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Genetic Analysis and Molecular Markers for Yield and its Components Traits in Faba Bean (*Vicia Faba* L.)

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Abstract: The aim of this investigation was to study combining ability effects and gene action for seed yield and their components in faba bean. Seven faba bean genotypes and the resultant twenty one hybrid combinations were evaluated using the diallel cross analysis according to Griffing (1956) as method 2 model 1. Significant mean squares were detected for genotypes, general and specific combining ability effects for all traits. The ratio of GCA / SCA exceeded unity for all traits except No. of branches / plant indicating that additive gene action were more important than non-additive geneaction in the inheritance of these traits. The best general combining ability effects for seed yield / plant and one or more of its attributes were found in the parents 5, 7, 3. The hybrid combination 1×2, 1×4, 2×3, 4×6 and 5×7, showed highly significant desirable SCA effects for yield and most components. Estimates of broad sense heritability varied from 0.57 form plant height to 0.91 for both of seed yield / plant and 100 – seed weight. Results suggested that, the best five selected genotypes as detected by general selection criterion were 1×3, 5×7, 3×5, 1×2 and 1×4. These crosses were the highest in most characters and these characters revealed high significant and positive correlation among each other and also between them and seed yield / plant.Highly differences were observed in all the parental lines during RAPD-PCR analysis using (AR64, AR67, SOL18 and OA-13) primers, respectively.

Key words: faba bean, combining ability, heritability, correlation, selection,molecular markers.

INTRODUCTION

Faba bean (*viciafeba* L.) is one among the most important nutritive seed lagumesand widely considered as a good resource of protein, starch, cellulose and minerals (Haciseferogullari *et al*. 2003).

It is used in daily diets, especially, for lower income peoples. Therefore, the investigators in Egypt and in mang other developing countiries have tried to improve yield (Omar *et al*. (1999), Soliman *et al*. 2005).

The ultimate goal of the plant breeder is the release new varieties that are superior in some way to those already in commercial production. To accomplish this, he must devise a breeding program which will allow him to produce and reproduce genotypes that represent somewhere near optimum combinations of genes for a particular area (Abul-Naas *et al*. 1989). Many breeders used the diallel cross mating design to identify the best genetic marterial developed for breeding programmes or for commercial application (Hayward 1979). Combining ability analysis is associated with additive effects of genes, while SCA is attributed primarily to non-additive (dominance and epistasis) ones. Therefore, the breeder should evaluate the potentialities of the available germplasm for new recombination's and eventually combining ability which have proved to be of considerable use in breeding methods (Farag 2005). In this regard, several studies on faba bean reported that both additive and non-additive gene action are important (Farag2007, Alghamdi 2009 and Ibrahim 2010). El-Hosary *et al*. (1986), El-Tabbakh and Ibrahim (2000) and Farag and Darwish (2005) found that additive gene action was the dominant component for most traits of faba bean.

The main objective of this study was to estimate general (GCA) and specific combining ability (SCA) in 21 crosses among seven faba bean genotypes by using method (Griffing 1956) to develop the genetic basis needed for selection of high yielding varieties of faba bean.

MATERIAL AND METHODS

Seven varieties and / or lines of faba bean (viciafaba L.), representing a wide range of diversity for several characters, were selected for this study (P_1) I 131introduced from Libya, (P_2) mutant 4 induced from Giza 1 with 6kr + 0.02 DES, both (P_3) 61 / 1311 / 66 and (P_4) 61 / 536 /69 derived from cross Habashi × Rebaya, (P_5) Rina Blanca introduced from Spain, (P_6) Krist al, (P_7) G 461 from Giza 3 × I. I. B 938. The experiments were carried out at the experiment station of the National Research Center, Giza, during two successive seasons and 2009/2010.

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In2009/2010 season, all possible crosses (without reciprocals) were made among the seven parental line. The twenty one hybrids and their parents were evaluated in randomized complete block design with three replicates in 2010/ 2011 growing season. For evaluation plot size was one row 4 m. long and 60 cm wide. Hills interspacing was 20 cm, and the dry method of planting was followed. Recommended agronomic practices were carried out as usual for ordinary faba bean fields in the area. Data pertaining to the following traits were collected on 10 guarded plants in each plot: seed yield / plant (g), plant height, number of branches / plant, number of pods / plant, pod length, number of seeds / pod, weight of seeds / pod, 100-seed weight and days to flowering 50% of plants were recorded.

Data were analysed by (ANOVA). For diallel analysis, Griffing's (1956)method 2 model 1 was assumed. The relative importance of (GCA) and (SCA) was tested using the ratio GCA /SCA. Phenotypic and genotypic correlation coefficients were calculated for all possible pairs of characters according to Steel and Torrie (1980). Classical selection criterion was determined after Singh and Chaudhary (1985).

DNA Extraction and RAPD Amplification Condition:

Leaves of faba bean were obtained from 10 days old plantlets and ground to afine powder in liquid nitrogen. The genomic DNA was extracted using the Bio flux kit protocol RAPD analysis was performed using four random primers (table 1) produced from operon technologies (Metabion International AG).

RAPD assay was performed as described by Williams *et al*. (1990) with some modifications PCR reaction was used in afinal volume of 25 ul containing 12.5 ul of master mix (Bioteke), 2.5 ul of 5 um of each primer, 50 mg of template DNA. PCR amplification was performed in PTC-100 PCR version 9.0 from MJ Research. USA programmed for 95 °C for 5 min (denaturation), 36 cycles of (94 °C for 1 min, 36 °C for 1 min and 72 °C for 1 min (annealing) and afinal extension of 2 min at 72 °C. PCR products were analyzed using 1% agarose gel electrophoresis and visualized with ethidium bromide staining. The sizes of the fragments were estimated based on a DNA ladder of 100 bp (fermentas).

RAPD Data Analysis:

Clear and distinct amplification products were scored for presence (1), absence (0) Gel were photographed using a 35 mm color film (200 ASA) and scanned with Bio-Rad video densitometer model 620 USA, at a wavelength of 577. Soft ware data analysis for Bio-Red model 620 densitometer and computer were used as illustrated by the manufacture.

Table 1: List of random primers used in RAPD analysis:

Primer	SeQuences
(AR64)	5\- GCCAGTTACA-3\
(AR67)	5\- ACTCGGATCG-3\
(So L18)	5\- CATCCTGACT-3\
(oA-13)	5\- AACTGGATGC-3\

RESULTS AND DISCUSSION

Pertinent portions of analysis for variance for all the traits studied are presented in Table (2).Significant genotypes mean squares were detected for all traits. With the exception of number of branches / plant, significant mean squares due to parents and crosses were detected for all traits. These findings indicate that both parental lines and crosses differed in their performance in all traits.

Table 2: Mean squares estimates of ordinary analysis for some traits studied of faba bean.

S. O. V.	D.F	Seed yield/plant (g)	Plant height (cm)	Number of branches/plant	Number of pods/plant	Pod length (cm)	Number of seed/pod	Weight of seeds /pod	100 – seed weight (g)	Days to flowering 50% / plant
		F1	F1	F1	F1	F1	F1	F1	F1	F1
Replicates	2	23.25**	258.54**	3.31*	2.22	0.15	0.01	0.23	6.75	7.11
Genotypes	27	365.49**	211.22**	5.81**	37.45**	3.06**	0.26**	1.60**	215.24**	160.93**
Parents	6	582.64**	282.65**	1.10	51.97**	5.96**	0.33**	2.21**	417.52**	272.86**
Crosses	20	226.88**	195.14**	6.25**	32.35**	2.30**	0.26**	1.50**	163.42**	129.18**
Parents × crosses	1	1834.92**	104.14	25.27**	52.39**	0.72	0.05	0.01	38.11*	124.23**
Error	54	11.65	42.45	0.88	4.92	0.34	0.04	0.10	6.79	8.65

*: significant at 5%
**: significant at 1%

Results in Table (3) showed that both general (GCA) and specific (SCA) combining ability mean squares were significant for all studied traits. It is evident that both additive and non-additive gene effects were involved in determining the inheritance of all studied traits. The ratio of GCA / SCA exceeded the unity for all studied

traits except number of branches / plant. These indicating that the GCA (additive genetic effect) was more important than SCA variances and played the major role in the inheritance of these traits. These results are in agreement with those of El-Hosary et al (1986), El-Tabbakh and Ibrahim (2000), Farag and Darwish(2005), Farag (2007), Alghamdi (2009) and Ibrahim (2010), found that additive gene action was the dominant component for most traits of faba bean.

Estimates of general combining ability (GCA) effects of parents for studied traits are given in Table (4). Generally, wide variation could be observed among genotypes for their combining ability effects for the traits under study. The parental line (1) seemed to be good combiner for 100-seed weight. On the contrarily, it expressed either negative or non-appreciable positive " ĝ " values for the rest traits. The parental line (2) gave either significant negative value or insignificant (ĝ) effect for all traits. The parental line (3) expressed significant positive (ĝ) effects for seed yield / plant, plant height and number of seeds / pod. However, it gave either significant negative or in significant (ĝ) effects for the rest traits. The parental line (4) behaved as a poor one for all traits except days to50% flowering /plant. The parental line (5) showed highly significant and positive desirable GCA effects for all study traits except plant height and number of pods / plant. Therefore, this parent could be considered as good combiner and could be used as donor for improving to these traits. The parental line (6) exhibited significant positive GCA effects for plant length, no of pods / plant. Also, it gave significant negative values for the rest traits. The parental line (7) appeared to be one of the good combiners for seed yield / plant.

Table 3: Mean squares of general and specipic combining ability effects for some traits of faba bean.

S. O. V.	D.F	Seed yield/plant (g)	Plant height (cm)	Number of branches/ plant	Number of pods/plant	Pod length (cm)	Number of seed/pod	Weight of seed/pod	100-seed weight(g)	Days to flowering 50% / plant
		F1	F1	F1	F1	F1	F1	F1	F1	F1
G. C. a	6	263.08**	105.92**	1.39**	24.43**	2.55**	0.13**	1.27**	86.29**	87.38**
S.C a	21	81.47**	60.26**	2.09**	9.07**	0.58**	0.08**	0.32**	67.59**	44.00**
Error	54	3.88	14.14	0.29	1.64	0.11	0.01	0.03	2.26	2.88
G.C.A/S.Ca		3.23	1.76	0.67	2.69	4.40	1.63	3.97	1.28	1.98

*: significant at 5%
**: significant at 1%

Table 4: Estimates of general combining ability effects for the parental lines of faba bean.

D.F	Seed yield/plant (g)	Plant height (cm)	Number of branches/plant	Number of pods/plant	Pod length (cm)	Number of seed/pod	Weight of seed/pod	100-seed weight(g)	50%/plant flowering days to
	F1	F1	F1	F1	F1	F1	F1	F1	F1
P1	- 0.577	0.783	- 0.003	0.718	0.077	- 0.047	0.052	3.138**	1.011
P2	- 3.576**	0.820	- 0.443**	- 0.771	- 0.071	0.019	- 0.189	0.397	- 1.619**
P3	2.127**	4.153**	- 0.269	0.451	- 0.052	0.071*	- 0.115	- 1.492**	- 3.471
P4	- 4.169	- 0.921	0.267	0.740	- 0.412**	- 0.107**	- 0.244**	- 5.566**	1.085*
P5	8.386**	6.661**	0.612**	- 3.394**	1.107**	0.230**	0.822**	3.767**	6.048**
P6	- 6.910**	2.524*	0.234	1.555**	- 0.523**	- 0.114**	- 0.200**	0.101	- 1.804
P7	4.720**	- 0.698	- 0.396*	0.703	- 0.126	- 0.051	- 0.126*	- 0.344	- 1.249
L.S.D(gi) 5%	1.222	2.331	0.335	0.793	0.211	0.070	0.112	0.932	1.053
L.S.D(gi) 1%	1.611	3.074	0.442	1.046	0.278	0.092	0.148	1.229	1.388
L.S.D5%(gi-gj)	1.867	3.563	0.514	1.212	0.321	0.108	0.172	1.425	1.608
L.S.D 1% (gi-gi)	2.461	4.698	0.678	1.597	0.424	0.143	0.227	1.878	2.120

*: significant at 5% **: significant at 1%
P1: I (131) , P2: Mutant 4 , P3: 61/1311/66 , P4: 61/536/69 , P5: Rina Blanca , P6: Kristal , P7: G 461

Specific combining ability SCA effects of the crosses for the studied traits are presented in Table (5). In general, the most desirable crosses which had desirable values of SCA effects were 1×2, 1×4, 2×3, 4×6 and 5×7 for yield and most components. Some of these crosses showing high specific combining ability effects involving only one good combiner, such combinations would show with desirable transgressive segregates, providing that the additive genetic system present in the good combiner as well as the complementary and epistatic effects present in cross, acr in the same direction to reduce undesirable plant characteristics and maximize the character in view. Therefore, the previous crosses might be of prime importance in breeding program for traditional breeding procedures.

Table (6) presents genotypic and phenotypic correlations among all pairs of traits. Generally, there was a close agreement between genotypic and phenotypic significant, but the former was higher of all comparisons, suggesting that there are strong inherited association between correlated traits. This indicates that these traits were less subject to environmental stresses. Both genotypic and phenotypic correlation coefficients among the all studied traits were positive and highly significant except seed yield / plant with each of plant height, no of pods / plant and days to flowering, plant height with each of no. of branches / plant, no of seeds / pod and 100 – seed weight; no of branches / plant with each of no of pods / plant and days to flowering were had negative association. A know ledge of the correlations that exit between important characters may facilitate the

interpretation of results already obtained and provide the basis for planning more efficient programs for the future. Also, correlations between important and non – important characters may reveal that some of the later are useful as indicators of one or more of the former (Herbert et al. 1955). These results are in a good coincidence with those reported by Farag et al. (2005), Farag (2007), Alghamdi (2007), Alghamdi (2009) and Ibrahim (2010).

Table 5: Estimates of specific combining ability effects for all combinations studied of all traits in faba bean.

Crosses	Seed yield /plant (g)	Plant height	Number of branches/ plant	Number of pods/ plant	Pod length (cm)
	F1	F1	F1	F1	F1
P1 × P2	5.296**	12.611**	- 0.431	4.986**	- 0.386
× P3	4.926**	8.944**	0.428	2.764**	0.595*
× P4	4.222**	9.019**	0.291	1.475	0.888**
× P5	- 3.667*	- 6.907*	3.046**	- 5.058**	0.503
× P6	8.630**	- 4.426	- 0.775	- 1.673	1.166**
× P7	- 8.6667**	- 17.870**	- 1.146**	- 0.821	- 0.364
P2 × P3	11.259**	- 5.425	1.669**	- 3.413**	0.843**
× P4	- 0.778	- 6.019*	- 1.202**	- 1.369	0.104
× P5	- 3.333*	0.389	- 2.113**	4.097**	- 1.249**
× P6	7.630	- 6.130*	0.565	- 2.851**	0.314
× P7	2.667	1.425	0.361	1.334	0.051
P3 × P4	- 1.148	- 0.019	0.157	1.742	- 0.516
× P5	- 3.703	11.056**	- 0.353	1.208	0.032
× P6	- 0.741	- 2.463	- 0.942*	- 2.073*	0.495
× P7	- 1.037	- 1.241	- 0.479	- 3.221**	- 0.701**
P4 × P5	7.593**	3.130	0.309	2.919**	- 1.142**
× P6	15.222**	3.944	1.620**	2.971**	0.255
× P7	- 0.074	9.167**	1.650**	1.157	0.192
P5 × P6	- 6.667**	5.019	1.676**	2.105*	- 0.497
× P7	19.707**	- 0.426	0.972*	- 0.043	1.206**
P6 × P7	- 0.667	- 0.278	1.350**	3.342**	- 0.664*
L.S.D 0.05 (S_{ij})	3.025	5.774	0.834	1.965	0.522
L.S.D 0.01(Sii)	3.988	7.613	1.099	2.591	0.689
L.S.D 0.05 (S_{ij} - S_{ik})	5.282	10.080	1.457	3.433	0.912
L.S.D0.01(S_{ij} - S_{ik})	6.964	13.289	1.921	4.526	1.203
L.S.D 0.05 (S_{ij} - S_{kl})	4.940	9.428	1.362	3.209	0.854
L.S.D 0.01(S_{ij} - S_{kl})	6.513	12.431	1.796	4.232	1.126

Table 5: Cont.

Crosses	Number of seed/pod	Weight of seed/pod	100-seed weight (g)	Days to flowering 50%/plant
	F1	F1	F1	F1
P1 × P2	0.108	- 0.321*	4.870**	- 4.713**
× P3	0.023	0.005	2.093	0.472
× P4	0.268**	0.234	7.500**	- 5.083**
× P5	0.297**	1.201**	2.833*	10.620**
× P6	0.208*	0.590**	1.500	- 0.194
× P7	- 0.721**	- 1.117**	- 7.722**	1.583
P2 × P3	0.323**	0.345*	11.167**	- 0.565
× P4	- 0.032	0.442**	- 5.093**	- 0.454
× P5	0.064	- 0.658**	- 0.093	6.917**
× P6	0.042	- 0.069	3.574**	2.769*
× P7	- 0.055	0.090	5.685**	0.213
P3 × P4	- 0.084	0.499**	- 9.870**	- 2.602
× P5	- 0.221*	- 0.099	- 9.537**	- 2.898*
× P6	0.077	0.123	3.796**	4.287**
× P7	- 0.040	0.316*	8.241**	- 1.269
P4 × P5	- 0.476**	- 1.069**	0.537	- 14.787**
× P6	0.134	- 0.047	9.870**	- 3.269*
× P7	0.271**	0.345*	6.648**	- 2.824*
P5 × P6	- 0.302**	- 0.647**	- 8.130	- 11.565**
× P7	0.334**	0.679**	- 13.351**	7.213**
P6 × P7	0.245**	0.101	- 6.352**	1.398
L.S.D 0.05 (Sij)	0.176	0.281	2.307	2.604
L.S.D 0.01(Sij)	0.233	0.371	3.042	3.434
L.S.D 0.05 (Sij - Sik)	0.309	0.490	4.030	4.551
L.S.D 0.01(Sij - Sik)	0.408	0.646	5.313	5.999
L.S.D 0.05 (Sij - Skl)	0.289	0.458	3.770	4.255
L.S.D 0.01(Sij - Skl)	0.381	0.604	4.971	5.610

*: significant at 5% **: significant at 1%

P1: I (131) , P2: Mutant 4 , P3: 61/1311/66 , P4: 61/536/69 , P5: Rina Blanca , P6: Kristal , P7: G 461

Heritability estimates in broad sense (Table 6)were generally high for all studied traits. It ranged from 0.57 to 0.91 for plant height and both of seed yield / plant and 100 – seed weight, respectively. These results indicated that, the environment had a small effect on the inheritance of such traits. In these case selection based on mean performance would be successful in improving these traits. Similar findings were also reported by Omer (2003), Toker (2004), Abd El-Maksoud et al (2007) and Ibrahim (2010).

Table 6: Genotypic correlation (above diagonal), phenotypic correlation (below diagonal) and heritability (diagonal) among all studied characters in F1 generation in faba bean.

Characters	Seed yield/plant (g)	Plant height (cm)	Number of branches/ plant	Number of pods/plant	Pod length (cm)	No. of seed/pod	Weight of seed/pod	100-seed weight (g)	Days to flowering 50%/plant
Seed yield/plant	0.91	- 0.13	0.34**	- 0.20	0.69**	0.65**	0.50**	0.35**	- 0.11
Plant height	- 0.10	0.57	- 0.01	0.80**	- 0.46**	- 0.11	- 0.47**	- 0.03	0.75**
No. of branches/plant	0.26**	0.02	0.65	- 0.03	0.33**	0.34**	0.40**	0.08	- 0.07
No. of pods/plant	- 0.14	0.57**	- 0.11	0.69	- 0.79**	- 0.48**	- 0.80**	- 0.27*	0.67**
Pod length	0.54**	- 0.23*	0.24*	- 0.45**	0.73	0.70**	0.87**	0.44**	- 0.53**
No. of seed/pod	0.48**	- 0.01	0.29**	- 0.29**	0.66**	0.65	0.82**	0.50**	- 0.46**
Weight of seed/ pod	0.44**	- 0.27*	0.34**	- 0.54**	0.78**	0.72**	0.83	0.42**	- 0.71**
100-seed weight	0.33**	- 0.03	0.06	- 0.23*	0.36**	0.38**	0.37**	0.91	- 0.09
day to flowering 50% plant	- 0.09	0.56**	- 0.03	0.50**	- 0.42**	- 0.33**	- 0.55**	- 0.07	0.85
L.S.D at 0.05	5.68	10.85	1.56	3.69	0.98	0.33	0.52	4.33	4.89
at 0.01	7.44	14.19	2.05	4.83	1.28	0.43	0.69	5.67	6.40

*: significant at 5%
**: significant at 1%

The selection index which has been illustrated by Smith (1936) gives proper weight to each of two or more characters to be considered for selecting better genotypes. When the economic importance of plant type is considered, thus the entry with the highest yield may not get the highest score resulting from use of the selection index (Robinson et al. 1951). Selection index based on a combination of nine major characters were studied. The 21 crosses and 7 their parents arranged descendly according to classical selection values and their corresponding means for all studied traits are presented in Table (7). Results revealed that, the best five selected genotypes as detected by general selection criterion among 28 ones were 1×3, 5×7, 3×5, 1×2 and 1×4. It is worthy to mention that, these crosses were the highest in most studied characters. However, these characters revaled high significant and positive correlation among each other and also between them and seed yield / plant (Table 6).

It is note worthy to indicate herein that the mean performance of some parental lines of faba bean favored their respectively GCA and SCA effects. Such cases included the parents: P1 (I 131) introduced from Libya, (P2) mutant 4 induced from Giza 1, (P3) 61/1311/66, (P4) 61/536/69 which derived from cross Habashi × Rebaya, (P5) Rina Blanca introduced from Spain, (P6) Kristal, (P7) G 461 from Giza 3 × I. I. B 936 and the crosses, P1 × P2, P1 × P4, P4 × P6 and P5 × P7, respectively. These findings indicated that the intrinsic performance of these genotypes gave a good index of their GCA and SCA effects. Therefore selection for improving such traits could be practiced either on mean performance or Genetic parameters basis.

RAPD – PCR Markers:

The densitometric of of RAPD-PCR products of faba bean " parental lines " using (**AR 64**) primer are showed in table (8) and Figure (1).The bands number 6, 7, 8, 9 and 10 with molecular weight of 750, 550, 400, 180 and 120 bp respectively were appeared in all genotypes except p6 for the band number 10, which means that these bonds were common bands in these cultivars, while, the bands number 4 and 5 with molecular weight of 900 and 850 bp were observed in all genotypes except the parents number 4 and 5 for the band number 4 and the patent number 5 for the band number 5,in addition to the bands number 1,2 and3 with molecular weight of 1450,1300 and 110 bp were observed in the parents number 7 for the first band,2 and 6 for the second band and 1 for the third band,respectively;which means that,these bands were primer for these cultivars in faba bean (table 8) and figure (1).

The results in table (9) and fig. (2) showed that the bands number 4, 5, 6, 7, 8 and 9 with molecular weight of 1000, 650, 530, 400, 370 and 200 bp were appeared in all parental lines of faba bean, which indicated that these bands were common bands in these cultivars, while the band number 2 with molecular weight of 1300 bp was observed in all genotypes except P2 and P6 using (**AR 67**) primer.On the other hand, the bands number 1,3 and 10 with molecular weight of 1380,1050 and 100 bp were appeared in the parents;(p4,p7),(p2,p3,p7) and (p4,p5);only respectively,which indicated that these bands were index for these genotypes.

Table 7: The 28 entries arranged descendly according to classical selection values and their corresponding means for all studied traits in faba bean.

	Classical selection values	Seed yield/ plant	Plant height	No. of branches /plant	No. of pods/ plant	pod length (cm)	No. of seed/ pod	Weight of seed/ pod	100-seed weight (g)	Days to flowering 50%/plant
P1 × P3	294.52	67.33	111.67	6.63	21.33	10.30	3.73	3.27	74.67	42.67
P5 × P7	293.75	93.67	90.00	7.67	14.67	11.87	4.20	4.70	61.00	28.66
P3 × P5	291.23	67.66	106.33	6.46	15.66	10.77	3.77	3.93	63.67	41.00
P1 × P2	288.21	62.00	112.00	5.60	22.33	9.30	3.76	2.87	79.33	46.00
P1 × P4	284.55	60.33	106.67	7.03	20.34	10.23	3.80	13.36	76.00	43.67
P2 × P3	284.27	70.67	97.33	7.43	13.67	10.40	4.10	3.37	81.00	46.33
P4 × P7	282.79	61.33	105.34	8.00	20.00	9.33	3.80	3.30	71.67	43.67
P4 × P6	282.54	65.00	103.33	8.60	22.67	9.00	3.60	2.83	75.33	44.66
P4 × P5	281.19	72.67	93.33	7.67	17.66	9.23	3.33	2.82	67.67	48.33
P3 × P7	279.91	66.66	100.00	5.33	15.33	8.80	3.67	3.40	77.33	46.67
P3	277.28	60.33	100.67	5.70	19.80	9.20	3.86	3.00	65.00	46.33
P7	276.90	64.34	101.00	4.33	17.93	9.57	3.57	2.87	73.67	46.34
P5 × P6	276.59	55.67	98.67	9.00	17.67	9.76	3.50	3.30	66.66	48.00
P2 × P7	274.93	64.66	99.33	6.00	18.66	9.53	3.60	3.10	76.67	43.33
P1 × P6	274.88	62.00	96.67	5.93	18.00	10.40	3.73	3.77	75.66	41.67
P6 × P7	271.32	58.00	99.33	7.67	23.00	8.37	3.77	3.10	64.33	42.33
P3 × P4	270.66	57.67	101.00	6.63	20.33	8.70	3.56	2.47	54.00	45.67
P3 × P6	265.99	55.33	102.00	5.50	17.33	9.60	3.57	3.13	73.33	41.66
P1	258.39	54.34	98.7	5.77	18.00	8.63	3.50	3.12	71.67	40.00
P2 × P6	257.95	58.00	95.00	6.83	15.33	9.40	3.63	2.87	75.00	41.33
P2	257.57	42.33	101.00	6.17	14.46	9.70	3.50	3.03	61.66	46.00
P5	255.26	72.67	78.33	5.93	8.00	12.47	4.30	5.27	92.33	26.33
P2 × P4	254.61	52.34	91.67	5.10	16.00	9.30	3.57	3.33	60.67	41.66
P1 ×P5	254.50	65.00	85.00	10.13	9.67	11.37	4.16	5.40	80.66	23.00
P2 × P5	248.09	62.33	92.33	4.53	17.33	9.46	4.00	3.30	75.00	29.33
P6	245.71	35.34	105.00	5.20	19.60	8.10	3.33	2.90	69.00	41.00
P1 × P7	233.14	56.33	80.00	4.93	18.00	9.27	2.87	2.13	66.00	39.33
P4	211.95	40.00	86.33	5.60	14.43	8.96	3.43	3.14	55.00	24.00

P1: I (131) , P2: Mutant 4 , P3: 61/1311/66 , P4: 61/536/69 , P5: Rina Blanca , P6: Kristal , P7: G 461

Table 8: The densitometeric analysis of RAPD-PCR products of the parental lines for faba bean against (AR64) primer.

Band No.	Base pairs	P1	P2	P3	P4	P5	P6	P7
1	1450	0	0	0	0	0	0	1
2	1300	0	1	0	0	0	1	0
3	1100	1	0	0	0	0	0	0
4	900	1	1	1	0	0	1	1
5	850	1	1	1	1	0	1	1
6	750	1	1	1	1	1	1	1
7	550	1	1	1	1	1	1	1
8	400	1	1	1	1	1	1	1
9	180	1	1	1	1	1	1	1
10	120	1	1	1	1	1	0	1

RAPD-PCR markers produced by (**SOL18**) primer are presented in figure (3) and table (10).

This primer succeeded in exhibiting nine RAPD bands over all studied genomic DNA. Molecular weight of these bands ranged from 150 bp to 1550 bp.

The bands number 4, 5, 6, 7 and 8 with molecular weight of 1000, 850, 650, 450 and 250 bp were appeared in all cultivars of faba bean, which means that these bands were common bands in these parents.

On the other hand, the bands number 1,2,3 and 9 with molecular weight of 1550,1370,1050 and 150 bp were showed in the genotypes ;(p1,p2,p3,p5) for the first band,(p1,p2,p3,p7) for the second band,(p1) only for the third band and(p3) only too for the band number nine , respectively.

The date of table (11) and fig. (4) in RAPD-PCR markers produced by (**OA-13**) primer revealed that, the bands number 1, 2, 3, 4, 5 and 10 with molecular weight of 1450, 1370, 1250, 1050, 1000 and 100 bp, were appeared in all the parental lines of faba bean ,except(p2,p7,p3 and p4) for the bands number 1,2,5 and 10 respectively, which indicated that these bands were common bands in all used plant materials.

The difference was in the band number 8 with molecular weight of 300 bp, where this band was appeared in all genotypes studied except P1,P5 and P6, while, the bands number 6, 7 and 9 weren't appeared in all cultivars.

It is evident from the aforementioned discussion that faba bean under Egyptian conditions which are greatly affected by multiple genes and environmental factors. However, marker assisted selection could enhance the identification of faba bean genotypes.

This approach would enable the molecular plant breeder to grasp the promising varieties with more confidence in their merits as variety selection will be based on genetic rather than phenotypic basis with the elimination of the environmental factors. Moreover, this process is fact, reliable and cost-effective which can reduce the required time for faba bean breeding program. These findings stand in conformity with those recorded by several workers among them Quirin and Chandra (2005), El-Said (2007) and Weerakoon *et al*. (2008).

Table 9: The densitometric analysis of RAPD-PCR products of the cultivars in faba bean against (AR 67) primer.

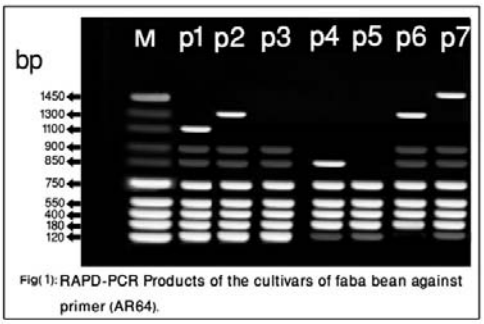
Band No.	Base pairs	P1	P2	P3	P4	P5	P6	P7
1	1380	0	0	0	1	0	0	1
2	1300	1	0	1	1	1	0	1
3	1050	0	1	1	0	0	0	1
4	1000	1	1	1	1	1	1	1
5	650	1	1	1	1	1	1	1
6	530	1	1	1	1	1	1	1
7	400	1	1	1	1	1	1	1
8	370	1	1	1	1	1	1	1
9	200	1	1	1	1	1	1	1
10	100	0	0	0	1	1	0	0

Table 10: The densitometric analysis of RAPD-PCP products of the cultivars in faba bean against (SOL 18).

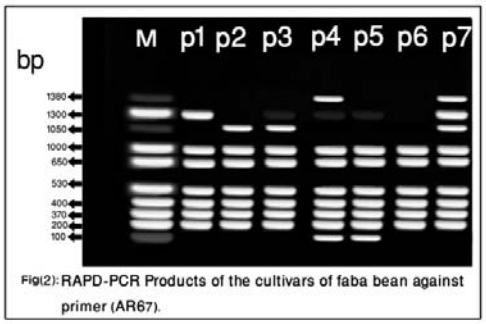
Band No.	Base pairs	P1	P2	P3	P4	P5	P6	P7
1	1550	1	1	1	0	1	0	0
2	1370	1	1	1	1	0	0	1
3	1050	1	0	0	0	0	0	0
4	1000	1	1	1	1	1	1	1
5	850	1	1	1	1	1	1	1
6	650	1	1	1	1	1	1	1
7	450	1	1	1	1	1	1	1
8	250	1	1	1	1	1	1	1
9	150	0	0	1	0	0	0	0
10	50	0	0	0	0	0	0	0

Table 11: The densitometric analysis of RAPD-PCR products the cultivars faba bean against (OA-13).

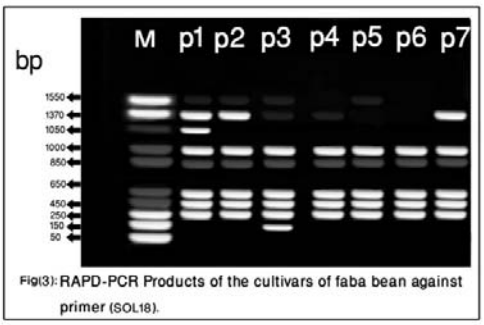
Band No.	Base pairs	P1	P2	P3	P4	P5	P6	P7
1	1450	1	0	1	1	1	1	1
2	1370	1	1	1	1	1	1	0
3	1250	1	1	1	1	1	1	1
4	1050	1	1	1	1	1	1	1
5	1000	1	1	0	1	1	1	1
6	750	0	0	0	0	0	0	0
7	500	0	0	0	0	0	0	0
8	300	0	1	1	1	0	0	1
9	200	0	0	0	0	0	0	0
10	100	1	1	1	0	1	1	1



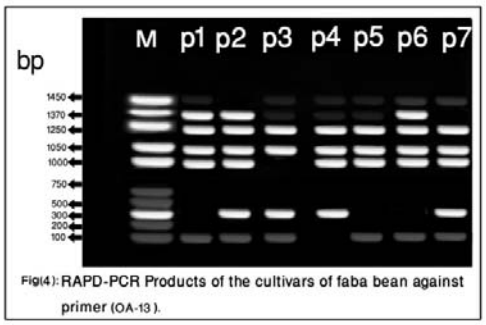
Fig(1): RAPD-PCR Products of the cultivars of faba bean against primer (AR64).



Fig(2): RAPD-PCR Products of the cultivars of faba bean against primer (AR67).



Fig(3): RAPD-PCR Products of the cultivars of faba bean against primer (SOL18).



Fig(4): RAPD-PCR Products of the cultivars of faba bean against primer (OA-13).

Conclusion:

The most desirable mean values, GCA and SCA effects and other genetic parameters were detected from the genotypes; P1 (I 131), P2 (mutant 4), P3 (61/ 1311/ 66), P4 (61/ 536/ 69) and P7 (G 461) in addition to the crosses; P1 × P2, P2 × P3, P3 × P5, P1 × P4 and P5 × P7, which were positive and highly significant for all other genetic parameters.

From the previous results it could be concluded that; the seven parental lines of faba bean were highly differences by using four primers in RAPD-PCR markers, namely; AR 64, AR 67, SOL 18 and OA-13, respectively. So, Abig chance was performed for breeders to select the best genotypes of faba bean for highly yielding , salinity and drought tolerance, ……. and so on, under Egyptian conditions.

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