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STATISTICAL AND GENETICAL ANALYSIS FOR SOME EARLY SEGREGATING POPULATIONS IN FABA BEAN

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ABSTRACT

Eight F_2 faba bean populations and their seven parental varieties were evaluated at Sids Research station, Beni Sueif Governorate, Egypt during 2010/2011-2012/2013 under the insect free cage during three successive seasons. The present work aimed to estimate some genetic parameters as (heritability and genetic advance) through variance and its components, correlation coefficients and prediction equations of full model and stepwise regression and factor analysis for yield and some of its components.

Highly significant variation was noted for all the studied traits. Misr1 had the highest parental values for traits seed yield per plant, number of seeds per plant and number of pods per plant among seven parents. Meanwhile, F_2 populations recorded the highest values than parental ones for traits number of pods per plant, number of seeds per plant and seed yield per plant. Results also, showed that hybrids had the highest mean performance, and the selection prospects within this parents and its F_2 genotypes can be used to improve the performance through breeding program.

Higher estimates of heritability coupled genetic advance were observed for seed yield per plant, number of seeds per plant and number of pods per plant. This indicating that these characters are mainly controlled by additive genes and selection of such traits may be effective for the improvement of seed yield. All the studied traits exhibited positive and highly significant

genotypic correlation with seed yield except hundred seed weight that showed negative and insignificant one.

Results showed that full model regression including all traits recorded 95.4%, while stepwise regression recorded 91.9% for number of seeds per plant only, and 97.5 for number of seeds per plant and hundred seed weight. Factor analysis showed that factor one had four variables (number of branches per plant, number of pods per plant, number of seeds per plant and seed yield). These traits could be used for the improvement of seed yield and evolution of high yielding studied populations of faba bean.

INTRODUCTION

Faba bean (*Vicia faba* L.) is an important legume crop in Egypt and in other countries of the world, due to high nutritive value for both human and livestock. Its seeds exhibit high levels of protein 28-36% of seed dry matter) and are, therefore, potential protein source for animal nutrition (Duc *et al.,* 1995). It has been classified botanically on the basis of seed shape and weight into three commonly recognized categories; minor, equina and major. The minor and equina groups comprise small and medium seeded varieties, respectively, while the major group comprises large seeded varieties (Witcombe, 1982). Great genetic variation between groups as well as within groups exists and intercrossing can be occurred freely. The success of an autogamous plant-breeding program depends on the choice of populations capable of producing progeny with desired trait combinations. The promising segregating populations make it possible to select lines with superior performance. Careless choice can cause resource and time loss. Procedures making possible early detection of unpromising populations have been the target of many investigators (Oliveira *et al.,* 1996). Seed yield is a complex trait that is quantitatively inherited with low heritability value (Yassin, 1973). The low heritability and consequent limited genetic advance for yield through selection had led many scientists to search for characters which are associated with yield but which are more highly heritable (De Pace, 1979).

Since genotypic and environmental factors determining yield and quality in plants, a primary aim should be determination of effect of

genotypic factors in selection. As the effect of environment on yield and quality in plants is not hereditable, effects of genotypic factors on yield and quality in plant breeding research need to be examined.

Seed yield is a complex character which is determined by some yield components which exhibited highly correlated with each others. Selection is an integral part of a breeding program by which genotypes with high productivity in a given environment could be developed. However, selection of high yielding genotypes is more difficult because its components have several characters, which are polygenic in inheritance and thus are highly influenced by environment. Therefore, only little progress could be made over along span of time through direct selection for yield (Tadesse *et. al.* 2011). The improvement of faba bean (*Vicia faba* L.) production is focused on increasing both seed yield and its components

Different statistical techniques have been used in modeling crops yield, including correlation and regression analysis. These are an important statistical procedure to evaluate breeding programs for high yield. Moreover, full model regression is used to determine the best predictive equation for yield. Factor analysis has been widely used to identify growth and plant characters related to faba bean.

The aim of this study were, 1) estimate some genetic parameters (PCV, GCV, $h_b{}^2$ and GA) and correlation between the main characters and their influence in faba bean selection. 2) Find out the nature of multiple and stepwise regression, and factor analysis. 3) In addition, using some statistical procedures to identify growth and plant characters related to faba bean, and determine the predictive equation for yield.

MATERIALS AND METHODS

Seven faba bean genotypes (Giza 843, Giza 716, Nubaria 1, Misr 1, Sakha 1, X -1671 and X -1881) along with eight F_2's population resulted from these genotypes were evaluated. The origin and characteristics of these genotypes are shown in Table 1 and Table 2.

Table 1:Origin, Pedigree and special characteristics of seven faba bean parental genotypes.

Genotype	Origin	Pedigree	Seed type	Characteristics
Giza 843	*FCRI, ARC, Egypt	561/2076/85 × 461/845/83	Equina	Resistant to *Orobanche* and foliar diseases,
Giza 716		461/843/83 × 503/453/84	Equina	Resistant to foliar diseases and early maturing.
Nubaria 1		Single plant selection from Giza Blanca	Major	Recommended for planting in newly reclaimed lands and resistant to foliar diseases.
Misr 1		Derived from Giza3 × 123A/45/76	Equina	Tolerant to *Orobanche*
Sakha 1		716/724/88 × 620/283/85	Equina	Resistant to foliar diseases
X -1671		Giza667 × Composite16	Equina	Tolerant to *Orobanche*
X -1881		(Giza40×Misr2) × Giza461	Equina	Tolerant to *Orobanche*

*FCRI: Field crops Res. Institute

Table 2:List of the eight F_2 faba bean populations.

Populations	Code	Parents
1	X -2078	G843*x-1617
2	X -2079	Misr 1*x-1881
3	X -2081	Sakha 1*x-1881
4	X -2084	Sakha 1*Misr1
5	X -2085	Nubaria1*Misr1
6	X -2089	G716*G843
7	X -2090	Nubaria1*Sakha1
8	X -2091	G843*Sakha1

The seven genotypes and their F_2 populations were evaluated during (2012/2013) season in a randomized complete block design with three replications in single row plot 3m long with 60 cm apart (approx.10 seeds/row), at Sids Research station, Beni Sueif Governorate, Egypt. Twenty plants for parents and 149 plants for F_2 populations were random selected to study, plant height (P.H) ,

number of branches (bra.), number of pods per plant (pods/pl.) , number of seeds per pod(s/p), number of seeds per plant (seeds/pl.), hundred seed weight, (100-s.w.) and seed yield per plant (yield/pl.).

*Statistical analysis:-

The analysis of variance was carried out to test the significance for studied traits. Mean comparisons for these traits were done according to Duncan's Multiple Range Test at P $\leq$ 0.05 **Duncan (1955).**

Multiple linear regression analysis and partial coefficient of determination (R^2) was estimated to evaluate the relative contribution and to develop the prediction model for grain yield (Y) according to the formula Snedecor and Cochran, (1981):

$$Y = a + b_1X_1 + b_2X_2 + b_3X_3 + \dots\dots + b b_n X_n$$

Moreover, stepwise multiple linear regression procedure was used according to Draper and Smith (1966) to determine the variable accounting for the majority of total yield variability.

Breeding value of the material was evaluated by estimate some genetic parameters, according to the methods used by Johnson *et al.* (1955) and Kumar *et al.* (1985). The phenotypic (*PCV %*) and genotypic (*GCV %*) coefficients of variation were estimated as a percentage of their corresponding phenotypic (V_{ph}) and genotypic (V_g) standard deviations to the trait grand mean. Heritability in broad sense (h_b^2) and expected genetic advance (*GA*) as percent of the mean assuming selection of the superior 5% of the genotypes were estimated in accordance with the methods illustrated by Fehr (1987). Genotypic correlation coefficient was calculated between all possible pairs combinations of traits based upon the method proposed by Falconer (1989).

Genetic variance = V_g = (MSG - MSE)/r

Phenotypic variance = V_{ph} = MSG/r

Phenotypic standard deviation (*PCV %*) = $\sqrt{Vph}$ / $\bar{x}$ * 100

Genotypic standard deviation (*GCV %*) = $\sqrt{Vg}$ / $\bar{x}$ * 100

Heritability (h_b^2) = V_g / V_{ph}

Genetic advance (*GA*) = k * V_{ph} * h_b^2

Genetic advance percent of population mean (*GA* %) = *GA* / x̄ * 100

Where, MSG and MSE: are genotypic and error mean squares, respectively from analysis of variance, r: is the number of replications x̄ is population mean and k: is constant = 2.06 at 5% selection intensity.

The factor analysis method reduces the large number of correlated variables to number of clusters called factors (Cattell, 1965). After extraction, the matrix of factor loading was submitted to a varimax orthogonal rotation, as applied by Kaiser (1958). The array of communality, the amount of variance of a variable accounted by the common factors together was estimated by the highest correlation coefficient in each array as suggested by Seiller and Stafford (1985).

RESULTS AND DISCUSSION
* Genotypes' mean performance:

As shown in Table 3, highly significant differences were detected among the investigated generation and their respective parents. Data revealed that the X -1881 possessed the tallest plants (104.96 cm) and Nubaria 1 had the highest estimates of branches (5.79) and 100-seed weight (118.04). Meanwhile, Misr 1 showed the highest values for number of pods, seeds and seed yield per plant and recorded 23.85, 71.51 and 59.15g, respectively.
Difference (Duncan, 1955).

All F_2 populations possessed the highest values for number of pods, seeds per pod, seeds/plant and seed yield per plant and recorded values higher than those in the parental populations. From the above-mentioned results, it could be concluded that the selection prospects within this parents and its F_2 genotypes can be used to improve the performance through breeding program.

Table 3: Mean performance of studied traits for seven faba bean genotypes and their F_2's genotypes.

Genotype	Traits						
	PH	bra/pl	p/pl	s/p	s/pl	100-sw	y/pl
Parents: 1- G 843	92.06^{de}	5.16^{bcde}	18.79^{ef}	3.03^{de}	56.93^{d}	87.34^{def}	48.51^{d}
2- G 716	92.7^{de}	4.19^{e}	16.35^{fg}	2.83^{ef}	46.1^{de}	92.38^{cde}	41.78^{d}
3- X -1671	86.31^{ef}	4.73^{de}	13.90^{g}	2.56^{g}	35.5^{ef}	84.52^{def}	29.21^{e}
4- X -1881	104.96^{abc}	4.56^{e}	20.01^{def}	2.73^{fg}	54.24^{d}	79.61^{f}	42.15^{d}
5- Nubaria 1	93.57^{de}	5.79^{abcd}	12.57^{gh}	3.06^{cde}	38.43^{ef}	118.04^{a}	43.10^{d}
6- Misr 1	99.01^{bcd}	4.61^{e}	23.85^{bcd}	3.00^{de}	71.51^{c}	82.06^{ef}	59.15^{c}
7- Sakha 1	79.01^{f}	2.60^{f}	9.60^{h}	3.10^{bcd}	29.73^{f}	101.82^{bc}	28.59^{e}
F_2 populations: x-2078	111.17^{a}	5.30^{abcde}	29.84^{a}	3.33^{ab}	99.62^{a}	78.44^{f}	77.19^{b}
x-2079	110.79^{a}	6.30^{a}	28.06^{ab}	3.41^{a}	95.56^{ab}	83.14^{def}	78.97^{b}
x-2081	106.85^{ab}	6.19^{ab}	31.60^{a}	3.35^{ab}	105.77^{a}	89.15^{def}	94.02^{a}
x-2084	99.67^{bcd}	5.07^{bcde}	28.13^{ab}	3.34^{ab}	94.27^{ab}	84.08^{def}	78.20^{b}
x-2085	99.58^{bcd}	6.08^{abc}	24.87^{bc}	3.37^{ab}	83.71^{bc}	93.89^{cd}	77.29^{b}
x-2089	93.33^{de}	5.00^{cde}	25.27^{bc}	3.11^{bcd}	78.60^{c}	108.45^{b}	81.93^{b}
x-2090	89.44^{de}	5.28^{abcde}	22.83^{cde}	3.31^{abc}	75.11^{c}	107.21^{b}	79.61^{b}
x-2091	95.65^{cde}	5.31^{abcde}	27.17^{abc}	3.40^{a}	92.28^{ab}	85.91^{def}	78.21^{b}

plant height (PH) , number of branches (bra), number of pods per plant (p/pl) , number of seeds per pod(s/p), number of seeds per plant (s/pl), hundred seed weight, (100-sw) and seed yield per plant (y/pl.).

* Means followed by the same letter (s) are not significantly differed by the least significant

*Genetic parameter:

Highly significant differences were observed for all the traits. This considerable variability provides a good chance of improvement in studied faba bean populations. In general, phenotypic coefficient of variability (*PCV %*) was higher than corresponding genotypic coefficient of variability (*GCV %*) for all the traits which demonstrated the effect of environment upon the traits (Table 4). The highest phenotypic and genotypic coefficient of variability were recorded for number of seed per plant (35.4 and 69.83%), seed yield (34.12 and 67.57 %), number of pods per plant (29.62 and 57.29%) and hundred seed weight (12.47 and 23.04%), respectively. This

indicates the presence of exploitable genetic variability for these traits. Heritability (h^2 %) estimates were generally high for most studied traits and recorded values from 92.41% for number of seed per plant to 68.54% for number of branches per plant. In general, the traits as number of seed, seed yield, number of pods per plant and hundred seed weight had higher heritable values. Hence it can be assumed that phenotypes of almost all the traits are mainly determined by their genotypes. High estimates of heritability indicated that selection based on mean would be successful in improving these traits (Attia, 2007 and El-Hady *et al.* 2009).

Table4: Genetic parameter for seed yield and some yield characters in *Vicia faba* L. in all studied populations.

Characters	V_{ph}	V_g	GCV%	PCV%	$h^2{}_b$	GA	GA%
Plant height	101.66	70.68	8.67	14.90	69.52	14.44	14.90
Branches/plant	1.08	0.74	0.35	0.60	68.54	1.46	0.60
Pods/plant	49.00	43.20	29.62	57.29	88.16	12.71	57.29
Seeds/Pod	0.08	0.06	8.01	14.23	74.37	0.45	14.23
Seeds/plant	679.18	622.71	35.40	69.83	91.69	49.22	69.83
100-seed weight	162.52	130.82	12.47	23.04	80.49	21.14	23.04
Seed yield/plant	492.65	455.24	34.12	67.57	92.41	42.25	67.57

V_{ph} = Phenotypic variance, V_g = Genotypic variance, PCV% = Phenotypic coefficient of variability, GCV% = Genotypic coefficient of variability, h^2 = heritability, G.A= Genetic advance and G.A% = Expected genetic advance as mean percent.

Higher estimates of genetic advance were observed for number of seeds per plant (69.83%), seed yield per plant (67.57%) number of pods per plant (57.29%) and hundred seed weight (23.04%). High heritability values coupled with high genetic advance were observed for all last traits. From the results it can be concluded that all these traits are controlled by additive type of gene action as reported by other workers. Similar results were also obtained by Alghamdi (2007 and El-Hady *et al.* (2009) who reported high heritability coupled with high genetic advance for most of the quantitative characters. Improvement in all these traits (number of seeds per plant, seed yield per plant, number of pods per plant and hundred seed weight) can be achieved through mass selection. But plant height and number of

branches per plant showed low heritability and low genetic advance, indicating limited scope improvement of these traits by selection.

*Correlation studies:

The estimates of genotypic correlation coefficients for all comparisons among the studied traits are presented in Table 5. Hundred seed weight had negative and significant genotypic correlation with plant height ($r = - 0.590^{**}$), number of pods per plant ($r = - 0.448^{**}$) and number of seeds per plant ($r = - 0.372^{**}$). Significant positive correlation values were detected between seed yield per plant and each of plant height ($r = 0.640^{**}$), number of branches ($r = 0.746^{**}$), number of pods per plant($r = 0.933^{**}$), number of seeds per pod ($r = 0.871^{**}$) and number of seeds per plant ($r = 0.955^{**}$) at the genotypic level. Similar results were observed by Ulukan *et al.* (2003), Alghamdi (2007) and Tadesse *et al.* (2011). These findings indicate that indirect selection for each or both of plant height, number of branches, number of pods per plant, number of seeds per pod and number of seeds per plant would be accompanied by high yielding and more effective for the improvement of seed yield in faba bean.

Table 5: Estimates of genotypic (g) correlation coefficient of yield and yield components traits in *Vicia faba* L. in all studied populations (n = 289).

Characters	Plant height	Branches /plant	Pods/ plant	Seeds/ Pod	Seeds/ plant	100-seed weight	Seed yield /plant
Plant height	1.00	0.791**	0.822**	0.500**	0.794**	- 0.590**	0.640**
Branches/plant		1.00	0.724**	0.519**	0.719**	- 0.043	0.746**
Pods/plant			1.00	0.752**	0.970**	- 0.448**	0.913**
Seeds/Pod				1.00	0.830**	0.084	0.871**
Seeds/plant					1.00	- 0.372**	0.935**
100-seed weight						1.00	- 0.099
Seed yield/plant							1.00

*, ** and ns indicates significant, highly significant and insignificant at the 0.05 and 0.01 level of probability

*Multiple and stepwise regression analysis

Data presented in **Table 6** shows regression coefficients and the probability of the estimated variables in predicting seed yield/plant. The obtained results showed that the prediction equation for seed yield/plant ($\hat{Y}$) is formulated using the faba bean variables as follows:

- Seed yield /plant:

Yield = - 58.3 - 0.024 Plant height + 0.064 branches/ plant + 0.835^{**} pods/ plant + 5.730^{**} seed/pod + 0.619^{**} seed/plant + 0.464^{**} Hundred seed weight.

Table 6: The regression coefficient (b), standard error (SE) and t value in predicting faba bean seed yield by the multiple linear regression analysis.

Variables	Regression coefficient (b)	Standard error	t
Plant height	-0.02439	0.02666	0.91
Branches/plant	0.0636	0.1995	0.32
Pods/plant	0.8345^{**}	0.2574	3.24
Seeds/Pod	5.734^{**}	1.540	3.72
Seeds/plant	0.61874^{**}	0.07747	7.99
100-seed weight	0.46358^{**}	0.01858	24.95
Intercept= - 58.31, R^2 = 95.4%, Adjusted R^2 = 95.3%			

*, ** and ns indicates significant, highly significant and insignificant at the 0.05 and 0.01 level of probability.
ns = insignificant   * = significant   ** = highly significant

The seed yield formula explains 95.4% of the total variation within the studied traits, while the remaining 4.6% maybe due to residual effects. The t-test showed that number of pods per plant, number of seeds per pod, number of seeds per plant and hundred seed weight have contributed significantly towards seed yield, while the other two variables did not. The results reflect the importance of the mentioned commensurate four variables in seed yield selection in programs. These findings are in agreement with the results obtained by ALbayrak and Tongel (2006) in *Vicia sativa* L..

Stepwise multiple regression analysis showed that 97.5% of total variation in seed yield could be explained by the variation in number

of seeds per plant and hundred seed weight (**Table 7**). From these results it could be concluded that the number of seeds per plant and hundred seed weight was the most suitable inputs to the model of prediction equation for seed yield/plant ($\hat{Y}$) which formulated as follows:

Yield = - 40.296 + 1.032** seed/plant + 0.346** Hundred seed weight.

ALbayrak and Tongel (2006),reported that using simple correlations and stepwise regression, the pods per plant was the most important selection traits to increase seed yield in a *Vicia sativa* L.

Table 7: Stepwise regression method of relative proportion of yield components in faba bean

Independent variable	intercept	Regression coefficient		Accumulative partial R-Square
		b1	b2	
No. of seeds per plant	7.875	0.919**		0.919
Hundred seed weight	- 40.296	1.032**	0.346**	0.975

** Significant at 1% of probability levels.

* Factor analysis

Data in Table (8) show that three main factors (groups) were accounted for 78.9% of the total variability in the dependent structure. The first factor (group) included number of branches per plant, number of pods per plant, number of seeds per plant and seed yield, which accounted for 40.1% of the total variability in the dependent structure. The second factor included plant height and hundred seed weight which accounted for 23.1% of the total variability in the dependent structure. The third factor included number of seeds per pod only which represented 15.7% of the total variability in the dependence structure.

Table 8: Rotated (Varimax rotation) factor loadings and communalities for the estimated variables of faba bean.

Variable	Loading	Communality	Latent roots	Factor variance (%)
Factor1:			**2.805**	**40.1**
Branches/plant	**0.620**	**0.415**		
Pods/plant	0.859	0.945		
Seeds/plant	0.857	0.959		
Seed yield/plant	0.924	0.923		
Factor2:			1.620	23.1
Plant height	0.665	0.523		
100-seed weight	- 0.868	0.763		
Factor3:			1.099	15.7
Seeds/Pod	0. 987	0.995		
Cumulative variance				78.9

According to the multiple statistical procedures used in this study it could be concluded that the number of pods per plant, number of seeds per pod, number of seeds per plant and hundred seed weight were the most important yield variables to be considered. This was relatively clear with another statistical procedure (Factor analysis). Thus, high yield of faba bean can possibly be obtained by selecting breeding materials with high productive number of seeds per plant.

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التحليل الاحصائى والوراثي لبعض عشائر الفول البلدي الانعزالية في الأجيال المبكرة

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*المعمل المركزي لبحوث التصميم والتحليل الاحصائى – مركز البحوث الزراعية- الجيزة - مصر

**قسم بحوث المحاصيل البقولية- معهد بحوث المحاصيل الحقلية

مركز البحوث الزراعية-الجيزة– مصر

أجريت هذه الدراسة خلال الثلاث مواسم ٢٠١٠/٢٠١١ – ٢٠١٢/٢٠١٣ بمحطة البحوث الزراعية بسدس محافظة بني سويف تحت الصوبة السلكية في تصميم القطاعات الكاملة العشوائية في ثلاث مكررات بهدف التقييم الوراثي لثمانية عشائر هجينية في الجيل الثاني بين سبعة أصناف أبوية من الفول البلدي. وكان الهدف هو تقدير بعض المقاييس الوراثية (كفاءة التوريث بالمعنى العام، معدل التحسين الوراثي المتوقع) من خلال التباين ومكوناته، والعلاقة بين المحصول و ستة من مكوناته باستخدام معامل الارتباط الوراثي ، ومعادلات التنبؤ بالمحصول للنموذج الكامل للانحدار للصفات المدروسة ،والتحليل العاملى وذلك لتحديد أكثر الصفات تأثيرا فى المحصول.

وقد أوضحت النتائج وجود اختلافات معنوية كبيرة بين التراكيب الوراثية فى العشائر تحت الدراسة مما يدل على وجود تباين وراثى واسع ،وقد سجل الصنف مصر١ قيما عالية لصفات عدد القرون/النبات، عدد البذور/النبات، ووزن محصول النبات خلال السبعة آباء. بينما سجلت الهجن الثمانية تفوقا أعلى من الآباء لنفس الصفات (عدد القرون/النبات، عدد البذور/النبات، ووزن محصول النبات)، مما يدل على تفوق الهجن وأهمية استخدامها في برامج التربية .

لوحظ أيضا اقتران كفاءة التوريث العالية مع معدل التحسين الوراثي المتوقع العالى لصفات وزن محصول النبات، عدد البذور/النبات، عدد القرون/النبات مما يدل

على أهمية التأثير الوراثى (المضيف) مما يدل على إمكانية تحسين هذه الصفات فى الفول البلدى بالانتخاب. كما وجدت علاقة ارتباط معنوية موجبة لجميع الصفات تحت الدراسة عدا صفة وزن ١٠٠- بذرة التى أظهرت ارتباط غير معنوي سالب.

وقد أوضحت نتائج تحليل الانحدار الكلى أن معامل التقدير سجل ٩٥,٤% ،بينما تحليل الانحدار المرحلى سجل ٩١,٩% لصفة عدد البذور/النبات ، و٩٧,٥ لصفتى عدد البذور/النبات ووزن ١٠٠- بذرة ، وبناء عليه يمكن الاعتماد على هاتين الصفتين فى زيادة محصول البذرة. وقد حدد التحليل العاملي أكثر الصفات أهمية وتأثيرا فى المحصول فكان لعدد الأفرع/النبات وعدد القرون/النبات، وعدد البذور/النبات ومحصول البذور/النبات هى الأكثر أهمية حيث تقع جميعا فى العامل الأول. وعليه يجب أخذ هذه الصفات فى الاعتبار عند تنفيذ برامج التربية لتحسين انتاجية الفول البلدى بالانتخاب لهذه الصفات.