Genetic Variation Within F_2 Populations for Some Crosses of Broad Bean (*Viciafaba* L.)

A.F. Ibrahim,A.M. El-Gamal* and S.M. Abd-Allah****
[*]Plant Production Department, Faculty of Agriculture (Saba Basha), Alex. University
[**]Horticulture Research Institute, Agriculture Research Center, Egypt

ABSTRACT: The present investigation was carried out during the winter seasons of 2013-2014 and 2014-2015 under field conditions at Sabahya Horticultural Research Station, Alexandria Governorate, Egypt. Plant materials for this study were consisted of 4 parents and 5 second generations, produced from self pollination F_2, from five crosses occurred among four cultivars of broad bean (*Vicia faba* L).The obtained results reflected, generally, all genotypes were showed highly significant differences for all the studied characters. This concept indicated that the evaluated populations differed in their genetic potential with respect to these traits. The mean squares for the parents F_2 and PvsF$_2$were significant for most of the studied characters. The obtained data, showed that the parent p1; gave the highest mean values for the following traits: flowering date (day), plant height (cm), pod length (cm), pod weight (gm, number of seeds/pod and seeds weight per pod (g). Heritability estimates were high in flowering date (days), fruiting date (days), height of the first flowering nod (cm), number of branches / plant, pod weight (gm), number of seeds / pod, seeds weight / pod (gm), number of pods / plant and total seeds yield / plant. The relationships were significant and positive between flowering date and fruiting date (days), height of the first flowering nod (cm), height of the first flowering pod(cm), number of pods / plant, and total fresh yield / plant which affect on total yield of broad bean. Regarding path analysis the direct effect of Flowering date (days) date, height of the first flowering pod (cm), plant height (cm) and number of branches / plant seemed to be close to correlations between them and seed yield so, it may indicate a true relationship and direct selection through these traits may be effective for improving seed yield of faba bean.

Key words: *Viciafaba*L.,F_2 generation, heritability, genetic advance, correlation coefficient and path analysis.

INTRODUCTION

Broad bean (*Vicia faba* L.) is one of the main crops grown for seed in Egypt. It is widely considered as a good source of protein, starch, cellulose and minerals in developing countries and for animals in industrialized countries (Chaieb *et al.*, 2011). In addition, faba bean have bacteria root ganglia which 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 N2-fixation (El-Refaey *et al.*, 2006). Broad bean is a self-pollinating plant with significant levels of outcross and inter-cross, ranging from 20% to 80% depending on genotype and environmental effects. Grain legume crops are important to the economy of Egypt and provide a balanced protein component in the mainly cereal diets of the people (Abd-Allah and Tolba, 2009). Egyptian production of faba bean in 2013 was 192,096tons produced from 138,000hectars as reported by FAO (2013).The promising segregating populations make it possible to select lines with superior performance. Heritability is considered one of the most important estimates to express relative genetic variability whether in broad or narrow senses. Therefore, heritability estimates provide values of relative importance of genetic components to phenotypic variation and is useful in predicting the expected genetic advance from selection in segregating populations. The low heritability and consequent limited genetic advance for yield in response to selection had led many scientists to search for characters which are associated with yield but which are more highly heritable (Cengiz, 2004). 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 broad 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 (Ghareeb and Helal, 2014). Analysis of genetic relationships in crop species is an important component of crop improvement programs, as it provides information about genetic diversity to be used in plant breeding programs (Ullah *et al.*, 2010). Knowledge of genetic variation and relationships between accessions or genotypes is important as it helps to: (1) understand the genetic variability available and its potential use in breeding programs (2) choose genotypes to be given priority for conservation (Toker, 2009). This knowledge is essential and critical importance in establishing managing and ensuring a long – term success of crop improvement programs. The genetic improvement of various traits, which depends on the nature and magnitude of genetic variability, and hybridization, which plays a critical role for obtaining the new recombination and releasing new materials, will help the breeders to identify the best combinations to be crossed and exploit heterosis or build up the favorable fixable genes (Ghareeb and Helal, 2014).The objectives of the present study are to: 1) study the genetic variation inF_2segregated generation of some crosses of broad bean, 2) measure the heritability in the broad and narrow sense, and 3) calculate the correlation coefficients among traits of populations.

MATERIALS AND METHODS

The present investigation was carried out during the winter seasons of 2013-2014 and 2014-2015 under field conditions at Sabahya Horticultural Research Station, Alexandria Governorate, Egypt. Plant materials for this study were consisted of the second generation of five crosses occurred among four cultivars of broad bean (*Viciafaba,* L) produced from self pollination (Abd Allah and Tolba, 2009). The parental cultivars were two Spanish cultivars named as Reina mora (P1) and Luz de otono (P2), one local cultivars named Giza planka (P3), and a selected line Equadols cv. (Sabaaty) [P4], originated from selection and improving of broad bean which was obtained from the local market of Alexandria. The colours of mature seeds of all the studied genotypes are white except that of cultivar "Reina mora" is pink. Seeds of the 4 parental cultivars and five F_2 of crosses (9 entries) were sown on November 5th during 2013-2014 and 2014-2015 winter seasons. The nine entries were, randomly, distributed on a randomized complete blocks design with 3 replicates. The seeds were sown in hills spaced 40 cm apart at the rate of one seed per hill. The other normal agricultural practices for faba bean production, i.e., irrigation, fertilization, weeds and pests control were practiced as recommended in the district.

Recorded measurements

The following traits were determinate as the mean of all plants per entry flowering date and fruiting date (days) were determined as the number of days from sowing to the first flower opening and fruiting set, respectively height of the first both of flowering node and pod (cm) were measured in centimeter, plant height (cm) and number of branches / plant all fresh pods were used from each entry to measure the following pod specifications; pod length (cm), pod width (cm), pod weight (g), net weight % which measured as a ratio between pod weight and seed weight. At harvest, all plants were used from each entry to record the following characters, number of seeds/pod, seeds weight /pod (g), number of pod/plant, total seeds yield (g/plant), dry seeds and total, fresh pods yield (g/plant) fresh seeds. Three random samples, 100 seeds each, were used from each entry for determination of protein content according to AOAC (2000)

Statistical procedures

Data of the studied characters were, statistically, analyzed, using a combined analysis of variance for both evaluated seasons according to Herbert *et al*., (1955). Differences between means measured Duncan multiple range. Heritability in broad sense was calculated as illustrated by Falconer (1989), using the following formula:

$$Heritability\ in\ broad\ sense(H_{bs}^2) = \frac{Genetic\ variance(\sigma_g^2)}{\text{Phenotypic}\ variance(\sigma_{ph}^2)} \times 100$$

The estimates of broad-sense heritability were used to predict effectiveness of selection as genetic advance (G_A) at specific selection intensity (20%) in the four F_2 broad bean populations as illustrated by Falconer(1989) using the following formula:

$$G_A = i\sqrt{\text{Phentypic}\ variance(\sigma_{ph}^2) \times Hritabilityinbroadsense(H_{bs}^2)}$$

Coefficient of variation; whereas, the genotypic and phenotypicco efficient of variation (GCV, PCV) were estimated according to the procedure outlined by Burton (1952) as follows:

$$GCV = \frac{\sqrt{(\sigma_g^2)}}{General\ mean\ (\bar{x})} \times 100\ and\ PCV = \frac{\sqrt{\sigma_{ph}^2}}{General\ mean\ (\bar{x})} \times 100$$

Coefficient of correlation (r) between various pairs of characters (calculated over both evaluated seasons) according to Dospekhove (1984).In the path diagram (Figure 1), the doubled-arrowed lines indicate mutual association as measured by correlation coefficients r_{ij} the single arrowed lines represent direct influence as measured by path-coefficient Pix, and h represents residual factors.

$$P_{16} + r_{12} P_{26} + r_{13} P_{36} + r_{14} P_{46} + r_{15} P_{56} = r_{16}$$
$$r_{12} P_{16} + P_{26} + r_{23} P_{36} + r_{24} P_{46} + r_{25} P_{56} = r_{26}$$
$$r_{31} P_{16} + r_{32} P_{26} + P_{36} + r_{34} P_{46} + r_{35} P_{56} = r_{36}$$
$$r_{41} P_{16} + r_{42} P_{26} + r_{43} P_{36} + P_{46} + r_{45} P_{56} = r_{46}$$
$$r_{51} P_{16} + r_{52} P_{26} + r_{53} P_{36} + r_{54} P_{46} + P_{56} = r_{56}$$

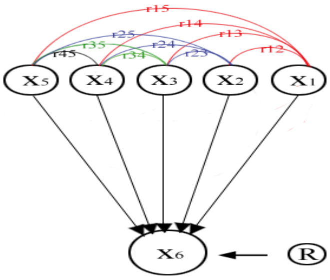

Fig. (1): Path diagram with 5 predictor variables "X_1" to "X_5" and the response variable X_6. The variable "h" is the remainder portion or residual. $(1-R^2)^{½}$

Each normal equation represents a partitioning of correlation coefficient of a predictor variable with the response variable into the component terms, the direct effect or path coefficient for that predictor variable and two indirect effects, each involves the product of a correlation coefficient between two predictor variables and the appropriate path coefficient in accordance with the path diagram.

Table (1): Monthly mean weather data recorded during the experimental period from November 2013 to May 2014 and November 2014 to May 2015 at location of the study according to meteorology unit of Sabahya horticulture research station at Alex. Governorate.

Months		Soil temperature [°C]	Wind speed [m/sec]	Air temperature [°C]		Relative humidity [%]	Dew Point [°C]
				min	max		
2013 - 2014	11/2013	14.7	1.1	14.7	15.8	60.6	6.5
	12/2013	13.8	1.1	13.6	14.7	48.4	4.1
	1/2014	13.4	1	12.8	13.9	72.9	9.9
	2/2014	14.3	1.1	14.5	15.5	73.2	10
	3/2014	16.3	1.3	16.8	17.8	74.6	11
	4/2014	18.4	1.6	18.8	19.6	74.7	13
	5/2014	22.2	1.4	22.6	23.5	79.9	18
2014 - 2015	11/2014	13.4	1.1	13.2	14.5	62.6	5.9
	12/2014	13.4	1.3	13.6	14.4	49.3	3.3
	1/2015	13.3	1.2	12.9	13.9	75.9	8.5
	2/2015	13.6	1.1	13.3	14.4	76.1	9
	3/2015	17.1	1.4	16.1	16.9	77.5	12
	4/2015	20.3	1.7	17.2	18.2	76.7	13
	5/2015	25.1	1.5	21.3	22.2	77.9	17

RESULTS AND DISCUSSION

Data in Table (2) showed that mean squares of both years, were highly significant for flowering date, height of the first flowering nod, height of the first flowering pod, plant height, number of branches / plant, pod weight and number of pods / plant, but seeds weight / pod was significant only, indicating differences between both seasons concerning those traits only. These findings may reflect the more or low, different environment conditions between both years of the study as shown in Table (1). Similar trend, of these results were found by Chaieb *et al*. (2011) significant genotypes' mean squares were detected for all traits. Also significant genotype differences by season interaction mean squares were obtained for height of the first flowering nod, number of branches / plant, pod weight, seeds weight / pod, number of pods / plant and total fresh yield / plant. Sharifi and Aminpana (2014) reported that the tested faba bean genotypes varied from each other and ranked differently from season to another, regarding these traits. The parental cultivars were, significantly, different in all traits (Table 2), indicating the wide diversity between the parental materials used in this study. However F_2' mean squares were found, herein, to be significant for all studied traits. Mean squares for parents *versus* crosses and parents *versus* crosses by season as indicator for average segregations overall F_2crosses were significant for all studied traits (Table 1). In this regard, El-Refaey *et al*. (2006) reported that mean squares of parents *vs.* crosses were highly significant for all seeds yield traits except number of seeds / pod. El-Hosary (1984) found that significant year's means squares were detected for all traits number of seeds / pod. Mean squares for genotypes, parents and hybrids were highly significant for all traits. Significant parents *vs.* hybrids mean squares were shown for all traits. Data in Table (3) showed that the parent P1 followed by F_2 of cross 2×1 were the earliest genotypes for both flowering and fruiting set dates. They gave the lowest more value of height of the first flowering nod and the first flowering pod (cm). Moreover, cultivar Reina morahad the highest mean values for plant height, pod length, pod weight, number of seeds / pod and seeds weight / pod. However, parent P4 scored the highest mean values for number of branches/plant, pod width and number of pods / plant. Parent P2 (cultivar Luz de otono) had the highest mean values for total seeds and fresh yields / plant (g).The results obtained, generally, showed that the estimated coefficient of variation (CV%), variance and somewhat ranges for all studied traits of the derived populations were found to be lower and narrower relative to those of the F_2 populations. Similar trends, more or low of those results of Barri and Shtaya (2013), they reported that the ranges become narrow in parents because the parents more homogeneity and the F_2 population have more segregations which may be the main reason to the coefficient of variation become more.

Table (2). Mean squares for the studied traits of the four parents and five F_2 of some broad bean, calculated from the combined data over both 2013/ 2014 and 2014 / 2015 winter seasons.

S.O.V.	D.F.	Earliness			
		Flowering date (days)	Fruiting date (days)	Height of the first flowering nod (cm)	Height of the first flowering pod (cm)
Blocks	2	55.7	72.2	0.9	8.1
Years(Y)	1	572.6**	1.7	466.0**	1079.8**
Genotypes	8	598.7**	779.0**	368.8**	510.0**
GxY	8	81.2	113.1	35.7*	154.4
Parent(P)	3	730.3**	902.0**	322.6**	409.0**
F_2	4	433.7**	402.9**	357.5**	1186.0**
P vs F_2	1	2003.8**	2380.1**	1234.5**	2134.3**
Error	34	34.2	59.4	12.9	92.8

To be continued

Cont.,

S.O.V.	D.F.	Growth attributes		Characteristics of fresh pods	
		Plant height (cm)	Number of branches / plant	Pod length (cm)	Pod width (cm)
Blocks	2	116.8	1.2	1.6	0.003
Years(Y)	1	4605.3**	17.4**	0.2	0.007
Genotypes	8	1719.3**	43.9**	25.5**	0.232*
GxY	8	595.5	3.2*	6.7	0.040
Parent(P)	3	1922.3**	49.5**	29.4**	0.265**
F_2	4	3739.0**	17.1**	15.6**	0.176**
P vs F_2	1	7970.9**	131.2**	86.3**	0.732**
Error	34	153.2	1.4	4.0	0.045

S.O.V.	D.F.	Fresh yield of pods and its components				
		Pod weight (g)	Net weight (%)	Number of seeds / pod	Number of pods / plant	Total fresh yield of pods/ plant
Blocks	2	0.4	2.6	0.4	14.1	11390.7
Years(Y)	1	156.1**	13.6	0.2	127.5**	6427.9
Genotypes	8	126.5**	55.1**	12.5**	516.4**	170201.6**
G x Y	8	10.3*	9.3	1.3	64.7**	57843.3**
Parent(P)	3	90.8**	40.9**	14.1**	596.1**	214186.8**
F_2	4	149.4**	77.5**	5.5**	288.6**	167577.3**
P vs F_2	1	414.7**	176.1**	36.7**	1591.8**	610260.4**
Error	34	4.2	14.1	1.1	11.9	15487.6

S.O.V.	D.F.	Seed yield and its components		
		Seeds weight / pod(g)	Total seeds yield / plant (g)dry weight	Protein content (%)
Blocks	2	0.2	677.1	7.4
Years(Y)	1	6.5*	2156.7	0.7
Genotypes	8	18.4**	15572.9**	15.9*
G x Y	8	2.8**	1534.1	6.0
Parent(P)	3	14.7**	16887.1**	19.4*
F_2	4	13.3**	10907.4**	16.3*
P vs F_2	1	47.9**	46334.8**	58.9**
Error	34	0.9	1197.1	5.3

*, ** Significant at 5% and 1% levels of probability, respectively.

Table (3). Mean performance, range, coefficient of variation and variance of the studied traits of the four parents and five $F_2$for some crosses of broad bean, calculated from the combined data over both2013 / 2014 and 2014 / 2015 winter seasons.

Genotypes		Earliness															
		Flowering date(days)				Fruiting date (days)				Height of the first flowering nod (cm)				Height of the first flowering pod(cm)			
		Mean	Range	C.V	variance	Mean	Range	C.V	variance	Mean	Range	C.V	variance	Mean	Range	C.V	variance
(Parent)	P1	43.2^{e}	36.0-47.7	12.3	28.4	50.5^{d}	47.0-52.6	4.6	5.4	29.3^{de}	25.6-39.0	17.1	25.0	30.6^{e}	23.7-34.1	13.0	15.8
	P2	63.5^{bcd}	56.4-68.4	7.4	21.98	75.2^{c}	55.4-80.0	12.9	9.76	32.8^{bcd}	31.2-34.1	3.4	1.2	50.3^{abc}	39.8-60.2	13.0	14.00
	P3	70.8^{b}	69.5-72.8	1.7	1.50	83.7^{ab}	81.8-85.7	2.0	2.79	49.8^{a}	47.3-52.5	4.4	4.8	56.3^{a}	51.7-67.5	10.3	33.47
	P4	79.9^{a}	78.6-81.4	1.4	1.23	90.1^{a}	87.6-93.7	2.2	4.07	47.9^{a}	45.3-49.7	3.5	2.9	53.5^{ab}	46.2-60.7	11.3	36.50
(F_2)	1×2	64.9^{bc}	49.8-78.8	15.0	61.09	78.4^{bc}	49.8-92.1	21.0	45.01	35.4^{bc}	29.9-47.3	19.0	36.9	54.7^{ab}	32.5-78.8	30.5	320.57
	2×1	56.8^{d}	46.6-70.3	13.7	35.03	74.1^{c}	46.6-89.0	20.3	35.47	27.3^{e}	19.2-35.0	22.2	45.2	42.8^{bcde}	23.1-70.3	41.6	202.60
	1×3	59.7^{cd}	48.2-77.6	17.3	118.16	75.0^{c}	46.8-83.5	18.8	60.68	31.4^{cde}	27.2-42.6	19.0	57.0	35.2^{de}	29.6-40.9	16.7	292.52
	3×1	64.7^{bc}	46.2-76.9	16.8	107.03	77.1^{c}	46.2-87.2	20.2	197.86	37.3^{b}	29.5-46.2	20.3	35.4	47.8^{abcd}	35.0-76.9	35.1	134.87
	3×4	64.1^{bcd}	45.1-78.5	17.4	124.89	80.4^{ab}	54.1-87.7	16.1	167.39	33.1^{bcd}	29.2-43.8	16.5	29.9	39.0^{cd}	27.4-51.1	27.9	118.77

Genotypes		Growth attributes								Characteristics of fresh pods							
		Plant height (cm)				Number of branches / plant				Pod length (cm)				Pod width (cm)			
		Mean	Range	C.V	variance	Mean	Range	C.V	variance	Mean	Range	C.V	variance	Mean	Range	C.V	variance
(Parent)	P1	141.2^{a}	133.3-150.0	4.7	44.2	5.8^{e}	5.0-6.7	11.0	0.4	19.8^{a}	18.7-20.5	3.1	0.4	1.7^{ab}	1.6-1.9	4.2	0.0
	P2	82.7^{d}	80.0-86.0	3.3	7.30	8.6^{cd}	8.0-9.1	5.8	0.24	15.9^{b}	13.4-17.2	8.2	1.65	1.8^{ab}	1.6-1.8	5.2	0.01
	P3	128.5^{ab}	120.7-136.3	4.2	29.36	12.5^{b}	10.6-14.2	11.6	2.09	14.2^{bc}	12.7-15.9	11.1	2.55	1.2^{c}	1.0-1.7	23.6	0.09
	P4	111.4^{bc}	102.9-120.0	5.7	40.24	15.0^{a}	13.1-16.2	7.3	1.19	12.4^{c}	10.7-15.6	13.7	2.92	1.9^{a}	1.8-2.1	5.0	0.01
(F_2)	1×2	88.4^{cd}	49.8-123.4	33.4	747.21	7.9^{d}	6.0-10.3	19.5	2.99	14.6^{bc}	11.4-17.8	18.4	5.71	1.7^{ab}	1.6-1.8	7.2	0.04
	2×1	92.6^{cd}	46.6-135.0	38.2	250.71	8.8^{cd}	7.3-12.0	19.6	2.34	14.6^{bc}	12.8-19.3	16.4	7.13	1.5^{a}	1.2-1.8	12.9	0.01
	1×3	104.5^{bcd}	90.4-145.0	20.2	396.81	8.9^{cd}	7.1-10.5	19.1	3.27	14.3^{bc}	13.1-19.5	17.6	5.60	1.7^{ab}	1.2-1.9	15.1	0.08
	3×1	87.3^{cd}	46.2-128.3	30.4	446.30	9.8^{c}	6.3-11.0	18.4	2.91	15.8^{b}	11.2-17.9	15.0	6.41	1.7^{ab}	1.2-1.9	16.2	0.07
	3×4	108.6^{bcd}	80.5-137.0	28.3	942.05	8.3^{cd}	5.0-10.5	21.7	3.25	13.6^{bc}	11.8-18.5	18.1	6.15	1.5^{b}	1.0-1.7	16.5	0.06

To be continued

Cont.,

Fresh yield of pods and its components

	Genotypes	Pod weight (g)				Net weight %				Number of seeds / pod				Number of pods / plant				Total fresh yield / plant (g) fresh seeds			
		Mean	Range	C.V	variance	Mean	Range	C.V	variance	Mean	Range	C.V	variance	Mean	Range	C.V	variance	Mean	Range	C.V	variance
(Parent)	P1	24.4^{a}	20.6-26.8	9.5	5.3	29.5^{c}	27.2-31.2	5.7	2.8	8.4^{a}	6.6-9.0	10.7	0.8	12.2^{g}	10.1-14.1	13.5	2.7	227.4^{c}	200.0-270.2	13.2	906.7
	P2	20.6^{b}	17.4-23.5	14.6	8.94	37.6^{a}	37.0-39.4	2.5	0.92	4.9^{bc}	4.4-5.7	10.3	0.26	23.5^{ef}	21.3-24.6	5.5	1.85	876.1^{a}	811.0-979.7	8.5	5510.89
	P3	14.0^{c}	11.3-16.7	14.4	4.07	36.8^{a}	35.6-38.3	2.4	0.79	4.5^{bcd}	4.1-5.7	13.1	0.36	20.9^{f}	17.9-24.6	13.2	7.61	563.3^{b}	500.0-621.2	8.8	2481.75
	P4	12.7^{cd}	12.0-13.4	3.7	0.21	35.9^{a}	32.2-38.9	7.1	6.49	3.3^{d}	3.0-3.9	10.1	0.11	45.4^{a}	43.0-48.6	5.2	5.56	625.6^{b}	582.9-654.8	3.8	569.76
(F_2)	1×2	13.0^{cd}	8.2-17.8	31.3	7.32	30.2^{c}	24.3-39.8	19.8	15.35	5.3^{b}	3.5-7.8	31.2	1.81	28.7^{cd}	26.0-36.0	13.1	111.01	585.3^{b}	505.9-731.8	18.7	45434.74
	2×1	14.4^{c}	10.4-17.3	18.8	16.49	36.0^{a}	28.3-39.6	10.9	35.56	4.6^{bcd}	3.8-7.3	29.1	2.68	30.7^{bc}	18.2-46.9	34.3	14.09	511.2^{b}	312.0-862.2	41.7	11933.75
	1×3	12.1^{cd}	8.3-15.8	31.2	14.88	31.0^{bc}	29.1-38.6	12.1	21.44	3.8^{cd}	3.4-5.6	22.8	2.06	31.6^{bc}	22.5-35.9	14.9	16.35	586.4^{b}	327.9-978.0	45.8	46832.17
	3×1	19.4^{b}	12.6-22.5	19.9	14.22	34.0^{abc}	25.2-37.9	13.6	14.07	5.0^{bc}	4.2-7.9	28.9	0.74	34.3^{b}	26.3-36.9	11.8	22.08	534.1^{b}	302.2-821.0	40.5	72238.66
	3×4	11.0^{d}	9.3-14.8	18.9	4.40	35.2^{ab}	27.3-39.3	11.9	17.27	4.1^{bcd}	3.5-6.1	23.7	0.94	25.4^{de}	19.9-31.80	23.2	34.51	470.1b	346.2-630.0	28.4	17788.81

Seed yield and its components

	Genotypes	Seeds weight / pod (g)				Total seeds yield / plant (g) dray seeds				Protein content %			
		Mean	Range	C.V	variance	Mean	Range	C.V	variance	Mean	Range	C.V	variance
(Parent)	P1	9.6^{a}	8.0-10.7	9.3	5.1	112.6^{e}	101.5-118.7	5.6	39.7	22.39^{c}	20.50-23.30	4.47	1.0
	P2	7.3^{b}	6.2-8.3	14.4	1.09	290.3^{a}	280.4-298.5	2.9	69.81	28.58^{a}	28.00-29.20	1.65	0.22
	P3	5.7^{c}	4.4-6.6	14.3	0.67	179.4^{cd}	171.5-187.4	3.0	28.05	25.89^{ab}	22.80-29.67	8.46	4.85
	P4	3.6^{d}	3.0-4.0	9.5	0.13	161.7^{d}	121.8-180.5	14.3	530.00	25.48^{b}	23.10-29.57	8.68	4.93
(F_2)	1×2	5.1^{c}	3.6-7.8	33.0	1.62	189.9^{cd}	149.8-237.9	16.2	1817.16	24.42^{bc}	20.10-28.83	12.48	6.81
	2×1	5.2^{c}	3.9-7.3	24.0	2.86	176.5^{cd}	124.0-246.6	24.1	945.98	25.32^{bc}	20.29-27.20	10.31	9.25
	1×3	5.3^{c}	4.4-7.5	22.1	2.48	213.2^{bc}	120.5-232.8	21.3	4670.88	24.62^{bc}	20.80-29.20	10.98	1.73
	3×1	6.9^{b}	4.2-8.0	23.0	1.37	248.6^{b}	146.2-298.4	27.5	2061.79	24.74^{bc}	22.90-29.86	10.41	7.31
	3×4	4.7^{cd}	3.9-6.7	22.2	1.08	195.0cd	134.3-235.0	17.3	1134.04	25.55b	21.30-28.60	10.88	7.72

*Means with the same alphabetical litter in the column are not significantly different from each other using Duncan's Multiple Range Test at 5% probability.

Genotypic and phenotypic variance' values presented in Table (4) revealed that the large portion of genotypic variance for flowering date, fruiting date, height of the first flowering nod, plant height, number of branches / plant, pod width, pod weight, number of seeds / pod, seeds weight / pod, number of pods / plant and total seeds yield / plant. The coefficient of genotypic (GCV) and phenotypic (PCV) variability may serve as a reference point for breeders who try to detect genotypic difference of the most important economic characters. It, also, makes selection of forms with valuable genotypes more effective (Abd El-Salam and Marie 2002). Values of genotypic and phenotypic coefficient of variances (GCV and PCV) showed that the characters: flowering date, fruiting date, height of the first flowering nod, number of branches / plant, pod weight, number of seeds / pod, seeds weight / pod, number of pods / plant, and total seeds yield / plant, demonstrated low differences between values of both GCV and PCV. The differences between GCV and PCV were large for the rest of other studied characters, indicating that these characters are affected by the environmental conditions. The same trend, more or low, of these results was found by Ghareeb and Helal (2014), who found that values of (GCV) and (PCV) were, nearly, equal to flowering date, fruiting date, height of the first flowering node. Differences between (GCV) and (PCV) values were low for height of the first flowering pod and plant height. Mohamed and Abd-El-haleem (2011) found that characters which expressed nearly equal values for GCV and PCV: plant length, flowering and pod width. On the other hand, the differences between GCV and PCV values were low for net weight and protein content, and they, also, reported that these results make selection for quantitative characters more effective owing to these characters were large dependent on ratio between the levels of the genotypic and phenotypic variability within the population. So, the characters which have equal or approximate ratio for GCV and PCV values, the selection would be effective.

Heritability percentage (h^2%)in the broad sense is presented in Table (3) specifies the proportion of the total variability that is due to genetic variance, were high for flowering date, fruiting date, height of the first flowering nod, number of branches / plant, pod weight, number of seeds / pod, seeds weight/ pod, number of pods/ plant and total seeds yield / plant. Moderate values for pod length, pod width and total fresh yield / plant, while low values were noticed in the rest of characters. Similar results were found by many researchers as Mohamed and Abd-El-haleem (2011) and Soleiman and Ragheb (2014), who found high heritability values for number of branches / plant, pod weight and total seeds yield / plant. Cengiz (2004) found high broad-sense heritability in net weight and moderate values in flowering date, fruiting date and height of the first flowering nod and reported that the low broad-sense heritability may be reflect the high effect of the environmental conditions. The results of Prakash and Ram (2014) illustrated that the highest values of heritability were number of seeds / pod, seeds weight / pod and total yield / plant. However, it should be mentioned that in stating any value of heritability of a character, it must be related to the particular population in which it was estimated and under what particular condition, as illustrated. So, it can be concluded from data that the character which possessed high broad sense heritability combined with relatively high ratio for genetic coefficient of variability and genetic advance might be rapidly improved by selection (Ibrahim, 2012).

Table (4).Values of genotypic and phenotypic (GCV & PCV), heritability and genetic advance over two years of the study (2013/2014 and 2014/2015 winter seasons).

Traits	Coefficient of variability		Heritability, %	Genetic Advance
	GCV	PCV		
Flowering date(days)	7.6	10.1	55.9	972.0
Fruiting date (days)	6.9	8.9	60.3	1145.0
Height of the first flowering nod (cm)	10.5	13.6	60.4	810.5
Height of the first flowering pod(cm)	8.6	16.0	28.7	577.0
Plant height (cm)	6.3	11.6	29.4	1039.5
Number of branches / plant	14.0	16.4	72.9	311.2
Pod length (cm)	6.0	9.5	40.4	157.7
Pod width (cm)	5.5	8.4	43.2	16.5
Pod weight (g)	14.2	18.0	62.5	487.3
Net weight (%)	4.1	6.8	37.5	236.7
Number of seeds / pod	14.3	18.1	62.5	151.4
Seeds weight / pod(g)	13.9	17.8	60.7	175.9
Number of pods / plant	15.7	18.8	70.3	1018.4
Total seeds yield / plant (g)DW	12.5	15.7	63.7	5405.6
Total seeds yield / plant (g)FW	12.6	19.8	40.3	12167.2
Protein content (%)	2.6	5.3	23.6	87.2

Correlation values among pairs of characters for all cross combinations are illustrated in Table (5). Flowering date (days) showed a significant positive correlation with fruiting date, height of the first flowering nod, height of the first flowering pod, number of pods / plant, and total fresh yield / plant. On the other hand, pod length, net weight, number of seeds/ pod, and seeds weight/ pod exhibited significant negative correlation with flowering date. Meanwhile, fruiting date exhibited significant positive correlation with height of the first flowering pod, number of branches, number of pods / plant, and total fresh yield / plant, and negative correlation with pod length, pod weight, number of seeds / pod, and seeds weight / pod. Height of the first flowering node showed positive correlation with height of the first flowering pod. Height of the first flowering pod explained positive correlation with number total fresh yield / plant. Plant height (cm) exhibited significant negative correlation with number of branches / plant, total seeds yield / plant, total fresh yield / plant and protein content %. Number of branches / plant exhibited significant positive correlation with number of pods / plant, total fresh and seeds yields / plant and negative correlation with pod length, number of seeds / pod and seeds weight / pod. However, Pod length showed positive correlation with pod weight, number of seeds / pod and seeds weight / pod and significant negative with number of pods / plant. Pod weight showed significant positive correlation with number of seeds / pod and seeds weight / pod. Total fresh yield / plant, exhibited significant positive correlation with pod weight, number of pods / plant and total seeds yield / plant and significant negative correlation with number of seeds / pod. Protein content (%) showed significant positive correlation with net weight %, total fresh and seed yields / plant. Number of seeds / pod showed significant negative correlation with seeds weight / pod, number of pods / plant, total fresh and seed yields / plant. Number of seeds/pod and pod length with pod weights which were significant positive correlated. These findings may suggest that number of pods/plant and pod weight showed to be the first concern for improving yield of faba bean. In this regard, Ulukan *et al.* (2003) stated that positive and significant relationships were determinate statistically between pod length and plant height, between first pod height and plant height, between pod number/plant and plant height, between pod number and 1st pod height, between grain number and first pod height, between biological yield and pod length,and between biological yield and first pod height. Similar, more or less, results were obtained by Gyanendra *et al*. (1993) and Chaieb *et al*. (2011).It could be noted that, from Table (6), the direct effect of flowering date, height of the first flowering pod, plant height and number of branches / plant seemed to be close to correlations between them and seed yield. Results indicate a true relationship and direct selection through these traits may be effective for improving seed yield of faba bean. It worth mentioning that the residual effect for seed yield/plot was low. Such result indicated that this character may depend on the most of the studied traits, thus, it may not be needed to investigate more attributes affecting seed yield in faba bean. Ulukan *et al*. (2003) reported that grain number pod could be a useful selection criterion because jointed or bilateral relations with this character have been given almost biggest value. Kuraczyk *et al*. (1989) indicated that seed yield structure was studied by path analysis of 18 yield characteristics of faba bean varieties, number of pods/ plant and number of seeds from the main stem in var. major had the most significant effect on seed yield. Katiyar and Singh (1990) stated that in 40 indigenous and exotic strains positive and significant association among grain yield and number of pods/ plant.

Table (5). Correlation coefficient values (r) for pair of characters of the studied traits of broad bean combined analysis over two seasons

Traits	Flowering date(days)	Fruiting Date (days)	Height of the first flowering nod (cm)	Height of the first flowering pod(cm)	Plant Height (cm)	Number of branches / plant	Pod Length (cm)	Pod Width (cm)	Pod Weight (g)	Net Weight (%)	Number of seeds / pod	Seeds weight / pod (g)	Number of pods/plant	Total seeds yield / plant (g) dry	Total seeds yield / plant (g) fresh
Fruiting date (days)	0.85**														
Height of the first flowering nod (cm)	0.81**	0.57													
Height of the first flowering pod(cm)	0.73*	0.78**	0.72**												
Plant height (cm)	-0.31	-0.41	0.23	-0.23											
Number of branches / plant	0.57	0.73*	0.10	0.39	-0.79**										
Pod length (cm)	-0.83**	-0.92**	-0.49	-0.53	0.38	-0.68*									
Pod width (cm)	-0.01	-0.11	-0.20	-0.16	-0.29	0.09	0.12								
Pod weight (g)	-0.55	-0.75**	-0.29	-0.26	0.15	-0.50	0.90**	0.26							
Net weight (%)	0.64*	0.48	0.40	0.51	-0.50	0.42	-0.48	-0.30	-0.17						
Number of seeds / pod	-0.83**	-0.86**	-0.43	-0.46	0.55	-0.79**	0.96**	0.05	0.81**	-0.55					
Seeds weight / pod(g)	-0.74*	-0.87**	-0.42	-0.44	0.28	-0.59*	0.98**	0.07	0.94**	-0.35	0.90**				
Number of pods / plant	0.71*	0.74*	0.35	0.41	-0.46	0.71*	-0.74*	0.46	-0.53	0.25	-0.76**	-0.75**			
Total seeds yield / plant (g) dry	0.28	0.33	-0.07	0.34	-0.87**	0.70*	-0.21	0.12	0.02	0.43	-0.61*	-0.04	0.20		
Total seeds yield / plant (g)fresh	0.58*	0.58*	0.24	0.61*	-0.79**	0.59*	-0.50	0.15	-0.21	0.58*	-0.61*	-0.36	0.59*	0.80**	
Protein content (%)	0.54	0.47	0.21	0.52	-0.75**	0.49	-0.44	-0.10	-0.16	0.83**	-0.55	-0.28	0.19	0.75**	0.90**

* ** Significant at 5% and 1% levels of probability, respectively.

Table (6).Direct effects (Diagonal, under line) and indirect effects of some studied traits onseed yieldof broad bean genotypes.

Character	Flowering date (days)	Fruiting date (days)	Height of the first flowering pod(cm)	Plant height (cm)	Number of branches / plant	Total effect
Flowering date (days)	0.2729	0.0994	0.2306	0.3351	-0.3580	**0.5800**
Fruiting date (days)	0.2320	0.1170	0.2464	0.4432	-0.4585	**0.5800**
Height of the first flowering pod(cm)	0.1992	0.0912	0.3159	0.2486	-0.2450	**0.6100**
Plant height (cm)	-0.0846	-0.0480	-0.0727	-1.0810	0.4962	**-0.7900**
Number of branches / plant	0.1556	0.0854	0.1232	0.8540	-0.6281	**0.5900**

Residual effect = 0.3127

REFERENCES

Abd- Allah, S. A. M. and M. H. Tolba (2009). Genetic studies on growth, earliness yield and its components, and seed quality in broad bean (*Viciafaba* L.). 1.J. Agric. Sci. Mansoura Univ., Egypt .34(4):3349-3366.

Abd-El-Salam, M.M.M and R. Marie. (2002). Genetically studies for improvement of fruit quality and yield of sweet melon (Ismaellawy). J. Agric. Sci. Mansoura. Univ., 27(11):7583-7593.

AOAC, (2000). Association of Official Analytical Chemistry.Official method of analysis (AOAC).International, 17thedition.Mary land. USA.

Barri, T. and M. Shtaya, (2013). Phenotypic Characterization of Faba Bean (*Viciafaba*L.)Landraces Grown in Palestine. J. of Agric. Sci., 5(2): 110-117.

Burton, G.W. (1952). Quantitative inheritance in grass.Proceeding of the 6 international grassland congress. Pennsylvania, U.S.A. : 217-283.

Cengiz ,T. (2004). Estimates of broad-sense heritability for seed yield and yield criteria in faba bean (Viciafaba L.). Hereditas, 140: 222-225.

Chaieb, N., M. Mouslama and M. Mars. (2011). Growth and yield parameters variability among faba bean (*Viciafaba*L.) Genotypes, J. Nat. Prod. Plant Resour., 1 (2): 81-90.

Dospekhov, P.A. (1984). Field experimentations.StatisticalProcedurs, Mir bublifhebro Moscow, pp. 349.

El-Hosary, A.A. (1984). Heterosis and combining ability in diallel crosses among seven varieties of faba bean. Pl genet&breed., 9(1-2): 17-28.

El-Refaey, R. A., M. S. El-Keredy, M. A.El-Hity and G. G. A. Zied, (2006). Estimation of heterosis and combining ability in faba bean under two plant population densities. II - Yield and some of its components. Annals of Agricultural Science, Moshtohor,33(2): 157–167

Falconer, D.S. (1989). Introduction to quantitative genetics.third edition, Longman, New York, U.S.A.

FAO (2013). Egyptian production of broad bean, (www.FAO.com).

Gyanendra. S., K.R. Dhuman, and S. Major (1993). Variability, correlation and path analysis in broad bean, Int. J. Trop. Agric., 11: 36-39.

Ghareeb E. Z. and A.G. Helal. (2014). Diallel analysis and separation of genetic variance components in eight faba bean genotypes. Annals of Agric.l Sci., 59(1): 147–154.

Herbert, W.J., H.F. Robinson and R.E. Comstock. (1955). Estimates of genetic and environmental variability in soybeans. Agron. J., 47: 314-318.

Ibrahim, E. A. (2012). Variability, heritability and genetic advance in Egyptian Sweet melon (*Cucumismelo* Var. *Egyptiacus*, L.) under water streesconditions.International J. Pl. Breed.&Genet., 6(4): 238.

Kuraczyk, A., M. Idzkowska, J. Golaszewski and I. Koczowska, (1989). Path coefficient studies for yield and yield componenb in faba bean (Viciafabci L.), In Proc. of the Synip. Biological Progress and the Effectiveness of Crop Plant Production, 11-12 January, Radzikow, Poland, pp: 1 -7.

Katiyar.R.P. and A.K. Singh. (1990). Path coefficient studies for yield and yield components in faba bean (*Viciafaba* L.), Fabis News, 26: 3-5.

Mohamed, G. I. A. and S. H. M. Abd-El-Haleem (2011). Pedigree selection in two segregating populations of Faba Bean (Viciafaba L.)I- Agro-Morphological traits.World J. of Agric. Sci., 7(6): 785-791.

Sharifi, P. and H. Aminpana, (2014). A study on the genetic variation in some of faba bean genotypes using multivariate statistical techniques. Trop. Agric. (Trinidad), 91 (2): 87-97.

Prakash, J. and R.B. Ram. (2014). Genetic variability, correlation and path analysis for seed yield and yield related traits in french bean (Phaseolus vulgaris L.) under Lucknow conditions. Internat J. Innovative Sci., Eng. & Tech.,1. (6): 41-50.

Soleiman, T. H. I. and E. I. M. Ragheb (2014). Two selection method and estimation of some important genetic parameters in Broad Bean (*ViciaFaba*, L.). Asian J. of Crop Sci., 6(1): 38-48.

Toker, G. (2009). Estimates of broad-sense heritability for seed yield and yield criteria in faba bean (Viciafaba L.). Hereditas, 140 (3): 222–225.

Ulukan, H., M. Gű̃lar and S. Keskin. (2003). A Path Coefficient Analysis Some Yield and Yield Components in Faba Bean (*Viciafaba* L.)Genotypes.Pakistan J. Biol. Sci., 6(23): 1951-1955.

Ullah, H.,I. H. Khalil, D. A. Lightfoot and R. H. Iltafullah, (2010). Estimation of genetic divergence among elite mungbean (*Vignaradiata*) genotypes by RAPD analysis.Biological Diversity Conserv.(BioDiCon), 3(1): 75-82.

الملخـص العربــى

التباينات الوراثية داخل عشائر الجيل الثاني لبعض الهجن من الفول الرومى

عادل فهمى إبراهيم[**]، أحمد محمود الجمل[*] و سامح محمد عبد الله[**]
[*] قسم الانتاج النباتى- كلية الزراعة سابا باشا- جامعة الاسكندرية
[**] معهد بحوث البساتين – مركز البحوث الزراعية – مصر

أجريت هذه الدراسة خلال الموسمين الشتويين لعامى ٢٠١٣/٢٠١٤ ، ٢٠١٤/٢٠١٥ بمزرعة بحوث بساتين الصبحية بالإسكندرية، مركز البحوث الزراعية. وأستخدمت التراكيب الوراثية الناتجه من الجيل الثاني الناتج من التلقيح الذاتي لخمس هجن تم الحصول عليها من التهجين بين ٤ سلالات من الفول الرومي . توضح نتائج تحليل التباين وجود اختلافات معنوية مابين التراكيب الوراثية بالنسبة لكل الصفات المدروسة مما يوضح مدي الاختلاف الوراثي بين هذه التراكيب الوراثية.أيضا توضح نتائج تحليل التباين لكلا من الاباء والجيل الثاني والتداخل بينهما وجود اختلافات معنوية فيما بينهم بالنسبة لكل الصفات المدروسة ، ايضا توضح النتائج أن الاب الاول (Reina mora (P1)) اعطي اعلي القيم بالنسبة لصفات ميعاد الازهار ، ارتفاع النبات ، طول وعرض القرن وعدد ووزن البذور في القرن. بالنسبه لقيم درجة التوريث كانت عاليه فى صفات تاريخ التزهير و تاريخ العقد وارتفاع أول عقده زهريه وعدد الفروع و وزن القرن و عدد البذور للقرن ووزن البذور للقرن و عدد القرون للنبات و المحصول البذرى للنبات (جاف). بالنسبه لأهم علاقات الارتباط كانت معنويه وايجابيه بين تاريخ التزهير وكل من تاريخ العقد و ارتفاع اول عقده زهريه وارتفاع اول عقده ثمريه و عدد القرون للنبات و المحصول الكلى. فيما يخص تحليل معامل المرور العلاقات المباشره لكل من تاريخ الإزهار و ارتفاع أول عقده زهريه وطول النبات و عدد الأفرع للنبات و قريبه فى قيمها من قيم الأرتباط مما يشير إلى تأثير هذه الصفات تأثيرا مباشرا على المحصول الكلى لنبات الفول الرومى وهذه الصفات لها تأثير كبير على المحصول الكلى عند الأنتخاب لها.