

GENETIC STUDIES FOR SOME AGRONOMIC CHARACTERS IN FABA BEAN (*Vicia faba* L.)

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Abstract: The objectives of this work were to analyze the genetic systems controlling variation in some quantitative characters (plant height, number of branches/plant, green (immature) pod length, green pod width, number of dry pods/plant, weight of dry seeds/plant and Protein content) in six faba bean lines (Assiut 174, Golden, Assiut 99, Assiut 12 (Romy), Assiut 195 and Assiut 16) and their F₁'s which produced by diallel crossing system. Also, to determine the association between these characters and randomly amplified polymorphic DNA (RAPD) as based similarity estimates. The results indicated that there were significant differences among genotypes in all the studied characters. Heterosis was present for all characters and both additive and non-additive gene effect were important in the control of these traits. Dominance played the major role in controlling the

variation in most the studied traits whereas over-dominance effects were found for number of dry pods/plant, weight of dry seeds/plant and protein content (%). The range of Euclidean distance grouped the six lines into two main clusters, the first cluster contained one line and the other contained the other five lines. Five random primers were used for RAPD experiments that generated 77 fragments with 59 % polymorphism. The range of Nei and li similarity coefficients calculated for the RAPD experiments was 0.55-0.83. The dendrogram based on RAPD marker created two main groups, the first group contained two lines (Assiut 16 and Assiut 195) and the other subdivided into three sub-clusters. The Euclidean distance based on morphological traits was not significantly correlated with the genetic distance based on RAPD markers.

Key words: *Vicia Faba*, diallel analysis, heterosis, RAPD marker

Introduction

Cultivated faba bean (*Vicia faba* L.) is used as human food in developing countries and as animal feed in industrialized countries. It is one of the most important winter crops for human consumption in the Middle East. Wide variation in protein content (20-41%) has been

reported (Chavan *et al.*, 1989). Protein content is influenced by both genetic and environmental factors and it has been reported that the inheritance of this trait is controlled by additive genes with some partial dominance (Bond *et al.*, 1985).

Diallel cross analysis (Waly, 1982) revealed that additive genetic variance was predominant for most of the quantitative characters in local faba bean cultivars. However, Filippetti and Pace (1983) showed that dominance effects and heterosis were operating for yield components. Mitkees and Hassan (1983) in a 6 parents diallel in *Vicia faba* found that additive and dominance gene effects were significant for seed protein character. Habetinek (1985) emphasized that the importance of additive gene effects in controlling 100-seed weight which were modified slightly by non-allelic interactions. Mahmoud *et al.* (1984) found that seed yield/plant, 100-seed weight, number of pods/plant, pod length and seed protein content characters were influenced by both additive and non-additive genetic variance, and all had high estimates of heritability. Waly and Abdel-Aal (1986) found that both additive and dominance were highly significant on protein and cellulose content in broad bean. Bargale and Billore (1990) found that a high level of heterosis was observed for seed yield and a number of yield components. El-Morsy (1990) performed a genetic analysis for morpho-physiological traits, yield and its components. Heterosis was presented for these traits, except number of branches/plant. Dominance gene effects were found to be important in the inheritance of the number of pods/plant and seed yield/plant.

Additive and non-additive gene actions were involved in the inheritance of plant height in the F₁. Kaul and Vaid (1996) found that both additive and dominance effects were highly significant on yield/plant and seed protein content. El-Hady *et al.* (1998) indicated that dominance effects played an important role in the inheritance of all traits in *Vicia faba*. Non-additive genetic variance was more important than additive genetic variance for pods/plant. Bashoot (2000) revealed the presence of epistasis in all characters for all the five studied crosses in faba bean. El Hosary *et al.* (2002) found that additive gene action was more pronounced compared with the dominance for both number of seeds/plant and seed yield/plant.

Genetic diversity is the basis of successful crop improvement and can be estimated by different methods, which include the use of agronomic characterization and DNA fingerprinting (Helms *et al.*, 1997; Becelaere *et al.*, 2005). One of the most widely used applications of the RAPD technique is the identification of markers linked to traits of interest without the necessity of mapping the entire genome (Bardakci 2001). Molecular markers have been repeatedly applied to study the genetic diversity in faba bean (Zeid *et al.*, 2003). The level of association between agronomic characterization and DNA marker-based genetic similarity may vary among different crop species. In

corn a close association was found (Messmer *et al.*, 1993), but in others such as, wheat, barley, oat and cotton moderate to low associations have been observed (Graner *et al.*, 1994; Kim and Ward 1997; Becelaere *et al.*, 2005). Therefore, it is necessary to determine within each species whether agronomic characterization and DNA marker-based genetic similarity provide similar information about the genetic distance among available germplasm.

The objectives of this work were (1) to study the genetic systems controlling quantitative characters using a diallel cross among six faba bean lines. (2) to apply RAPD technique for the identification of the genetic relationship between these lines and (3) to find out the association between morphological traits and RAPD markers.

Materials and Methods

The present study was carried out at the Experimental Farm, Faculty of Agriculture, Assiut University, Assiut, in the winter seasons of 2005/2006 and 2006/2007. The inheritance studies were carried out using diallel cross analysis among six faba bean breeding lines produced from the general research breeding program of Prof. Dr. Esmat A. Waly and Prof. Dr. Sayed Abas Abdel-Aal (Dept. of Hort., Assiut University), namely: Assiut 174, Golden, Assiut 99, Assiut 12 (Romy), Assiut 195 and Assiut 16. In October 2005, hand emasculation and pollination

were done, hybridization among the six faba bean lines in a diallel pattern (without reciprocals) to obtain all the possible 15 F₁ hybrid seeds. In October 2006, the seeds of 21 entries (6 parents and 15 hybrids) were planted. The material was laid out in three replicates each consisted of 15 plots for the F₁ hybrids and 6 plots for the parents. Each plot consisted of three rows of 12 plants spaced 30 cm with 60 cm between rows. Normal culture practices were applied. The harvesting date was in early April 2007.

Characters measured:

The following characters were measured for 10 plants/plot.

- 1-Plant height (cm)
- 2-Number of branches/plant
- 3-Green (immature) pod length (cm) at the time of green harvest
- 4-Green (immature) pod width (cm) at the time of green harvest
- 5-Number of dry pods /plant
- 6-Weight of dry seeds/plant
- 7-Protein content was determined using micro Kjeldahl methods (A.O.A.C., 1975).

Statistical analysis

A diallel analysis as developed by Hyman (1954a, 1954b, 1957 and 1958) was performed on the collected data. Variance/Covariance (Vr/Wr) graphs were also prepared according to Jinks (1954).

RAPD experiments

Fresh young leaves were harvested from 15-day old seedlings and immediately ground in liquid nitrogen. The total

genomic DNA was extracted using a protocol as described by Poresbski *et al.* (1997). The DNA concentration was estimated by staining DNA with ethidium bromide after electrophoresis in 0.8% agarose mini-gel at 60V for 3 hours in TAE buffer (0.04M Tris-acetate, 0.001M EDTA, pH 8.0). RAPD technique was conducted using 5 arbitrary 10-mer primers (Table 5).

Amplification was carried out in a DNA Thermal Cycler (Techno-412, Germany) according to the methods described by Williams (1990). The RAPD assay was performed in a 25 μ l volume containing 2.5 μ l of 10 \times PCR buffer, 0.5 μ l of dNTPs (PRomyga, Madison, USA) 2 μ l of primer, 0.3 μ l of *Taq* DNA polymerase (PRomyga, Madison, USA), 6 μ l of Mgcl₂ (25mM), 9.7 μ l of sterile ultrapure deionized water and 1 μ l of 100ng DNA template. A negative-DNA control was performed by adding 1 μ l of sterile ultrapure deionized water.

The Thermal Cycler was programmed by an initial denaturation cycle at 90 °C for four minutes. The following 35 cycles were composed of: denaturation step at 90 °C for one minute, annealing step for 1 minute at 33 °C and elongation step at 72 °C for two minutes. The final cycle of polymerization was performed at 72 °C for ten minutes. The amplification products were electrophoresed in a 1.4% agarose gel stained with 0.2 μ l ethidium

bromide. The amplified fragments were visualized using UV trans-illuminator and photographed by Camera digital (Olympus SP-510UZ).

Data analysis

Data analysis on the means of all traits was initially performed based on the Euclidean distance matrix. The hierarchical cluster analysis (Kaufman and Rousseeuw 1990), was used to investigate patterns of phenotypic diversity existing in these parental lines. Group average hierarchical cluster analysis by MVSP (version 3.1) program used to develop a dendrogram.

The DNA banding patterns generated from RAPD analysis were analyzed by a computer program, Gene Profiler (version 4.03). A binary matrix reflecting the presence (1) or absence (0) of each band was generated for each line for the five primers used. Genetic similarities among all lines were computed based on Nei and Li (1979) method. A cluster diagram was constructed based on these similarities by the UPGMA method to develop a dendrogram.

Mantel test (1967) of matrix was applied to compare Euclidean distance and RAPD distance. The correlation between each distance pair using computer program NTSYS-pc Ver 2.1 was calculated.

Results and Discussion

Morphological characters

Plant height means of the sex parents ranged from 77.67 to 116.33 cm with an average of 89.40

cm (Table 1). The hybrid mean plant height exceeded the parental mean by 16.30 cm indicating directional dominance.

The average of number of branches indicated that Assiut 12 gave the highest value 2.92 while, both parents Assiut 174 and Golden gave the lowest values 1.33. The number of branches for F₁ hybrids ranged from 1.50 to 3.03. Hybrid (Assiut 12 x Assiut 16) gave the highest value and Hybrid (Assiut 174 x Assiut 195) gave the lowest value. The hybrid means greater than parent means indicated the presence of heterosis for this trait.

The mean values of green pod length ranged from 7.00 to 10.40 cm and from 7.17 to 9.63 cm for parental lines and hybrids, respectively (Table 1). The highest values for green pod length obtained from Assiut 12 and hybrid (Assiut 99 x Assiut 12). While the lowest values obtained from Golden and hybrid (Assiut 174 x Assiut 16). The hybrid mean was greater than parent mean indicating the presence of heterosis.

Data of green pod width (Table 1) indicated that the average green pod width of the parents ranged from 1.42 to 1.91 cm with an average of 1.54 cm. Assiut12 gave the highest value, while the Golden gave the lowest value. The average of hybrids ranged from 1.41 to 1.82 cm. The hybrid (Assiut174 x Assiut16) gave the lowest value while, hybrid (Assiut12 x Assiut195) gave the highest value.

Results of number of dry pods/plant of the parents and hybrids ranged from 14.11 to 30.00 with an average of 20.27 and from 14 to 41.67 with an average of 29.90, respectively. The Assiut16 gave the highest value, while Assiut12 gave the lowest. Furthermore, Assiut174 produced higher number of pods when compared with the mid-parents value. The highest value obtained from hybrid (Assiut174 x Assiut99) while the lowest value obtained from hybrid (Assiut12 x Assiut195). The differences between the hybrid means and parent means was 9.63, showing the presence of heterosis.

The average of weight of dry seeds/plant are presented in Table 1. Results showed that weight of dry seeds/plant of the parents ranged from 20.00 to 40.25 g with an average of 30.57g. Line Assiut 16 gave the highest value, while Assiut 195 gave the lowest value. Furthermore, Assiut 99 and Assiut 12 produced higher weight of dry seeds/plant when compared with the mid-parents value. Weight of dry seeds/plant for hybrids ranged from 35.00 to 89.44 g with an average 61.55 g. The highest value obtained from hybrid (Assiut 99 x Assiut12) while the lowest value obtained from hybrid (Assiut 12 x Assiut 195). The differences between the hybrid means and parent means was 30.98 g showing the presence of heterosis.

Average of protein content ranged from 23.18 to 31.15 % and

Table(1): The means of the 6 parents (diagonal) and their F₁ hybrids for all studied traits.

The average of plant height (cm)							The average of number of branches						
lines	Assiut 174	Golden	Assiut 99	Assiut 12	Assiut 195	Assiut 16	lines	Assiut 174	Golden	Assiut 99	Assiut 12	Assiut 195	Assiut 16
Assiut 174	116.3	115.5	111.5	125.3	107.0	100.0	Assiut 174	1.33	1.78	2.17	2.83	1.50	2.00
Golden		78.33	105.2	121.2	106.4	105.6	Golden		1.33	1.58	2.33	1.72	1.83
Assiut 99			88.33	109.0	107.3	82.61	Assiut 99			2.00	2.78	2.50	2.55
Assiut 12				81.25	81.00	109.7	Assiut 12				2.92	2.00	3.03
Assiut 195					77.67	97.92	Assiut 195					1.50	2.67
Assiut 16						94.53	Assiut 16						2.47
Parent mean=89.407 Hybrids mean=105.702							Parent mean=1.926 Hybrids mean=2.218						
The average of green pod length (cm)							The average of green pod width (cm)						
lines	Assiut 174	Golden	Assiut 99	Assiut 12	Assiut 195	Assiut 16	lines	Assiut 174	Golden	Assiut 99	Assiut 12	Assiut 195	Assiut 16
Assiut 174	7.09	8.14	7.90	8.53	7.89	7.17	Assiut 174	1.46	1.45	1.55	1.53	1.57	1.30
Golden		7.00	7.82	8.98	8.52	7.31	Golden		1.42	1.50	1.61	1.63	1.41
Assiut 99			7.68	9.63	8.64	8.21	Assiut 99			1.48	1.68	1.58	1.53
Assiut 12				10.40	9.17	9.18	Assiut 12				1.91	1.82	1.62
Assiut 195					7.33	8.68	Assiut 195					1.63	1.51
Assiut 16						7.96	Assiut 16						1.36
Parent mean=7.908 Hybrids mean=8.385							Parent mean=1.543 Hybrids mean=1.552						
The average of number of dry pods/plant							The average of weight of dry seeds/plant						
lines	Assiut 174	Golden	Assiut 99	Assiut 12	Assiut 195	Assiut 16	lines	Assiut 174	Golden	Assiut 99	Assiut 12	Assiut 195	Assiut 16
Assiut 174	23.00	26.53	41.67	40.00	24.33	28.00	Assiut 174	29.00	57.56	71.17	81.00	51.33	45.00
Golden		15.00	22.67	32.36	29.33	27.83	Golden		24.67	49.67	77.92	65.67	53.69
Assiut 99			21.67	30.11	37.50	22.00	Assiut 99			36.00	89.44	64.33	50.28
Assiut 12				14.11	14.00	36.33	Assiut 12				33.53	35.00	70.22
Assiut 195					18.00	30.78	Assiut 195					20.00	61.00
Assiut 16						30.00	Assiut 16						40.25
Parent mean=20.27 Hybrids mean=29.90							Parent mean=30.57 Hybrids mean=61.33						
The average of protein content (%)													
lines	Assiut 174	Golden	Assiut 99	Assiut 12	Assiut 195	Assiut 16							
Assiut 174	31.15	26.22	25.45	27.86	25.55	26.40							
Golden		23.18	29.19	29.53	29.49	27.72							
Assiut 99			26.00	28.18	24.94	31.10							
Assiut 12				26.23	31.66	29.19							
Assiut 195					30.00	26.70							
Assiut 16						25.17							
Parent mean=26.90 Hybrids mean=28.00													

24.94 to 31.66 % for the parental lines and hybrids, respectively. The highest values for protein content obtained from Assiut 174 and hybrid (Assiut 12 x Assiut 195). While the lowest values obtained from parent Golden and hybrid (Assiut 99 x Assiut 195). The hybrid mean was greater than the parental mean indicating the presence of heterosis.

Genetic parameters

The analysis of variance (Table 2) revealed highly significant differences among genotypes for all studied characters except for weight of dry seeds/plant character which was significant.

The diallel analysis of variance (Table 3) showed that both additive "a" and non-additive "b" gene effects were involved in controlling all studied traits. The additive variance (a) was consistently greater than the non-additive (b) variance indicated that the major proportion of the genetic variation for plant height, number of branches, green pod length and green pod width was controlled by additive gene effects. But the value of b item was greater than a item for the other characters indicated that the dominance gene action is the most important effect in controlling differences between parents in these traits.

On partitioning the non-additive effect item "b" into its components, there was significant mean square due to "b1" confirming the presence of heterosis. The "b2" and "b3" items were significant,

indicating unequal distribution of genes among the parents and the superiority of some specific combinations for all characters except for green pod width character, the b_1 item was not significant.

The D value estimating the additive component was smaller than H_1 and H_2 values which estimates dominance (Table 4) confirming that the additive components was more important than dominance for plant height, number of dry pods/plant, weight of dry seeds/plant and protein content characters. But H_1 and H_2 values were larger than D values for the other characters studied.

The ratio $(H_1/D)^{1/2}$ was more than one indicating over-dominance for plant height, number of dry pods/plant, weight of dry seeds/plant and protein content characters.

Broad-sense and narrow-sense heritability values (Table 4) were high for plant height, number of branches, green pod length and green pod width characters indicating that a great proportion of the total phenotypic variation was genetic. Therefore these characters could be improved by crosses and selection. While number of dry pods/plant, weight of dry seeds/plant and protein content characters revealed a high value of broad-sense heritability and low value of narrow-sense heritability indicated that these traits were influenced by environmental factors and dominance effects.

Table(2): Analyses of variance for 7 characters in a 6x6 diallel cross of faba bean.

Item	d.f.	Plant height	Number of branches	Green pod length	Green pod width	number of dry pods/plant	Weight of dry seeds/plant	Protein content
Blocks	2	60.937	0.466	1.909	0.0305	117.734	408.421	0.777
Genotypes	20	969.044**	1.395**	3.446**	0.0913**	390.199**	2126.81*	27.962**
Error	40	97.328	0.275	0.14	0.0016	48.418	333.602	0.372

**Significant at 0.05 probability level

Table(3): The diallel analysis of variance for the seven 7 characters.

Item	d.f.	Plant height	Number of branches	Green pod length	Green pod width	number of dry pods/plant	Weight of dry seeds/plant	Protein content
		MS	MS	MS	MS	MS	MS	MS
a	5	1248.35**	4.016**	10.511**	0.309**	258.815*	960.85*	9.031**
b	15	875.95**	0.522*	1.091**	0.0187**	433.993**	2515.46*	34.271**
b ₁	1	3982.899**	1.279*	3.401**	0.0013	1608.357**	14863.08**	35.082**
b ₂	5	595.387**	0.072*	1.010**	0.0183**	149.434*	1058.709*	65.828**
b ₃	9	686.601**	0.687*	0.88**	0.02083**	461.597**	1952.82*	16.649**
Error	40	97.328	0.257	0.14	0.0016	48.418	333.602	0.372

**Significant at 0.05 probability level

Table(4): Components of the genetic variation for the seven characters.

Item	Plant height	Number of branches	Green pod length	Green pod width	number of dry pods/plant	Weight of dry seeds/plant	Protein content
D	160.261	0.2869	1.535	0.0404	54.024	33.097	9.306
H ₁	567.96	-0.028	0.738	0.0141	248.75	1403.89	36.908
H ₂	475.82	0.062	0.571	0.0106	235.53	1306.3	22.433
F	135.329	-0.192	0.565	0.0098	49.252	98.062	22.86
(H ₁ /D) ^{1/2}	1.88	0.312	0.693	0.59	2.145	6.517	1.991
Heritability in broad-sense	76.14 %	58.8 %	89.8 %	95.5 %	71 %	64 %	96 %
Heritability in narrow-sense	25.00 %	54.4 %	71.7 %	82.5 %	9.4 %	3.5 %	7.3 %

Graphical analysis

The graphical analysis for studied characters is shown in Fig. 1. The regression line coefficient was significantly different from zero but not from unity for all studied characters indicated the existence of non-allelic interaction. The regression line cuts the W_r axis below the origin for plant height, weight of dry seeds and protein content characters indicating the presence of over-dominance. While, the line cuts the W_r in a positive position, showing the presence of partial dominance for the other characters.

The distribution of the parental arrays along the regression line in F_1 hybrids for the studied characters are presented in Fig. 1. Assiut 174 possessed an excess of dominant alleles for green pod length and green pod width characters but possessed an excess of recessive alleles for number of branches, number of dry pods/plant and weight of dry seeds/plant characters. Assiut 99 possessed an excess of dominant alleles for plant height character and possessed an excess of recessive alleles for green pod length and protein content characters. Assiut

12 possessed an excess of dominant alleles for number of branches, number of dry pods/plant and weight of dry seeds/plant characters while, possessed an excess of recessive alleles for plant height and green pod width characters.

The results in our study revealed that the additive and non-additive genetic effects were governing the genetic system of all studied characters. The additive genetic effect was the most important in the inheritance of number of branches, green pod length and green pod width characters. However, the non-additive genetic effect was the most important in the inheritance of plant height, number of dry pods/plant, weight of dry seeds/plant and protein content traits. These findings were in agreement with those reported by many workers such as Waly (1982), Filippetti and Pace (1983), Mitkees and Hassan (1983), Habetinek (1984), Kitiki and Demir (1984), Mahmoud *et al.* (1984), Waly and Abdel-Aal (1986), Bakheit (1992), Kaul and Vaid (1996), Mohamed (1997), El-Hady *et al.* (1998), Yamani (1998) and El Hosary *et al.* (2002).

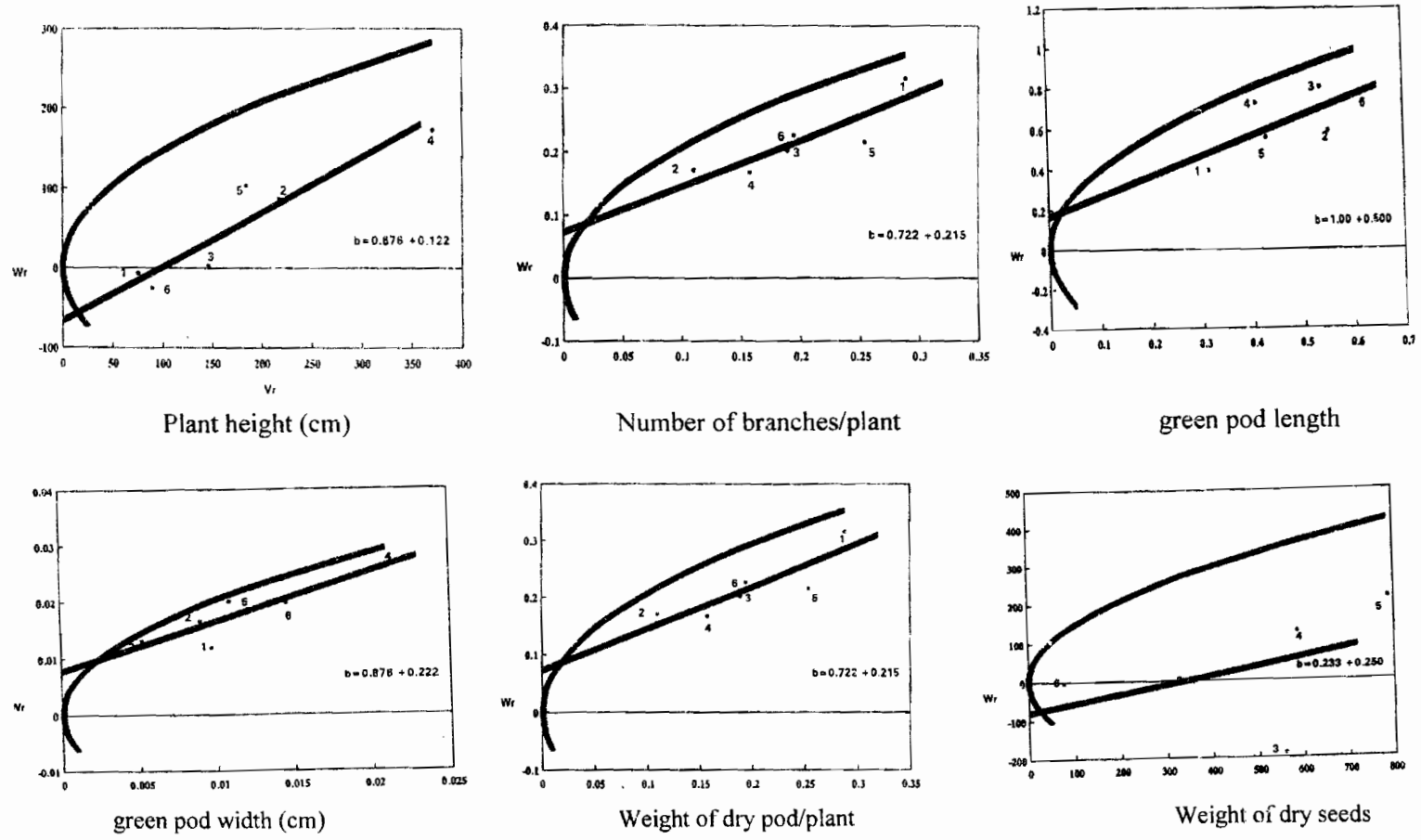


Fig.(1) : W_r, V_r graphs for all characters studied in faba bean.

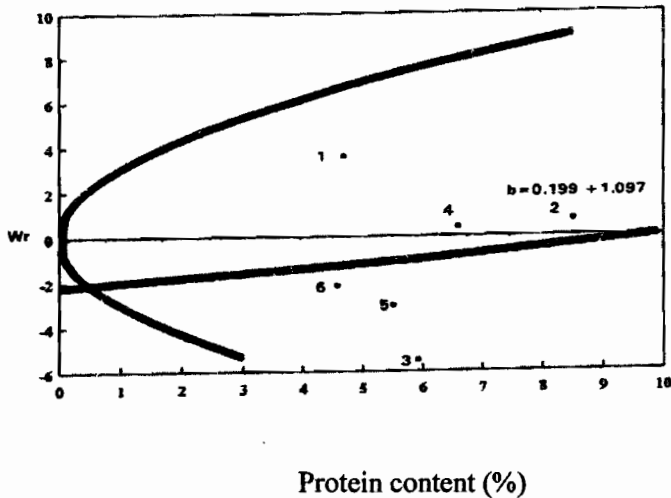


Fig (1) cont: W_r , V_r graphs for all characters studied in faba bean.

Heterosis was present for all characters studied. The results of the ratio of dominance at each loci, revealed that there were over dominance in inheritance of all characters except number of branches, green pod length and green pod width traits. These finding were in agreement with those reported by many workers such as Waly (1982), Mahmoud and Al-Ayobi (1987), E bmeyer (1988), Bargale and Billore (1990), El-Morsy (1990), Bakheit (1992) and Bashoot (2000).

Genetic advance through selection depends on the heritability of the characters in question. Heritability in broad-sense can be defined as being the genetic portion of phenotypic variance. However, the genetic variance includes all types of gene expression (including additive,

dominance, over-dominance and all types of epistasis). Also, heritability in narrow-sense which estimates the proportion of the total genetic variance which due to the fixable additive gene action. However, it must be known that heritability estimates vary greatly not only from one character to another but also within in one character depending on the genotypes of parents.

2-Cluster analysis based on morphological traits

In this study to find out relationship among the 6 parental lines, the Euclidean distance was calculated, it was based on the means of morphological traits. Euclidean distance ranged from 0.88 between Assiut 195 and Golden lines to 4.01 between Assiut 174 and Assiut 195 lines,

with an average 2.3 (Table 6). The range of Euclidean distance among the lines (0.88-4.01) was relatively wide. Also, the average Euclidean distance 2.3 among all lines was also high. Fahmi *et al.* (2004) obtained similar results among 11 Egyptian wheat varieties. Our result indicated that the amount of phenotypic variation among these parental lines was relatively high and reflects the genetic diversity of the genes controlling these characters.

Bootstrap values indicated on the dendrogram (Fig. 3) showed a high genetic variation pattern, where the Assiut 174 line formed one cluster, that were separated from the other of lines at a wide Euclidean distance of 3.45. The other of lines created two clusters at a wide Euclidean distance of 2.24, where the first cluster included Assiut 16 line only. The second cluster sub-divided at 1.6 Euclidean distance and created two sub-clusters. The first sub-cluster included Golden and Assiut 195 lines, which separated at 0.88 Euclidean distance. The second sub-cluster included Assiut 99 and Assiut 12 lines, which separated at 1.11 Euclidean distance (Table 6). The analysis of dendrogram based on morphological traits showed that Assiut 174 and Assiut 16 were the most unique lines. Morphologically these genotypes are different from the other lines and quit distinct from each other in most of characters studied. The dendrogram also revealed that

Assiut 195 and Golden showed morphological diversity less than Assiut 99 and Assiut 12.

Parental lines analyses using RAPD markers

After screening, only five out of twenty 10-mer arbitrary primers produced polymorphic. A total of 77 fragments were generated by the 5 primers with an average of 15.4 fragments per primer (Fig. 2 and Table 5). The number of amplification products by each primer varied from 9 to 22 (Table 5). In order to test the differences of band patterns from different primers among bean parental lines, a similarity matrix was first calculated, based on markers from each primer. It was found, a total of 59 bands were polymorphic across the entire sample with an average of 11.8 fragments per primer. The percentage of polymorphic bands ranged from 23.1 to 95.5 % with an average of 73.06 %.

RAPD similarity of Nei and Li (1979) coefficient matrix for the 6 parental lines was calculated and used for UPGMA cluster analysis (Table 7). The 6 parental lines were separated into two genetically diverted main clusters at 65.5 % level of similarity (Fig. 4). Cluster one contained only two lines Assiut 195 and Assiut 16 at 80.0 % level of similarity. Cluster two contained four lines Assiut 174, Golden, Assiut 49 and Assiut 12, this cluster sub-divided into three sub-groups. The first sub-group contained two

lines Assiut 49 and Assiut 12 at 82.9 % level of similarity. The second sub-group contained Golden line at 74.4 % level of similarity with the first sub-group. The third sub-group contained Assiut 174 line at 69.2.0 % level of similarity with the second sub-group (Fig. 4).

In our study, 77 DNA fragments were amplified with the 6 parental lines of bean, out of them 59 were polymorphic 76.6 %. The genetic similarity ranged from 0.55 to 0.83 between Assiut 174 and Assiut 16, and between Assiut 49 and Assiut 12, respectively. Similar result obtained by Zeid *et al.* (2003) among elite faba bean lines using AFLP markers, where the genetics similarity values of pairs of inbred lines ranged from 0.53 to 0.88.

Correlation between the two distance matrices generated by morphological traits and RAPD marker was calculated (Fig. 5). The correlation between Euclidean distance and RAPD distance was -0.40 ($P = 0.11$). The low association between agronomic traits and RAPDs markers was not surprising since the estimation of genetic relationship among different germplasm based on different approaches. (Schut *et al.*, 1997) reported a correlation of -0.1 for AFLP and agronomic data in Barley varieties. Also, a low

correlation of -0.26 between agronomic traits and RAPD in Hexaploid Wheat was obtained (Fahmi *et al.*, 2004). However, (Autrique *et al* 1996) reported a moderate correlation (0.47) between AFLP and agronomic characters in durum wheat. In commercial bean lines, morphological traits variation might reflect the result of adaptation to different environments. On the other hand, the observed relationships using molecular markers may provide information on the history and biology of cultivars but it does not necessarily reflect what may be observed with respect to agronomic traits (Metais *et al.*, 2000). RAPDs are dispersed throughout the genome and their association with agronomic traits is influenced by selection only in the region under selection pressure. The other loci are subjected to random genetic drift. The agronomic characterization and RAPD based on dendrogram were some what similar, indicating that the agronomic characterization information will continue to be useful to identify diverse germplasm in breeding programs of lupine and/or other species (Abd EL-AGani *et al.*, 2007).

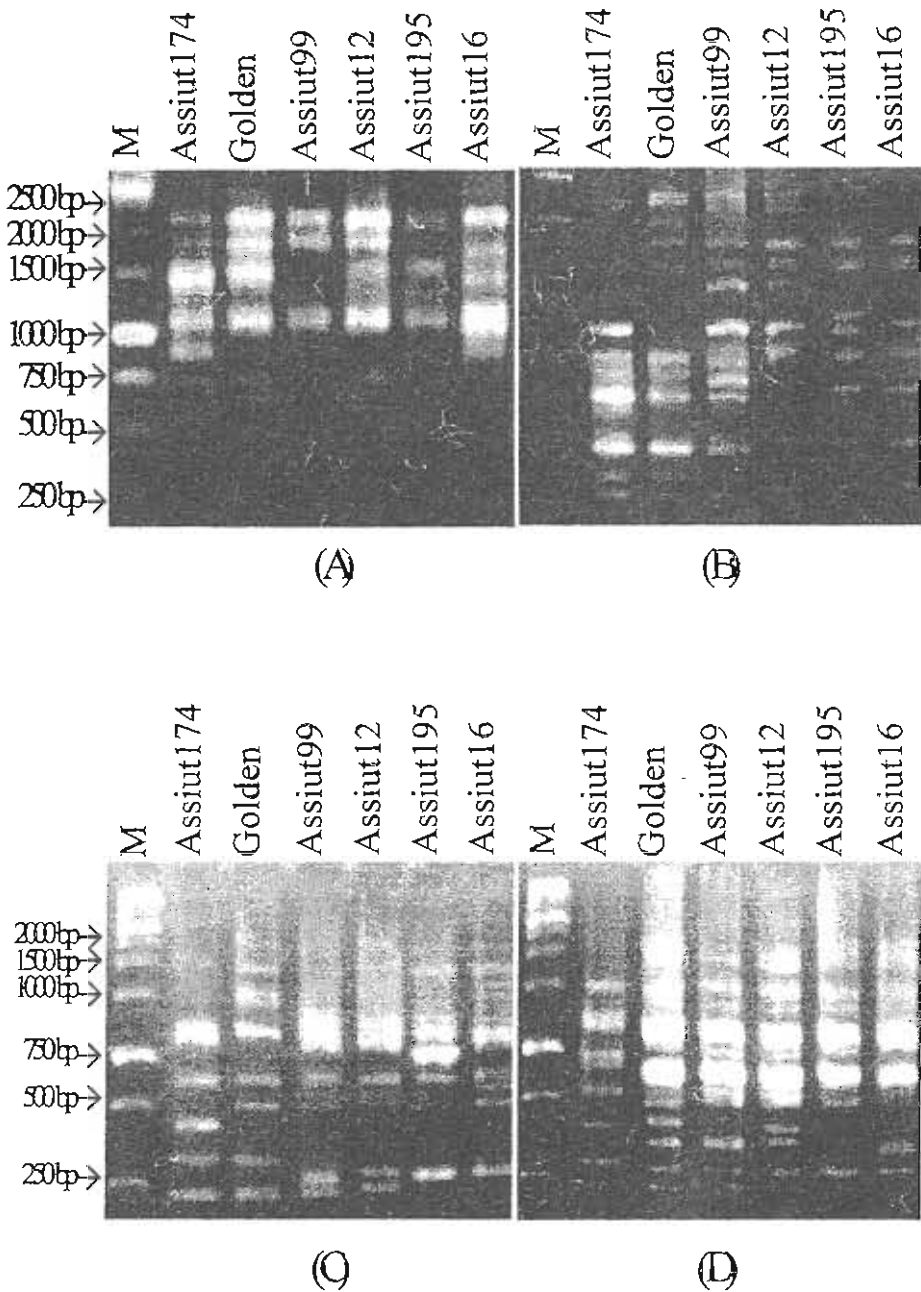


Fig.(2): RAPD profiles obtained for six faba bean lines amplified with primers OPW-15 (A), OPA-8 (B), OPC-7 (C) and OPQ-15 (D), M= 1000 bp ladder size marker.

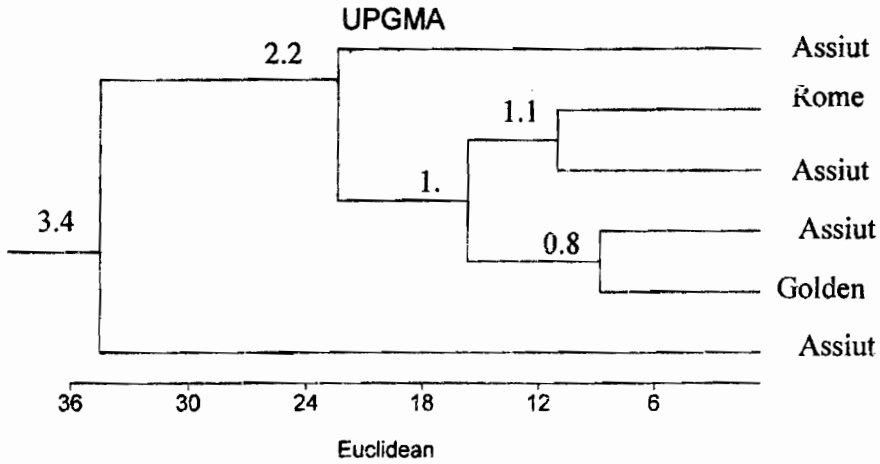


Fig.(3): Dendrogram based on UPGMA cluster analysis showing the genetic distances among parental lines using 7 morphological

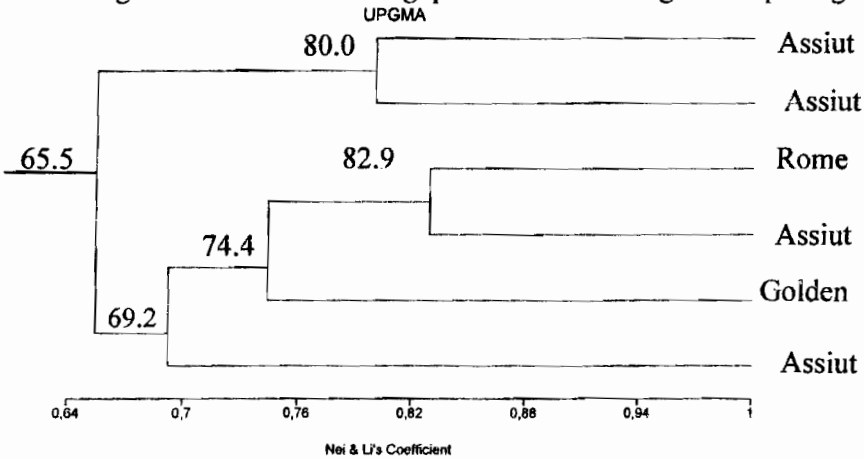


Fig. (4): Dendrogram generated by UPGMA cluster analysis according to Nei & Li's coefficient using 77 RAPD fragments among parental lines.

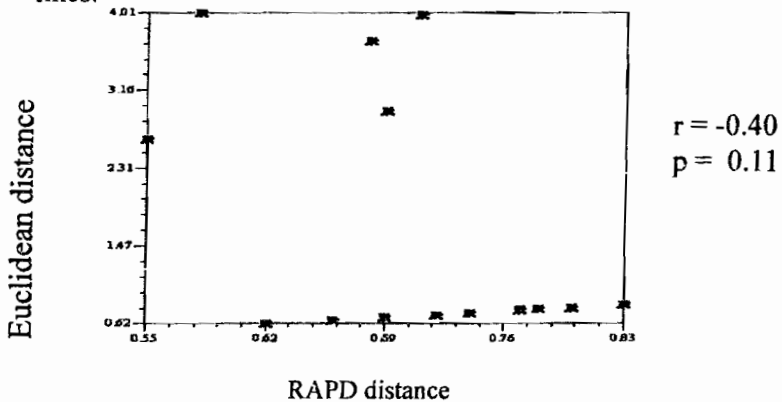


Fig.(5): Correlation between Euclidean distance and RAPD marker.

Table(5): Primers used in RAPD analysis, total number of fragments detected by each primer and polymorphism found among 6 bean lines.

RAPD Primer	Sequence (5'-3')	Amplified bands		Polymorphic bands %
		Polymorphic	Total number of fragments	
OPA-2	TGC CGAGCTG	3	13	23.1%
OPA-8	GTGACGTAGG	16	18	88.9%
OPC-7	GTCCCCGACGA	12	15	80.0%
OPQ-15	GGGTAACGTG	21	22	95.5%
OPW-15	ACACCGGAAC	7	9	77.8%
Total		59	77	
Mean		11.8	15.4	73.06%

Table(6): Euclidean distance matrix of 6 bean lines using averages of 7 morphological traits.

Lines	Assiut 174	Golden	Assiut 99	Assiut 12	Assiut 195	Assiut 16
Assiut 174	0.0					
Golden	3.99	0.0				
Assiut 99	2.94	1.68	0.0			
Assiut 12	3.70	1.06	1.11	0.0		
Assiut 195	4.01	0.88	2.00	1.54	0.0	
Assiut 16	2.63	2.71	1.13	2.20	2.94	0.0

Table(7): Similarity matrix for 6 bean lines according to Nei & li's coefficient obtained from 77 RAPD fragments.

Lines	Assiut 174	Golden	Assiut 99	Assiut 12	Assiut1 95	Assiut1 6
Assiut 174	1.0					
Golden	0.711	1.0				
Assiut 99	0.691	0.719	1.0			
Assiut12	0.675	0.769	0.829	1.0		
Assiut 195	0.582	0.621	0.692	0.775	1.0	
Assiut 16	0.554	0.615	0.659	0.738	0.80	1.0

Results from the marker data presented in this study revealed the presence of broad genetic base of the investigated faba bean germplasm. Although crossing between faba bean germplasm has carried out in the past and is still an ongoing process, a great potential for further cultivar improvement and hybrid production is still available. In conclusion, the agronomic traits and RAPDs markers are useful for classification of germplasm in faba bean, but a combination of different markers is preferred in studying genetic relationships among the lines of same species.

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دراسات وراثية لبعض الصفات المحصولية في الفول البلدى

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أجرى هذا البحث بغرض دراسة النظم الوراثية المتحكمة في تباين بعض الصفات الكمية وفي (طول النبات - عدد الأفرع في النبات - طول القرن الأخضر - عرض القرن الأخضر - عدد القرون الجافة - وزن حبوب النبات الجافة والمحتوى من البروتين) لستة سلالات من الفول البلدى وهي (أسيوط ١٤٧ وجلدن أسيوط ٩٩ و أسيوط ١٢ و أسيوط ١٩٥ و أسيوط ١٦) والهجن الـ ١٥ الناتجة من التهجين الدائرى. وكذلك تحديد العلاقة بين هذه الصفات باستخدام الواسمات الجزئية من نوع البادئات العشوائية على أساس معامل التماثل. وقد أظهرت النتائج وجود تنوع معنوى واسع بين هذه التراكيب الوراثية المستخدمة في كل الصفات المدروسة. كما أظهرت النتائج عن وجود قوة هجين في هذه الصفات. ولقد أوضحت النتائج معنوية كلا من التأثير المضيف والغير مضيف للحين وأتضح أن الجينات السائدة تلعب دورا رئيسيا في التحكم في تباين هذه الصفات. كما أظهرت النتائج أنه يوجد تأثير للسيادة الفائقة بالنسبة لصفات عدد القرون و وزن بذور النبات الجافة و محتوى البروتين. كما أظهر تحليل الدندروجرام على أساس متوسطات الصفات أن الستة سلالات الأبوية تنقسم الى مجموعتين، الأولى تحتوى على سلالة واحدة وهي أسيوط ١٧٤ والثانية تحتوى على باقى السلالات. أما فى تجارب البادئات العشوائية وجد أن ٥ من ١٨ بادئ كانت قادرة على إظهار ٧٧ شظية من الحامض النووى بنسبة تباين ٥٩%. بينما مدى معامل التماثل نى و لى على أساس تجارب الواسمات الجزئية كان من ٠,٥٥ إلى ٠,٨٣. كما أن تحليل شجرة الدندروجرام على أساس الواسمات الجزئية اظهر وجود مجموعتان أساسيتان الأولى تحتوى على سلالتين وهما (أسيوط ١٦ و أسيوط ١٩٥) و الثانية تنقسم الى ثلاثة تحت مجموعة. وأظهر تحليل المسافات البيئية على أن العلاقة بين الصفات المورفولوجية المدروسة و تحليل الواسمات الجزئية كانت غير معنوية.