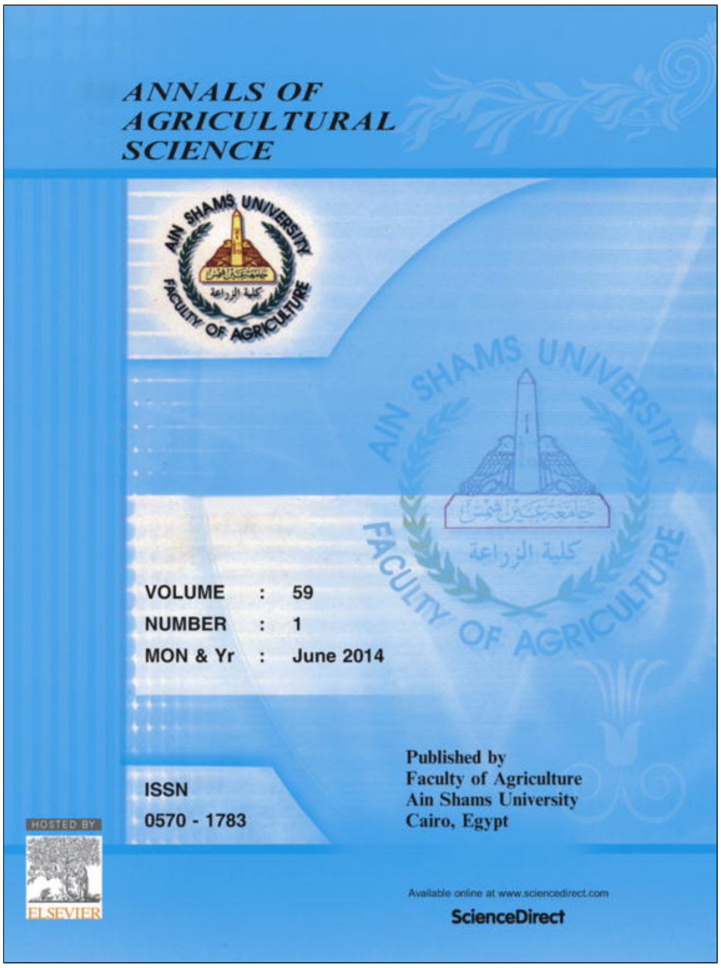
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ORIGINAL ARTICLE

Diallel analysis and separation of genetic variance components in eight faba bean genotypes

CrossMark

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Abstract The present investigation was carried out at Genetic Resources Department-Bahtim, to evaluate eight faba bean varieties in diallel crosses set. Twenty-eight crosses were constituted in the 2011/2012 season, whereas parents and crosses were evaluated in 2012/2013, in a randomized complete block design with three replications. Results revealed highly significant variations within parents and F_1 genotypes, indicating a wide genetic variability for the studied characters and the possibility of genetic improvement using such genetic pools of faba bean. Some crosses recorded significant desired heterotic percentages relative to mid parents and better parent for all studied traits except for number of branches per plant. Both general (GCA) and specific (SCA) combining abilities were significant for all studied traits revealing the important role of both additive and dominant components in the inheritance of the studied characters. The ratio of general and specific combining ability (GCA/SCA) indicated great additive effects for the majority of the studied characters. Giza 3 was proved to be a good combiner for all studied traits except for plant height and number of branches per plant. Several crosses exhibited significantly positive SCA effects for studied traits especially L.512 × NA112 and L.153 × Giza 3 which exhibited highest significant and positive SCA effects for seed yield per plant with high 100-seed weight and number of seeds per plant. Heritability in the broad sense (h_b^2 %) estimates was generally high for all studied traits. However, heritability in the narrow sense was high for number of pods per plant (76.42), 100-seed weight (75.53), plant height (70.53) and number of branches per plant (62.00), while it was low for seed yield per plant. High heritability values coupled with high genetic advance observed for 100-seed weight and number of pods per plant indicated that such traits would respond to selection. These two traits might contribute to the increasing seed yield since they are important yield components.

Introduction

Faba bean (*Vicia faba* L.) is one of the main pulse crops grown for seed in Egypt. It is widely considered as a good source of protein, starch, cellulose and minerals for humans in

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developing countries and for animals in industrialized countries (Haciseferogullari et al., 2003). In addition, faba bean is one of the most efficient fixers of the atmospheric nitrogen and, hence, can contribute to sustain or enhance total soil nitrogen fertility through biological N_2-fixation (Lindemann and Glover, 2003).

Faba bean is a self-pollinating plant with significant levels of outcross and inter-cross, ranging from 20% to 80% (Suso and Moreno, 1999) depending on genotype and environmental effects. The genetic improvement of crop desired traits depends on the nature and magnitude of genetic variability and interactions involved in the inheritance of these traits which can be estimated using diallel cross technique. This technique may also result in the production of new genetic combinations whose performance may exceed that of the parents, a phenomenon known as heterosis. Exploitation of heterosis could play an important role in improving yield potential and its components in faba beans. Heterotic effects for important yield components, i.e., number of branches per plant, number of pods per plant and seed index. These heterotic effects may range from significantly positive to significantly negative for different traits depending on genetic makeup of parents (Darwish et al., 2005; El-Hady et al., 2006).

In addition, an inference can be made from diallel crosses about general combining ability of parents and specific combining ability of hybrids. Such information may help breeders to identify the best combiners which may be hybridized to build up favorable fixable genes. Several researchers have reported the significance of both general and specific combining ability effects on seed yield and other important traits in faba bean (Attia and Salem, 2006).

On the other hand, the genetic improvement of faba bean desired traits depends on the nature and magnitude of genetic variability and interactions involved in the inheritance of these traits. It can be estimated using diallel crosses technique, which provide early information on the genetic behavior of these traits in the first (F_1) generation (Chowdhry et al., 1992). This technique may also result in the production of new genetic combinations performance which may be exceeding the parents. However, the superiority over parental value may not depend so much on their actual performance as on their ability to combine well and through transgressive segregates (Zhang and Kang, 1997). The combining ability is considered as an important criterion for plant breeders, where it is useful in connection with testing procedures to study and compare the performance of lines in hybrid combinations and the nature of gene action. So, the plant breeders are interested in the gene effect estimates to apply the most effective breeding procedure for the improvement of the desired attributes. Moreover, the choice of the most efficient breeding program mainly depends upon the type of gene action controlling the genetic behavior of most agronomic and economic characters. Nevertheless, for obtaining a clear picture of genetic mechanism of faba bean populations, the absolute value of variances must be partitioned into its genetic components. Hence, exploitation of the genetic components could encourage improvement of yield potential and its components in faba bean plants. Whereas, the superiority of crosses over parents for seed yield is associated with manifestation of gene effects in important yield components, i.e. number of branches per plant, number of pods per plant and seed index. These effects may differ from significantly positive to significantly negative for different traits depending on genetic makeup of faba bean parents. On the other hand, heritability estimates provide values of relative importance of genetic components to phenotypic variation and useful for predicting the expected genetic advance under populations selection. These heritability estimates for different characters were calculated by several researchers using different materials and methods and reported that heritability values were high for 100-seed weight, but low to moderate for seed yield, number of branches per plant and number of pods per plant. The importance of gene action and heritability was previously discussed by Awaad et al. (2005), Darwish et al. (2005), Attia and Salem (2006), El-Hady et al. (2006, 2007), El-Harty et al. (2009) and Bayoumi and El-Bramawy (2010).

The present study was carried out to investigate the nature of gene action influencing seed yield components, and general and specific combining abilities of eight faba bean diverse genotypes and their F_1 generation using diallel cross mating technique. Heritability was also to be estimated.

Materials and methods

Faba bean materials and cross model

Eight parental genotypes of *V. faba* were selected based on the presence of wide differences among them with respect to certain economically important traits (Table 1). The used lines in this study were obtained from Agriculture Research Center, Field Crop Research Institute, Genetic Resources Department-Bahtim.

The selected parents were crossed in a diallel model to obtain all possible combinations, excluding reciprocals during the first season of 2011/12 (total of 28 F_1's seeds). The parents and their respective F_1 hybrids were planted under field condition at the experimental farm during the second growing season of 2012/13. A randomized complete block design (RCBD) with three replications was used. Each plot consisted of one ridge of 3 m length and 60 cm width. Hills were spaced 20 cm with one seed by hill. Cultural practices were adopted as recommended for field beans' production in the area. At harvest, ten guarded plants were randomly sampled from each plot to provide measurements for plant height (cm), number of branches per plant, first fertile nod height (cm), number of pods per plant, number of seeds per plant, 100-seed weight (g) and seed yield per plant (g).

Statistical analysis

Data for seed yield and its component traits were subjected to statistical analysis of variance in (RCBD) according to Steel and Torrie (1997). The data were further subjected to the diallel analysis proposed by Griffing (1956), method 2, model 1 (all possible combinations excluding reciprocals) to determine the combining ability to separate some components of genetic variance.

Heterosis was determined as outlined by Foohad and Bassiri (1983). Appropriate "t" test was made for the significance of deviation of the F_1 s from the mid and better parent values (Wynne et al., 1970). Heritability and genetic parameters were determined through variance component method (Breese, 1972) as follows:

$$h_b^2 = VG/VP * 100$$

where VG is genetic variance, and VP is phenotypic variance.

Table 1 Name and pedigree history of faba bean parental genotypes.

Parent	Pedigree	Special remarks
L.155 (P_1)	Selected from breeding material in Benisuf – Egypt	High fertile with light seed coat color and tolerant to insects' storage
L.512 (P_2)	Selected from breeding material in Benisuf – Egypt	High fertile with light seed coat color and tolerant to insects' storage
L.153 (P_3)	Selected from breeding material in Assiut – Egypt	High fertile with light seed coat color and tolerant to insects' storage
L.1 (P_4)	Selected from breeding material in Assiut – Egypt	High fertile with light seed coat color and tolerant to insects' storage
Triple white (P_5)	Sudan	High autofertility, white flower with light seed coat color and colorless hilum, and susceptible to insects' storage
NA112 (P_6)	Pakistan	Black-spotted flower, small and dark seed coat with high protein content and resistant to insects' storage
Giza 3 (P_7)	Cross (Giza 1 × Dutch Intr.)	Resistant to foliar disease, high yield
L.16 (P_8)	Selected from breeding material in Aswan – Egypt	Medium seed type and susceptible to insects' storage

$$h_n^2 = [0.5D/(0.5D + 0.25H + E)] * 100$$

where D, H and E are the estimates of additive dominance and environmental components of variation, respectively.

Predicted genetic advance as mean percent from selection (GA %) was calculated according to Johnson et al. (1955).

Results and discussion

The progress in the breeding program of a certain crop characters depends on the variability in populations and the extent to which the desirable characters are heritable in this respect. However, the knowledge of the genetic architecture of yield and other characters helps to formulate a meaningful breeding strategy for developing improved genotypes. Therefore, the obtained results and their discussion will be presented in the following,

Diallel analysis and its genetic components

The preliminary statistical analysis revealed highly significant differences among the parents and their possible hybrids (F_1) for all the studied characters (Table 2). These findings provided evidence for the presence of high considerable amount genetic variability among the parental faba bean and their respective hybrids (F_1), which may facilitate genetic improvement using such genetic pools of faba bean. These results were in harmony with those reported by Awaad et al. (2005) and Bayoumi and El-Bramawy (2010).

In this concern, according to the above mentioned results, the detailed analysis of combining ability and type of gene action was therefore appropriate for estimating the characters investigated through this study. ANOVA of the diallel data set with respect to seed yield and its components attributes revealed a highly significant general and specific combining ability (GCA and SCA) effects (Table 2). The GCA variance contains additive epistasis effect, while SCA variance contains non-additive as outlined by Griffing (1956). Hence, the significant estimates of both GCA and SCA variances suggested that each of additive and non-additive nature of gene actions was involved in controlling these characters through all faba bean genotypes. These results confirmed those findings by Darwish et al. (2005), Attia and Salem (2006), El-Hady et al. (2007), Ibrahim (2010) and El-Bramawy and Osman (2012) who reported the significant genetic variation among faba bean genotypes (parents and their hybrids) in respect of yield and its components attributes.

The GCA/SCA ratio of mean squares for all studied characters in faba bean genotypes was higher than unity (1). Therefore, this means that greater considerable contribution of additive effects of genes in the genetic expressions, which controlling these characters. In contrast, non-additive (dominant) gene action was found to be less important for these characters. Therefore, selection can be effective in the improvement through our faba bean materials. However, it could be emphasized that GCA/SCA ratio may not always project the true picture of the gene action for a particular character. This

Table 2 Mean squares obtained from preliminary analysis and combining abilities in faba bean genotypes for the studied characters.

Character	Genotype	G.C.A	S.C.A	G.C.A/S.C.A	Error
Plant height	418.55**	261.67**	108.98**	2.4	6.2
No. of branches/plant	1.06**	0.6**	0.29**	2.07	0.03
First fertile nod	2.45**	0.99**	0.77**	1.29	0.03
No. of pods/plant	27.1**	19.5**	6.42**	3.04	0.55
No. of seed/plant	186.88**	85.95**	56.38**	1.52	2.65
100-Seed weight (g)	1669.32**	1162.37**	404.96**	2.87	28.57
Seed yield/plant (g)	234.48**	88.40**	75.60**	1.17	2.32

* Significant at the 0.05 probability level, respectively.
** Significant at the 0.01 probability level, respectively.

state is due to the deferential parental ability to combine well with each other. On the other hand, such combination depends considerably upon complex interaction between genes and genotype by environment (Mulusew et al., 2008; El-Bramawy and Osman; 2012).

Mean performance of parents and their hybrids

The mean performance of eight parents and their respective crosses are presented in Table 3. The parent P_7 (Giza 3) had the tallest plants (124.23 cm), whereas F_1 hybrids $P_1 \times P_5$ (L.155 × Triple white) and $P_3 \times P_7$ (L.153 × Giza 3) recorded the same value (125.57 cm). The parental genotype P_6 (NA112) exhibited the highest number of branches per plant (4.37), number of pods per plant (19.4) and, number of seeds per plant (49.4), meanwhile crosses $P_6 \times P_7$ (NA112 × Giza 3), $P_3 \times P_6$ (L.153 × NA112) and $P_3 \times P_7$ (L.153 × Giza 3) recorded the highest values for these traits (5.00, 22.10 and 51.40, respectively).The parent P_8 (L.16) showed the highest values for 100-seed weight (87.84 g) as well as seed yield per plant (42.24 g), moreover F_1's $P_1 \times P_4$ (L.155 × L.1) and $P_3 \times P_7$ (L.153 × Giza 3) revealed the highest values for the same traits (108.31 g and 42.37 g, respectively). On the other side, the parent P_5 (Triple white) possessed the lowest value for first fertile nod (3.63), while cross $P_2 \times P_4$ (L.512 × L.1) recorded the lowest one (2.77).

These results could confirm the possibility of selection for these characters through hybridization of respective parents. Moreover it allows plant breeders to build future breeding program for high potential yield in faba bean crop. These findings were in agreement with those reported by Bayoumi and El-Bramawy (2010), Ibrahim (2010) and El-Bramawy and Osman (2012).

Heterosis

Percentage of heterosis relative to mid ($\overline{\text{MP}}$ and better ($\overline{\text{BP}}$ parents for yield and its components are presented in Table 4.

Values of heterosis percentages relative to ($\overline{\text{MP}}$) were significantly positive in ($P_1 \times P_5$) and ($P_6 \times P_8$) crosses with (29.32%

Table 3 Mean performance of parents and their hybrids for all studied characters.

Genotype	Character						
	Plant height	No. of branches	1st Fertile nod	No. of pods	No. of seeds	100-Seed weight	Seed yield
L.155 (P1)	100.43	2.60	3.97	10.60	36.07	69.85	25.11
L.512 (P2)	95.50	3.03	5.47	13.33	37.97	62.73	23.75
L.153 (P3)	115.40	3.27	4.57	11.80	41.77	72.12	30.11
L.1 (P4)	123.63	3.50	5.83	11.13	26.87	113.00	30.28
Triple white (P5)	93.77	3.83	3.63	14.10	36.27	58.19	21.17
NA112 (P6)	82.17	4.37	3.73	19.40	49.40	26.61	13.20
Giza 3 (P7)	124.23	3.67	4.13	14.13	45.10	86.57	38.95
L.16 (P8)	88.93	2.47	4.87	15.97	48.13	87.84	42.24
P1 × P2	121.53	2.83	5.07	15.70	42.17	69.75	29.47
P1 × P3	111.87	3.60	4.60	13.20	36.13	36.75	12.87
P1 × P4	123.63	3.50	5.83	11.13	26.87	108.31	28.97
P1 × P5	125.57	3.23	4.63	13.43	27.17	81.87	22.13
P1 × P6	95.37	3.77	5.10	19.77	35.23	22.60	7.87
P1 × P7	107.2	3.90	3.90	19.17	28.53	51.53	14.70
P1 × P8	118.37	2.57	5.60	15.03	37.70	53.10	19.47
P2 × P3	115.47	2.53	4.77	16.73	30.87	71.31	21.77
P2 × P4	122.13	2.33	2.77	12.20	32.00	80.89	25.77
P2 × P5	118.40	3.20	5.27	13.97	28.10	67.40	18.97
P2 × P6	103.73	4.07	4.17	19.03	46.73	81.00	37.50
P2 × P7	110.47	3.13	2.90	16.77	33.80	77.17	26.13
P2 × P8	117.27	4.10	4.73	11.83	27.30	91.30	24.80
P3 × P4	116.20	2.80	5.13	10.63	21.60	105.54	22.70
P3 × P5	121.17	3.27	5.27	13.37	37.10	64.73	23.97
P3 × P6	122.07	3.70	5.87	22.10	48.13	27.08	13.00
P3 × P7	125.57	2.70	4.17	21.13	51.40	75.89	42.37
P3 × P8	115.53	3.17	4.77	14.40	22.03	85.75	18.73
P4 × P5	123.70	3.90	5.03	13.13	37.83	65.77	24.97
P4 × P6	118.10	3.77	5.80	13.37	33.43	30.78	10.23
P4 × P7	104.77	2.73	4.63	15.17	40.80	44.41	18.10
P4 × P8	112.10	3.07	4.43	12.17	24.77	58.40	14.33
P5 × P6	95.47	2.87	5.67	13.17	28.97	33.53	9.63
P5 × P7	100.47	3.57	5.03	16.17	42.37	47.40	20.03
P5 × P8	103.73	3.80	3.27	11.83	30.33	56.40	17.13
P6 × P7	93.93	5.00	3.00	15.63	36.07	42.82	15.07
P6 × P8	114.70	3.00	5.23	13.57	30.80	69.47	21.33
P7 × P8	105.67	3.50	2.80	12.17	32.90	34.08	11.17
Mean	110.78	3.34	4.60	14.62	35.35	64.22	22.17
LSD	7.02	0.46	0.49	2.08	4.59	15.07	4.32

Table 4 Percentage of heterosis relative to mid ($\overline{MP}$ and better ($\overline{BP}$ parents for all studied traits.

Cross	Plant height		No. of branches		1st fertile nod			
	$\overline{MP}$	$\overline{BP}$	$\overline{MP}$	$\overline{BP}$	$\overline{MP}$	$\overline{BP}$		
$P_1 \times P_2$	24.06	21.01	0.59	−6.59	7.42	−7.32		
$P_1 \times P_3$	3.66	−3.06	22.73	10.20	7.81	0.73		
$P_1 \times P_4$	10.35	0.00	14.75	0.00	19.05	0.00		
$P_1 \times P_5$	29.32*	25.02	0.52	−15.65	21.93	16.81		
$P_1 \times P_6$	4.45	−5.04	8.13	−13.74	32.47	28.57		
$P_1 \times P_7$	−4.57	−13.71	24.47	6.36	−3.70	−5.65		
$P_1 \times P_8$	25.01	17.86	1.32	−1.28	26.79	15.07		
$P_2 \times P_3$	9.50	0.06	−19.58	−22.45	−4.98	−12.80		
$P_2 \times P_4$	11.47	−1.21	−28.57	−33.33	−51.03**	−52.57**		
$P_2 \times P_5$	25.11	23.98	−6.80	−16.52	15.75	−3.66		
$P_2 \times P_6$	16.77	8.62	9.91	−6.87	−9.42	−23.78		
$P_2 \times P_7$	0.55	−11.08	−6.47	−14.55	−39.58*	−46.95*		
$P_2 \times P_8$	27.16	22.79	49.09	35.16	−8.39	−13.41		
$P_3 \times P_4$	−2.78	−6.01	−17.24	−20.00	−1.28	−12.00		
$P_3 \times P_5$	15.86	5.00	−7.98	−14.78	28.46	15.33		
$P_3 \times P_6$	23.57	5.78	−3.06	−15.27	41.37	28.47		
$P_3 \times P_7$	4.80	1.07	−22.12	−26.36	−4.21	−8.76		
$P_3 \times P_8$	13.08	0.12	10.47	−3.06	1.06	−2.05		
$P_4 \times P_5$	13.80	0.05	6.36	1.74	6.34	−13.71		
$P_4 \times P_6$	14.77	−4.48	−4.24	−13.74	21.25	−0.57		
$P_4 \times P_7$	−15.47	−15.67	−23.72	−25.45	−7.02	−20.57		
$P_4 \times P_8$	5.47	−9.33	2.79	−12.38	−17.13	−24.00		
$P_5 \times P_6$	8.53	1.81	−30.08	−34.35	53.85*	51.79		
$P_5 \times P_7$	−7.83	−19.13	−4.89	−6.96	29.61	21.77		
$P_5 \times P_8$	13.56	10.63	20.63	−0.87	−23.14	−32.88		
$P_6 \times P_7$	−8.98	−24.39*	24.48	14.50	−23.73	−27.42		
$P_6 \times P_8$	34.07*	28.97	−12.20	−31.30	21.71	7.53		
$P_7 \times P_8$	−0.86	−14.94	14.13	−45.5	−37.78	−42.47*		
Cross	No. of Pods		No. of Seeds		100−seed weight		Seed yiel	
	$\overline{MP}$	$\overline{BP}$	$\overline{MP}$	$\overline{BP}$	$\overline{MP}$	$\overline{BP}$	$\overline{MP}$	$\overline{BP}$
$P_1 \times P_2$	31.20	17.75	13.91	11.06	5.22	−0.14	20.63	17.40
$P_1 \times P_3$	17.86	11.86	−7.15	−13.49	−48.23	−49.05	−53.39	−57.27
$P_1 \times P_4$	2.45	0.00	−14.62	−25.51	18.46	−4.16	4.61	−4.34
$P_1 \times P_5$	8.77	−4.73	−24.88	−25.09	27.88	17.20	−4.33	−11.82
$P_1 \times P_6$	31.78	1.89	−17.55	−28.68	−53.14	−67.64	−58.92*	−68.66**
$P_1 \times P_7$	54.99	35.61	−29.69	−36.73	−34.11	−40.48	−54.11	−62.28*
$P_1 \times P_8$	13.17	−5.85	−10.45	−21.68	−32.65	−39.55	−42.18	−53.91
$P_2 \times P_3$	33.16	25.50	−22.58	−26.10	5.76	−1.12	−19.18	−27.71
$P_2 \times P_4$	−0.27	−8.50	−1.29	−15.72	−7.94	−28.42	−4.63	−14.91
$P_2 \times P_5$	1.82	−0.95	−24.29	−25.99	11.47	7.43	−15.56	−20.15
$P_2 \times P_6$	16.29	−1.89	6.98	−5.40	81.31	29.11	102.98*	57.87
$P_2 \times P_7$	22.09	18.63	−18.62	−25.06	3.38	−10.85	−16.67	−32.93
$P_2 \times P_8$	−19.23	−25.89	−36.59	−43.28*	21.27	3.94	−24.84	−41.29
$P_3 \times P_4$	−7.27	−9.89	−37.06	−48.28*	14.02	−6.60	−24.82	−25.03
$P_3 \times P_5$	3.22	−5.20	−4.91	−11.17	−0.65	−10.25	−6.53	−20.40
$P_3 \times P_6$	41.67	13.92	5.59	−2.56	−45.14	−62.45	−39.96	−56.82
$P_3 \times P_7$	62.98*	49.53	18.34	13.97	−4.36	−12.34	12.72	−0.09
$P_3 \times P_8$	3.72	−9.81	−50.98**	−54.22**	7.21	−2.38	−48.21*	−55.65*
$P_4 \times P_5$	4.10	−6.86	19.85	4.32	−23.17	−41.80	−2.95	−17.55
$P_4 \times P_6$	−12.45	−31.10	−12.33	−32.32	−55.90	−72.76*	−52.92	−66.20*
$P_4 \times P_7$	20.05	7.31	13.39	−9.53	−55.49*	−60.70*	−47.72*	−53.55
$P_4 \times P_8$	−10.21	−23.80	−33.96	−48.55*	−41.85	−48.32	−60.47**	−66.07
$P_5 \times P_6$	−21.39	−32.13	−32.37	−41.36*	−20.91	−42.37	−43.94	−54.50
$P_5 \times P_7$	14.52	14.39	4.14	−6.06	−34.51	−45.24	−33.37	−48.59*
$P_5 \times P_8$	−21.29	−25.89	−28.12	−36.98	−22.76	−35.79	−45.96	−59.44**
$P_6 \times P_7$	−6.76	−19.42	−23.67	−26.99	−24.34	−50.54	−42.23	−61.33**
$P_6 \times P_8$	−23.28	−30.07	−36.84*	−37.65	21.40	−20.91	−23.04	−49.49*
$P_7 \times P_8$	−19.16	−23.80	−29.42	−31.65	−60.92	−61.21	−72.50**	−73.56**

* Significant at the 0.05 probability level, respectively.
** Significant at the 0.01 probability level, respectively.

Table 5 Estimates of genotype general combining ability effects (GCA) for yield and its components.

Genotype	Character						
	Plant height	No. of branches/plant	1st Fertile nod	No. of Pods/ plant	No. of seeds/ plant	100-Seed weight (g)	Seed yield/ plant (g)
L.155 (P_1)	0.73	−0.15	0.13	−0.30	−1.22	−1.44	−1.38
L.512 (P_2)	0.29	−0.18	−0.08	0.13	−0.13	8.63**	3.24**
L.153 (P_3)	6.16**	−0.18	0.23	0.36	1.26	3.33*	1.61
L.1 (P_4)	7.08**	−0.10	0.39	−2.15**	−4.71**	14.21**	0.61
Triple white(P_5)	−2.10	0.14	0.002	−0.83	−1.38	−4.45**	−2.03*
NA112 (P_6)	−8.94**	0.48	0.09	2.38**	4.00**	−21.75**	−5.85**
Giza 3 (P_7)	−0.05	0.18	−0.67*	1.29*	3.79**	−3.15*	2.60**
L.16 (P_8)	−3.18**	−0.20	−0.08	−0.87	−1.61	4.62**	1.20
S.E. gi	0.74	0.05	0.05	0.22	0.48	1.58	0.45
S.E. gi−gj	1.11	0.07	0.08	0.33	0.73	2.39	0.68

* Significant at the 0.05 probability levels, respectively.
** Significant at the 0.01 probability levels, respectively.

and 34.07%, respectively) for plant height. First fertile nod height recorded highly significantly negative percentages relative to ($\overline{MP}$ for $P_2 \times P_4$ and $P_2 \times P_7$ with values of −51.03 and −39.58, respectively and to ($\overline{BP}$ for $P_2 \times P_4$, $P_2 \times P_7$ and $P_7 \times P_8$ with values of −52.57%, −46.95% and −42.47%, respectively. Based on the estimates of heterosis percentages; two crosses $P_2 \times P_4$ and $P_2 \times P_7$ exhibited significantly negative heterotic effects over both ($\overline{MP}$) and ($\overline{BP}$ for first fertile nod height. Meanwhile, heterosis percentages relative to ($\overline{MP}$) were significantly positive for $P_3 \times P_7$ (62.98%) for number of pods per plant. Moreover, heterosis percentages relative to ($\overline{MP}$) were significantly, positive for $P_2 \times P_6$ (102.98%) for seed yield per plant.

These data suggest that heterotic effects for seed yield per plant were associated with other yield components in several crosses, such as plant height, first fertile nod height and number of pods per plant. Moreover, various cross combinations exhibited different degrees of crosses superiority in some traits based on the genes in parental combinations that may contribute directly, or indirectly, to the expression of these traits. In addition, the heterotic estimates, compared to either $\overline{MP}$ or, for seed yield per plant and its major yield components indicated that there was sufficient genetic variability among the assessed parents to favor efficient breeding for these characters. Positive significant heterotic percentages over $\overline{MP}$ or $\overline{BP}$ were reported by several researchers for faba bean characters which varied according to the cross combinations and traits (Darwish et al., 2005; Attia and Salem, 2006; El-Hady et al., 2006; Ibrahim, 2010).

Combining ability

The estimates of GCA effects for different genotypes are listed in Table 5, which differed from one individual parent to another and from character to character.

Comparison between GCA effects associated with each parent revealed that the parental variety L.512 (P_2) was a good combiner for 100-seed weight (8.63) and seed yield (3.24). Also, the parent L.153 (P_3) showed positive and highly significant value for plant height (6.16) and significant positive value for 100-seed weight (3.33). While, L.1 (P_4) had highly significant positive GCA for plant height (7.08) and 100-seed weight (14.21). Moreover, NA112 (P_6) was proved to be a good combiner for number of pods (2.38) and seeds (4.00). However, the parental variety Giza 3 (P_7) had highly significant positive GCA effects for most studied characters. Similarly, L.16 (P_8) had highly significant positive GCA for 100-seed weight (4.62). Therefore, this parent could be considered as a good combiner for improving these studied characters, since they showed significant values, positive or negative according to the desirable trend of these characters.

Therefore, the parent Giza 3 (P_7) and L.512 (P_2) could be considered as a good source for improving the yield trait in faba bean crop. Consequently, it could be concluded that the studied parental genotypes and hybrids can be used in faba bean breeding programs and may be valuable for improving seed yield and its components. Similar findings were earlier reported by Darwish et al. (2005), El-Hady et al. (2007) Ibrahim (2010) and El-Bramawy and Osman (2012).

The values of SCA effects are shown in Table 6. Eleven crosses ($P_1 \times P_2$, $P_1 \times P_5$, $P_1 \times P_8$, $P_2 \times P_5$, $P_2 \times P_8$, $P_3 \times P_5$, $P_3 \times P_6$, $P_3 \times P_7$, $P_4 \times P_5$, $P_4 \times P_6$ and $P_6 \times P_8$) showed highly significant and positive values for plant height, while two crosses ($P_2 \times P_8$ and $P_6 \times P_7$) had significant and positive SCA effects for number of branches per plant. Five F_1s ($P_2 \times P_4$, $P_2 \times P_7$, $P_5 \times P_8$, $P_6 \times P_7$ and $P_7 \times P_8$) exhibited highly significant, or significant and negative SCA effects for first fertile nod height. Four crosses ($P_1 \times P_6$, $P_1 \times P_7$, $P_3 \times P_6$ and $P_3 \times P_7$) had highly significant positive SCA effects for number of pods per plant. Nine crosses ($P_1 \times P_2$, $P_1 \times P_8$, $P_2 \times P_4$, $P_2 \times P_6$, $P_3 \times P_6$, $P_3 \times P_7$, $P_4 \times P_5$, $P_4 \times P_7$ and $P_5 \times P_7$) exhibited highly significant, or significant and positive values for number of seeds per plant. Concerning 100-seed weight, ten crosses revealed highly significant and positive SCA effects ($P_1 \times P_4$, $P_1 \times P_5$, $P_2 \times P_6$, $P_2 \times P_7$, $P_2 \times P_8$, $P_3 \times P_4$, $P_3 \times P_7$, $P_3 \times P_8$, $P_6 \times P_7$ and $P_6 \times P_8$), while eight of these crosses exhibited highly significant, positive SCA effects for seed yield per plant ($P_1 \times P_2$, $P_1 \times P_4$, $P_1 \times P_5$, $P_2 \times P_6$, $P_3 \times P_5$, $P_3 \times P_7$, $P_4 \times P_5$ and $P_6 \times P_8$). These findings indicate that SCA for seed yield per plant may be influenced by SCA for yield components.

Table 6 Specific combining ability effects of the different crosses for the studied characters.

Cross	Character						
	Plant height	No. of branches/plant	1st Fertile nod	No. of pods/plant	No. of seeds/plant	100-Seed weight (g)	Seed yield/plant (g)
$P_1 \times P_2$	7.50**	−0.18	0.42	1.01	9.55**	0.59	7.13**
$P_1 \times P_3$	−8.03**	0.58	−0.36	−1.71	2.13	−27.11**	−7.83**
$P_1 \times P_4$	2.81	0.40	0.72	−1.27	−1.16	33.57**	9.27**
$P_1 \times P_5$	13.93**	−0.10	−0.10	−0.29	−4.20**	25.79**	5.08**
$P_1 \times P_6$	−9.44**	0.09	0.28	2.83**	−1.51	−16.18**	−5.37**
$P_1 \times P_7$	−6.49**	0.53	−0.16	3.32**	−8.00**	−5.84*	−6.99**
$P_1 \times P_8$	7.81**	−0.43	0.96*	1.34	6.56**	−12.05**	−0.82
$P_2 \times P_3$	−3.99**	−0.45	0.02	1.39	−4.24**	−2.61	−3.56*
$P_2 \times P_4$	1.75	−0.73	−2.14**	−0.63	2.87*	−3.92	1.44
$P_2 \times P_5$	7.20**	−0.10	0.74	−0.18	−4.36**	1.25	−2.71
$P_2 \times P_6$	−0.63	0.42	−0.44	1.67	8.89**	32.15**	19.64**
$P_2 \times P_7$	−2.78	−0.21	−0.95*	0.50	−3.83**	9.73**	−0.18
$P_2 \times P_8$	7.15**	1.13*	0.30	−2.28*	−4.93**	16.09**	−0.11
$P_3 \times P_4$	−10.05**	−0.27	−0.09	−2.42*	−8.92**	26.03**	0.004
$P_3 \times P_5$	4.10*	−0.04	0.43	−1.01	3.25*	3.89	3.92**
$P_3 \times P_6$	11.84**	0.05	0.95*	4.51**	8.90**	−16.47**	−3.24*
$P_3 \times P_7$	6.45**	−0.64	0.01	4.64**	12.38**	13.75**	17.68**
$P_3 \times P_8$	−0.45	0.20	0.02	0.06	−11.59**	15.83**	−4.54**
$P_4 \times P_5$	5.71**	0.51	0.04	1.27	9.96**	−5.96*	5.92**
$P_4 \times P_6$	6.95**	0.04	0.72	−1.72	0.18	−23.65**	−5.00**
$P_4 \times P_7$	−15.27**	−0.69	0.31	1.18	7.76**	−28.61**	−5.58**
$P_4 \times P_8$	−4.81**	0.02	−0.47	0.33	−2.88*	−22.40**	−7.95**
$P_5 \times P_6$	−6.50**	−1.10*	0.97*	−3.24**	−7.62**	−2.23	−2.96*
$P_5 \times P_7$	−10.38**	−0.10	1.10*	0.86	5.99*	−6.96**	−1.01
$P_5 \times P_8$	−3.99*	0.51	−1.25**	−1.32	−0.65	−5.73*	−2.50
$P_6 \times P_7$	−10.08**	1.00*	−1.02*	−2.89**	−5.69**	5.75**	−2.16
$P_6 \times P_8$	13.81**	−0.63	0.63	−2.80**	−5.56**	24.64**	5.51**
$P_7 \times P_8$	−4.10*	0.17	−1.05*	−3.11**	−3.25*	−29.35**	−13.10**
S.E.Sij	2.26	0.15	0.16	0.67	1.48	4.85	1.38
S.E.Sij-Sik	3.15	0.20	0.22	0.93	2.06	6.76	1.93

* Significant at the 0.05 probability level, respectively.
** Significant at the 0.01 probability level, respectively.

Table 7 Estimates of additive and non-additive genetic variances heritability, and genetic advance % of the studied traits.

Character	Additive variance	Non-additive variance	Heritability		GA % of mean
			Broad sense	Narrow sense	
Plant height	152.69	102.78	95.56	70.53	20.99
No. of branches	0.31	0.26	92.45	62.00	29.35
First fertile nod	0.22	0.74	96.33	33.85	33.76
No. of pods	13.08	5.87	93.95	76.42	34.46
No. of seed	29.57	53.73	95.75	47.90	38.14
100-Seed weight	757.41	376.39	94.87	75.53	62.17
Seed yield	12.80	73.28	97.03	23.67	79.75

GCA effects provide appropriate criterion for detecting the validity of a genotype in hybrid combination, while SCA effects may be related to heterosis. The results revealed that GCA effects, for some traits, were related to several SCA values of their corresponding crosses, where the two parents L.512 (P_2) and Giza 3 (P_7), which exhibited significant and positive GCA effects for seed yield per plant and 100-seed weight or number of seeds per plant, produced some crosses as L.512 × NA112 and L.153 × Giza 3 ($P_2 \times P_6$ and $P_3 \times P_7$) enjoying positive and highly significant SCA effects for these traits. This may indicate that additive and non-additive genetic effects in the crosses are acting in the same direction to maximize the characters in view. These findings are in agreement with Darwish et al. (2005), Attia and Salem (2006), El-Hady et al. (2006, 2007) and Ibrahim (2010).

Heritability

Heritability in the broad sense (h_n^2 %) estimates was generally high for all studied traits and recorded values ranging from 92.45% for number of branches per plant to 97.03% for seed yield per plant (Table 7). Meanwhile, heritability in narrow sense (h_n^2 %) was high for number of pods per plant (76.42), 100-seed weight (75.53), plant height (70.53) and number of branches per plant (62.00), while it was low for the remaining characters. Higher estimates of genetic advance were observed for seed yield per plant (67.58), 100-seed weight (62.37), number of seeds per plant (38.14) and number of pods per plant (34.46). High heritability values coupled with high genetic advance were observed for 100-seed weight and number of pods per plant which indicate that such traits would respond to selection better than those with high heritability and low genetic advance. Similar findings were reported by Salama and Salem (2001) and Toker (2009).

In conclusion, the present results revealed that several of the obtained crosses are highly promising be used in breeding programs of faba bean cultivars which possess genetic factors for high yield potentiality.

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