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GENETICAL ANALYSIS OF SOME LOCAL AND FOREIGN FABA BEAN CULTIVARS

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ABSTRACT

The present study was carried out during 2008/2009 and 2009/2010 seasons at the Experimental Farm of Faculty of Agriculture, Al-Azhar University, Assiut Branch. Seeds were planted in a randomized complete block design with three replications.15 F_1's obtained from a half diallel crossing system of faba bean cultivars were genetically analyzed according to Griffing (1956) Model I Method II. The studied characters were yield and its components.

Results showed that both general (G.C.A) and specific (S.C.A) combining abilities were significant for all studied characters and revealed that shoots number/plant, pods number/plant, seeds number/pod, 100-seed weight, seeds weight/plant and crude protein% were mainly affected by additive and non-additive effect. Both variances due to G.C.A and S.C.A were controlled all studied characters .

Heterosis percentage was significant for all studied characters. The best crosses for these traits in ranking were Assiut85×Misr1 in shoots/plant, pods/plant and seeds weight/plant traits, while the crosses Giza40×Misr1 and Giza40×Assiut98 were the superiors in seeds/pod trait and for 100-seed weight, the cross Giza40× Giza429 was the highest crosses, while the cross Giza429×Misr1 was the best in crude protein %, respectively.

Generally, it could be concluded that the best promising combinations were Assiut 85× Misr1. Also, more of these crosses which Looza (foreign parent) shared in them were a good crosses like Looza×Giza429 for shoots/plant, Looza×Assiut85 was very good for pods/plant, Looza×Assiut98, Looza×Misr1 were excellent for seeds weight/plant and Looza×Misr1 a good cross for crude protein %. Moreover, heritability was high for all studied characters

Keywords: Combining ability, heterosis, diallel, additive, dominance, faba bean, shoots number/plant, pods number /plant, seeds number/pod,100-seed weight, seeds weight/plant and crude protein%

INTRODUCTION

Faba bean *(Vicia faba* L) plays a significant role in critical areas of food security and economic stability of most countries of the world, and it is the important source of plant portion for both human and animal in Mediterranean area. It can be used as human food in developing countries and as animal feed in some other countries. Feeding value of faba bean is high, and it is considered in some areas to be superior to field peas or other legumes. It is one of the most important winter crops in the Middle East. The straw can be used for brick making and as fuel in parts of Sudan and Ethiopia.

In formation on the expression levels of heterosis are useful to help breeders to choose the best hybrid combinations which will serve as the basis for the selection of superior genotypes. Generally, combining analysis is associated with additive effective effects of genes while general combining ability and specific combining ability is attributed primarily to non-additive (dominance and epistasis) genes. Also, identification of gene action such as additive, dominance and epistasic effects are very important for any breeding program. In addition, heritability estimates and the magnitude of genetic variability for the different traits are very useful to identify the best progenies. Therefore, the breeder should evaluate the potentialities of the available germplasm for new recombination and eventually combining ability which have proved to be of considerable use in breeding methods.

In the present work, Griffing's model I method II mating system was used for analysis and partition the total genetic variance among six faba bean cultivars and their F_1 hybrids in order to evaluate these parents. The aim of this work was to determine the best parents and the best crosses according to the agronomic traits and studying general combining ability, specific combining ability, heterosis and heritability.

MATERIALS AND METHODS

A half diallel cross was made using six parents based on Griffing's model I method II (Griffing 1956). The parents involved Looza (P_1), Giza 40 (P_2), Giza 429 (P_3), Assiut 85 (P_4), Assiut 98 (P_5) and Misr 1 (P_6).
Where: The last fifth cultivars are local varieties, some of them are still cultivated in the present time in various locations in Egypt, and the first variety (Looza) is Spanish variety and it has high yield, long pod and big seed, but it is highly susceptible to fungal and viral diseases.

The seeds were sown in two dates at the Farm of Faculty of Agriculture, Al-Azhar University, Assiut Branch on first and half October 2008. Total 15 hybrids were obtained. The 6 parents and their 15 F_1s were planted on 15th of October 2009. The randomized complete block design with three replications was employed. Ridges in the plot were used with 4.0 m long and 0.40 m apart. The seeds were planted at a spacing of 25 cm within the row. Parents and F_1s were randomly assigned to each plot.
The agronomic characters were recorded as follow:
1-Number of Shoots/plant
2-Number of Pods/plant
3-Number of Seeds/pod
4-100-seed weight
5-Seeds weight/plant (g).
6-Crude protein% was determined in lab of the college by the semi-Kjeldahle method (A.O.A.C.,1980).

Statistical analysis:-

Data of the 2009/2010 growing season were subjected to statistical analysis as outlined by Snedecor and Cochran (1967) for the RCBD experiments.

Form of the analysis of variance and expectation of mean squares.

Source of variance	D.F	M.S	E.M.S
Replications	r-1	M3	$\sigma^2 E+g\sigma^2 r$
Genotypes	g-1	M2	$\sigma^2 E+r\sigma^2 g$
Error	(r-1)(g-1)	M1	$\sigma^2 E$

Where: r and g = number of replications and genotypes, respectively.
$\sigma^2 E$ =error variance.
$\sigma^2 g$ = genetic variance.

The phenotypic ($\sigma^2 P$) and genotypic ($\sigma^2 g$) variances were calculated according to the following formula:

$\sigma^2 P = \sigma^2 g + \sigma^2 E/r$

$\sigma^2 g = (M2-M1)/r$

Heritability (H) = ($\sigma^2 g$ / $\sigma^2 p$) x100

Heterosis was determined as the percentage of increase or decrease of F_1's means over the average of its parents:

Heterosis % = $\frac{\overline{F_1} - \overline{M.P}}{\overline{M.P}} \times 100$

It was also determined as the percentage of increase or decrease of F_1's mean over the better parent:

Heterosis % = $\frac{\overline{F_1} - \overline{B.P}}{\overline{B.P}} \times 100$

LSD for mid-parent heterosis = $t \times \sqrt{\frac{3MSe}{2r}}$

LSD for better-parent heterosis = $t \times \sqrt{\frac{2MSe}{r}}$

Where: t is the tabular t value at a stated level of probability for the experimental error degree of freedom, MSe is mean squares of the experimental error from the analysis of variance and r is number of replication.

RESULTS AND DISCUSSION

Analysis of variance:

Analysis of variance for the studied characters of the six parents and their 15 F_1's in Table 1 indicates that the differences between the genotypes means were highly significant for all the studied characters.

Table 1: Analysis of variance for the studied characters.

S.O.V	D.F	M.S					
		Number of Shoots/plant	Number of pods/ plant	Number of seeds/pod	100-seed weight	seeds weight/plant	crude protein %
Blocks	2	------	------	------	------	------	------
Genotypes	20	1.78**	193.69**	0.55**	560.71**	71.32**	69.02**
Error	40	0.187	3.88	0.11	25.52	18.89	0.01

Tabular f value: 1.84, 2.37

Means performance :

Means of the 21 genotypes (six cultivars and 15 F_1's) for shoots number/plant, pods number/plant, seeds number/pod, 100-seed weight, seeds weight/plant and crude protein % are shown in Table 2. With regard to shoots/plant, the means ranged from 2.78 (P_1×P_5) to 5.56 (P_4×P_6). With respect to pods/plant, the highest crosses were (P_4×P_6) 29.33 and (P_3×P_4)23.89, respectively, while lowest cross was (P_1×P_2)1.67. As for seeds/pod, the cross (P_2×P_6) 4.67 was the highest genotype and the lowest genotypes were Assiut 98, (P_1×P_2), (P_1×P_3) and (P_4×P_5) equal 3. Regarding to 100-seed weight, (P_2×P_4) was the best cross, it has 87.12, while (P_1×P_2) was the lowest cross and it has 24. For seeds weight/plant, the means ranged from 20 (P_1×P_2) to 150 (P_4×P_6). With regard to crude Protein % the means ranged from 10.94 (P_1×P_2) and (P_4×P_6) to 29.17 (P_2×P_5).

Table 2: Mean performance of 15 F_1's hybrids and their six parents for studied traits

characters / Genotypes	Number of shoots/plant	Number of pods/plant	Number of seeds/pod	100-seed weight	seeds weight/plant	crude Protein %
Looza	3.55	5.33	4.33	61.9	22.00	13.95
Giza 40	4.33	23.00	3.67	48.83	92.31	16.84
Giza 429	4.00	13.22	4.00	42.6	40.63	11.38
Assiut 85	3.22	10.67	3.33	61.55	65.18	18.59
Assiut 98	2.89	15.89	3.00	50.18	52.06	20.78
Misr 1	4.00	9.56	3.67	50.64	53.18	14.66
P1×P2	3.00	1.67	3.00	24	20.00	10.94
P1×P3	4.78	13.50	3.00	54.05	44.09	16.30
P1×P4	3.89	23.11	3.33	59.42	66.30	13.13
P1×P5	2.78	11.22	3.67	55.25	69.86	19.69
P1×P6	3.56	14.44	3.67	56.15	67.11	20.55
P2×P3	4.11	9.44	3.67	81.25	62.92	19.69
P2×P4	3.78	10.89	4.00	87.12	72.57	15.04
P2×P5	3.00	6.33	3.67	68.6	44.00	29.17
P2×P6	3.89	10.67	4.67	80.78	78.44	22.50
P3×P4	3.67	23.89	3.67	69.28	116.92	20.78
P3×P5	3.56	20.00	3.67	49.02	102.50	13.56
P3×P6	3.00	9.00	3.67	54.05	90.37	21.88
P4×P5	3.44	21.89	3.00	53.33	75.24	22.24
P4×P6	5.56	29.33	3.33	55.61	150.00	10.94
P5×P6	3.33	13.67	3.67	45.25	69.57	12.63
LSD at 5%	0.714	3.25	0.55	8.34	7.17	0.17
LSD at 1%	0.955	4.35	0.73	11.15	9.60	0.22
C.V	11.75	13.94	9.05	8.78	9.98	0.58

Partitioning of genetic variance:

Partitioning of the genetic variance mean square of genotypes into general combining ability and specific combining ability for all the studied characters was made according to Griffing (1956) using model 1 method 2 mating system.

The results showed that, both G.C.A and S.C.A were highly significant for studied traits Table 3. This result means that all studied characters are affected by both additive and dominant genes (dominance and epistasis) which means that importance of additive and non-additive genes effects in genetic control for all studied characters. These results are in line with obtained by Kitiki and Demir(1984), El-Hady *et al.* (1991), Bakheit (1992), El-Hosary *et al.* (1992), Hendawy *et al.* (1994), Kaul and Vaid (1996), El-Hady *et al.* (1997) , Helal (1997), Mohamed (1997), Youssef (1999), Salama and Mohamed (2004) and Farag (2007). Also, the data showed clearly that both of G.C.A and S.C.A variances controlled inheritance of shoots number/plant and seeds weight/plant, but G.C.A variance was greater than S.C.A variance. On the other hand the variance due to S.C.A were greater than that of G.C.A regarding pods/plant, seeds/pod, 100-seed weight and crude protein % but also these traits affected by G.C.A and S.C.A together. El-Hady *et al*. (1991) found similar results.

Table 3: Partitioning of genetic variance for all the studied characters.

S.O.V	D.F	M.S					
		Number of Shoots/ plant	Number of pods/plant	Number of seeds/pod	100-seed weight	seeds weight/plant	crude protein %
G.C.A	5	0.53**	45.84**	0.13**	135.78**	53.10**	15.26**
S.C.A	15	0.42**	50.76**	0.44**	226.59**	31.30**	25.59**
Error	40	0.06	1.29	0.04	8.51	6.30	0.004

G.C.A= general combining ability and S.C.A= specific combining ability

General combining ability effects:

Table 4 shows the values of general combining ability effects for each cultivar for the studied characters, when mention that positive and significant G.C.A, this means that this parent is a good combiner with other parents in this trait and vice-versa.

Result of Table 4, we can use P_3, P_4 and P_2, respectively in breeding program for shoots number/plant trait improving, and it can be employ P_4 then P_3 for improve pods number/plant trait, and we can use also P_2, P_3, P_6 and P_1, respectively to improve seeds number/pod trait, as we can use P_4 then P_2 for improve 100-seed weight trait. For seeds weight/plant it can be investment P_4, P_6 and P_3, respectively. We can use P_5 and P_2, respectively in breeding program for crude protein % trait improving. These results were similar with results of Mahmoud (1977), Waly (1982), Kitiki and Demir (1984), Mahmoud and Al-Ayoubi (1986), El-Hossary (1987), El-Hady *et al.* (1991), Hendawy *et al* (1994), Kaul and Vaid (1996), Mohamed (1997), and Abdel-Mohsen (2004).

Table 4: General combining ability effects for the studied traits.

Characters / Genotypes	Number of Shoots/ plant	Number of pods/plant	Number of seeds/pod	100-seed weight	seeds weight/plant	crude protein %
P_1	-0.08375**	-3.03833**	0.03333**	-3.78563**	-4.34292**	-1.63417**
P_2	0.08250**	-1.73833*	0.16083**	4.55687**	-0.56417**	1.16458**
P_3	0.16750**	0.42042**	0.07708**	-1.26313**	0.32458**	-0.82667**
P_4	0.12500**	3.94292**	-0.13417**	5.61313**	3.15833**	-0.33542**
P_5	-0.48625**	0.74792**	-0.17292**	-3.89313**	-0.49542**	2.11708**
P_6	0.19500**	-0.33458**	0.03583**	-1.22813**	1.91958**	-0.48542**
LSD at 5%	0.16	0.74	0.13	1.90	1.64	0.04
LSD at 1%	0.21	0.99	0.17	2.55	2.19	0.06

Specific combining ability effects:

S.C.A effects for the crosses are shown in Table 5 For shoots number/plant, generally, (P_4×P_6), (P_1×P_3), (P_2×P_3) and (P_1×P_4), (P_5×P_4) and (P_3×P_5), respectively, were the greatest crosses. This result means that mean of shoots number/plant crosses were more than mean of their parents. For pods number/plant, the crosses (P_4×P_6), (P_1×P_4), (P_3×P_4), (P_3×P_5), (P_1×P_6), (P_4×P_5) and (P_1×P_3) gave positive and highly significant S.C.A effects, respectively, in the most because mean of this crosses were more than mean of their parents. Regarding to seeds/pod the highest crosses were (P_2×P_6), (P_2×P_4), (P_1×P_5), (P_5×P_6), (P_3×P_5), (P_3×P_4), (P_2×P_5) and (P_1×P_6), respectively. With regard to 100-seed weight, the crosses (P_2×P_3), (P_2×P_6), (P_2×P_4), (P_2×P_5), (P_3×P_4), (P_1×P_5), (P_1×P_6) ,(P_1×P_3) and (P_1×P_4) gave positive and highly significant S.C.A effects, respectively. Regarding to seeds weight/plant the greatest crosses were (P_4×P_6), (P_3×P_5), (P_3×P_4), (P_1×P_5), (P_3×P_6), (P_1×P_4) and (P_2×P_6), respectively. For crude protein %, the crosses (P_2×P_5), (P_3×P_6), (P_1×P_6), (P_3×P_4), (P_2×P_6), (P_4×P_5), (P_2×P_3), (P_1×P_5) and (P_1×P_3) gave positive and highly significant S.C.A effects, It can be say that significant of S.C.A effects indicate that probability of heterosis presence, greatly. These results are in harmony with those obtained by Mahmoud and Al-Ayobi (1986), El-Hady *et al.* (1991), Mohamed (1997), and El- Hossary and Aziz (1997).

Table 5: Specific combining ability effects for studied traits.

Characters / Genotypes	Number of Shoots/ plant	Number of pods/ plant	Number of seeds/pod	100-seed weight	seeds weight/plant	crude protein %
$P_1{\times}P_2$	-0.68**	-7.68**	-0.77**	-34.34**	-4.95**	-6.03**
$P_1{\times}P_3$	1.01**	1.99**	-0.69**	1.53**	-1.02**	1.40**
$P_1{\times}P_4$	0.17**	8.08**	-0.15**	0.03**	0.59*	-2.18**
$P_1{\times}P_5$	-0.33**	-0.62**	0.23**	5.36**	4.95**	1.90**
$P_1{\times}P_6$	-0.23**	3.68**	0.02**	3.60**	1.98**	5.43**
$P_2{\times}P_3$	0.18**	-3.37**	-0.15**	20.39**	-1.04**	2.05**
$P_2{\times}P_4$	-0.11**	-5.44**	0.39**	19.39**	-1.94**	-3.12**
$P_2{\times}P_5$	-0.28**	-6.81**	0.10**	10.37**	-4.00**	8.59**
$P_2{\times}P_6$	-0.07**	-1.39**	0.89**	19.89**	0.48*	4.36**
$P_3{\times}P_4$	-0.31**	5.40**	0.15**	7.36**	6.04**	4.59**
$P_3{\times}P_5$	0.20**	4.70**	0.19**	-3.39**	6.81**	-5.08**
$P_3{\times}P_6$	-1.05**	-5.22**	-0.02**	-1.02**	1.97**	5.79**
$P_4{\times}P_5$	0.12**	3.07**	-0.27**	-5.96**	-1.47**	3.12**
$P_4{\times}P_6$	1.56**	11.59**	-0.15**	-6.34**	11.06**	-5.92**
$P_5{\times}P_6$	-0.06**	-0.87**	0.23**	-7.19**	-1.37**	-6.43**
LSD at 5%	0.44	2.03	0.36	5.23	4.50	0.11
LSD at 1%	0.59	2.72	0.48	6.99	6.02	0.15

Heterosis:

Heterosis was measured as a percent of the deviation of F_1 mean to its mid-parent mean or to its better parent mean. Heterosis percentages are shown in Tables (6 and 7).The data indicated they high desirable heterotic effects relative to their mid and better parent for all studied characters.

Heterosis was highly significant for shoots/plant, and ranged from -25.00 ($P_3{\times}P_6$) to 54.02 ($P_4{\times}P_6$) for mid-parent, and from -30.72 ($P_1{\times}P_2$), ($P_2{\times}P_5$) to 39.00($P_4{\times}P_6$) for better parent. Sizable heterosis was obtained for pods/plant 189.97, 174.88 ($P_4{\times}P_6$) from mid-parent and better parent, respectively. Concerning seeds/pod, the heterosis ranged from -27.97 ($P_1{\times}P_3$) to 27.25 ($P_2{\times}P_6$) from mid-parent and from -30.72($P_1{\times}P_2$), ($P_1{\times}P_3$) to 27.25 ($P_2{\times}P_5$) from better parent. Regarding to 100-seed weight, heterosis ranged from -56.65($P_1{\times}P_2$) to 77.73($P_2{\times}P_3$) percent to mid-parent and from -61.23($P_1{\times}P_2$) to 66.39 ($P_2{\times}P_3$). Heterosis in seeds weight/plant ranged from -65.01($P_1{\times}P_2$) to 153.46($P_4{\times}P_6$), and from -78.33 ($P_1{\times}P_2$) to 130.13($P_4{\times}P_6$) percent from mid-parent and better parent, respectively. With respect crude protein%, heterosis percentages to the mid-parent ranged from -36.40 ($P_4{\times}P_6$) to 68.01 ($P_4{\times}P_6$) and from -42.77 ($P_4{\times}P_6$) to 48.26 ($P_3{\times}P_6$) to better parent. It can be note that, not necessarily every genotype had high yield, also had high protein%. Also it can be conclude that the best cross was ($P_4{\times}P_6$) in shoots/plant, pods/plant and seeds weight/plant traits, while the crosses ($P_2{\times}P_6$) and ($P_2{\times}P_5$) were the superiors in seeds/pod trait, and for 100-seed weight, the cross ($P_2{\times}P_3$) was the highest crosses, while the cross ($P_3{\times}P_6$) was the best in crude protein %. Also, more of these crosses which P_1 (Looza) shared in them were a good crosses like $P_1{\times}P_3$ for shoots/plant, $P_1{\times}P_4$ was very good for pods/plant, $P_1{\times}P_5$, $P_1{\times}P_6$ were excellent for seeds weight/plant and $P_1{\times}P_6$ a good cross for crude protein %. These results are in harmony with those obtained by Abdalla (1977), Mahmoud (1977), Lawes et al (1979), Filippetti and Pace (1983), El-Hossary (1985), El-Hady et al (1991), Abd El-Aziz (1993), Hendawy et al (1994), El-Galaly (1997), Helal (1997), El-Harty (1999), Attia (2002), Abdel-Mohsen (2004), Farag (2007) and Alghamdi (2009).

Table 6: Heterosis percentages of the crosses for studied characters

Characters / Genotypes	Number of shoots/plant		Number of pods/plant		Number of seeds/pod	
	$\overline{M.P}$	$\overline{B.P}$	$\overline{M.P}$	$\overline{B.P}$	$\overline{M.P}$	$\overline{B.P}$
$P_1×P_2$	-23.86**	-30.72**	-88.21**	-92.74**	-25.00**	-30.72**
$P_1×P_3$	26.62**	19.50**	45.55**	2.12**	-27.97**	-30.72**
$P_1×P_4$	14.92**	9.58**	188.88**	116.59**	-13.05**	-23.09**
$P_1×P_5$	-13.66**	-21.69**	5.75**	-29.39**	0.14**	-15.24**
$P_1×P_6$	-5.70**	-11.00**	93.96**	51.05**	-8.25**	-15.24**
$P_2×P_3$	-1.32**	-5.08**	-47.87**	-58.96**	-4.30**	-8.25**
$P_2×P_4$	0.13**	-12.70**	-35.31**	-52.65**	14.29**	8.99**
$P_2×P_5$	-16.90**	-30.72**	-67.45**	-72.48**	10.04**	0.00**
$P_2×P_6$	-6.60**	-10.16**	-34.46**	-53.61**	27.25**	27.25**
$P_3×P_4$	1.66**	-8.25**	100.00**	80.71**	0.14**	-8.25**
$P_3×P_5$	3.34**	-11.00**	37.41**	25.87**	4.86**	-8.25**
$P_3×P_6$	-25.00**	-25.00**	-20.98**	-31.92**	-4.30**	-8.25**
$P_4×P_5$	12.60**	6.83**	64.83**	37.76**	-5.21**	-9.91**
$P_4×P_6$	54.02**	39.00**	189.97**	174.88**	-4.86**	-9.26**
$P_5×P_6$	-3.34**	-16.75**	7.43**	-13.97**	10.04**	0.00**
LSD at 5%	0.62	0.71	2.81	3.25	0.47	0.55
LSD at 1%	0.83	0.95	3.77	4.35	0.63	0.73

Table 7: Heterosis percentages of the crosses for studied characters

Characters / Genotypes	100-seed weight		seeds weight/plant		crude protein %	
	$\overline{M.P}$	$\overline{B.P}$	$\overline{M.P}$	$\overline{B.P}$	$\overline{M.P}$	$\overline{B.P}$
$P_1×P_2$	-56.65**	-61.23**	-65.01**	-78.33**	-29.23**	-35.50**
$P_1×P_3$	3.44**	-12.68**	40.80**	8.52**	29.90**	18.10**
$P_1×P_4$	-3.73**	-4.01**	52.10**	1.72**	-18.27**	-28.59**
$P_1×P_5$	-1.41**	-10.74**	88.66**	34.19**	15.04**	-3.90**
$P_1×P_6$	-0.21**	-9.29**	78.53**	26.19**	45.03**	40.29**
$P_2×P_3$	77.73**	66.39**	-5.34**	-31.84**	40.92**	17.90**
$P_2×P_4$	57.85**	41.54**	-7.84**	-21.38**	-14.54**	-18.45**
$P_2×P_5$	38.57**	36.71**	-39.05**	-52.33**	57.17**	42.64**
$P_2×P_6$	62.42**	59.52**	7.83**	-15.03**	42.40**	33.87**
$P_3×P_4$	33.04**	12.56**	121.00**	79.38**	40.00**	12.82**
$P_3×P_5$	5.67**	-2.31**	121.17**	96.89**	-14.95**	-34.13**
$P_3×P_6$	15.94**	6.73**	92.67**	69.93**	68.01**	48.26**
$P_4×P_5$	-4.54**	-13.35**	28.35**	15.43**	14.36**	8.48**
$P_4×P_6$	-0.86**	9.81**	153.46**	130.13**	-36.40**	-42.77**
$P_5×P_6$	-10.24**	-10.64**	32.21**	30.82**	-29.10**	-39.11**
LSD at 5%	7.22	8.34	6.21	7.17	0.14	1.18
LSD at 1%	9.66	11.15	8.31	9.60	0.19	1.58

Heritability:

Heritability in broad sense is shown in Table 8. It is clear that the values of heritability were high indicating that the possibility of selection programs in the subsequent generations specially when the heritability in narrow sense is high also. These results are in agreement with those obtained by Ibrahim (1972), Khalil (1977), El-Kady and Khalil (1979), El-Hossary (1981), Salem (1983), Kikiti and Demir (1984), Mohamed (1997), Youssef (1999) and Petel *et al.* (2008).

This result indicates that traits like seeds weight/plant can be used to increase seeds yield of faba bean genotypes.

Table 8: Heritability in broad sense for all studied characters.

Number of Shoots/plant	Number of pods/plant	Number of seeds/pod	100-seed weight	seeds weight/plant	crude protein %
89.49	98.00	80.00	95.45	73.51	99.99

Generally, it could be concluded that the best promising combinations were Assiut 85× Misr 1 in shoots/plant, pods/plant and seeds weight/plant. The crosses Giza40×Misr1, Giza 40 × Assiut 98 were the superiors in seeds/pod trait and for 100-seed weight, the cross Giza 40 × Giza 429 was the highest crosses, while the cross Giza 429 × Misr1. Also, Looza × Giza 429 for shoots/plant, Looza × Assiut 85 was very good for pods/plant, Looza × Assiut 98, Looza × Misr1 were excellent for seeds weight/plant and Looza × Misr1 a good cross for crude protein %, and we can invest these crosses during selection program in the subsequent generations to obtain so good lines.

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التحليل الوراثى لبعض الأصناف المحلية والأجنبية من الفول البلدى

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الهدف من هذه الدراسة هو تقييم ستة أصناف من الفول البلدي المحلية والأجنبية فيما يتعلق بمكونات المحصول ونسبة البروتين لتحديد أنسب الآباء لعمل أفضل توليفة من الهجن المبشرة . التقييم يشمل دراسة القدرة على التآلف ودراسة قوة الهجين وتقدير درجة التوريث العامة. وقد أجريت التجارب خلال موسمي ٢٠٠٨ /٢٠٠٩م و٢٠١٠/٢٠٠٩ بمزرعة كلية زراعة الأزهر بأسيوط حيث تم التهجين في اتجاه واحد في الموسم الأول للحصول على الهجن وتمت زراعة الهجن والآباء في الموسم الثاني في ثلاث مكررات في قطاعات كاملة عشوائية وتم أخذ البيانات وتحليلها على صفات مكونات المحصول الأساسية ونسبة البروتية الخام.

وكانت أهم النتائج تتمثل في الآتي:

١- وجود معنوية عالية في كل من القدرة العامة على التآلف والقدرة الخاصة على التآلف فى كل الصفات المدروسة مما يعنى أن عدد الأفرع بالنبات وعدد القرون بالنبات وعدد البذور بالقرن ووزن الـ١٠٠ بذرة ووزن البذور بالنبات ونسبة البروتين الخام كلها صفات يتحكم بها الجينات المضيفة وغير المضيفة (جينات السيادة والتفوق), لكن صفتى الأفرع بالنبات ووزن البذور

بالنبات يتحكم بهما جينات مضيفة أكثر قليلاً من الجينات غير المضيفة, وأما صفات عدد القرون بالنبات وعدد البذور بالقرن ووزن الـ١٠٠ بذرة ونسبة البروتين الخام يتحكم بهم الجينات الغير مضيفة أكثر قليلاً من الجينات المضيفة.

٢- كانت قوة الهجين عالية المعنوية لكل الصفات المدروسة, وكانت أفضل الهجن حسب الترتيب كالآتي:

الهجين أسيوط٨٥ ×مصر١ وذلك فى صفات عدد الأفرع بالنبات وعدد القرون بالنبات ووزن البذور بالنبات ثم الهجين جيزة٤٠×مصر١ والهجين جيزة ٤٠×أسيوط ٩٨ المتفوقة في عدد البذور بالقرن والهجين جيزة ٤٠×جيزة ٤٢٩ متفوق في صفة وزن الـ١٠٠بذرة أما الهجين جيزة ٤٢٩×مصر١ كان أعلى الهجن فى نسبة البروتين الخام.

وقد كانت للهجن التى يشترك فيها الأب الأجنبي (لوزا) نصيب وافر من قوة الهجين لأكثر الصفات حيث كان الهجين لوزا×جيزة ٤٢٩ له قوة هجين عالية جداً ومعنوية فى صفة عدد الأفرع بالنبات وكذلك الهجين لوزا×أسيوط٨٥ كان ممتازاً فى صفة عدد القرون بالنبات والهجينان لوزا×أسيوط٩٨ والهجين لوزا×مصر١ متميزان أيضاً فى صفتى وزن البذور بالنبات ونسبة البروتين الخام.

٣- كانت درجة التوريث العامة مرتفعة فى كل الصفات المدروسة.

ووفق ما تم الحصول علية من نتائج توصي الدراسة باستخدام الهجن التي تحتوي علي الأب الأجنبي للاستفادة منه في برامج التربية

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