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RESPONSE TO SELECTION FOR SEED YIELD AND ITS .COMPONENTS IN FABA BEAN (*Vicia Faba L.*)

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ABSTRACT

Two populations of faba bean (*Vicia faba L.*) derived from the crosses of Giza٤٢٩ x Misr١ (population I) and Giza٤٢٩ x Assiut ٢١٥ (population II) were made for selection by two methods, i.e. pedigree selection (PSM) and bulk selection (BSM) from $F_{٣}$ to $F_{٥}$ generation. The selection criteria were number of pods/plant (PP), seed index (SI) and seed yield/plant (SYP). Results revealed highly significant differences among genotypes (selected families, parents, bulk population and checks varieties) for $F_{٤}$ and $F_{٥}$ generations in the two populations. For two selection methods, $F_{٥}$ progenies had the highest means for all traits of the two crosses except for days to maturity compared to $F_{٣}$ progenies. The mean values for days to maturity, plant height, number of branches/plant, number of pods/plant, ١٠٠-seed weight and seed yield/plant in population I and II were higher by PSM than BSM. Therefore, PSM was found to be the best method for faba bean breeding for higher yield compared to the other method. The results also indicated that pedigree selection decreased the genetic variability measured as a genotypic coefficient of variability of the selection criterion and other studied traits after two cycles of selection in both populations. Correlation study for $F_{٥}$ indicated that, seed yield/plant was positive correlated with plant height, number of branches/plant, number of pods/plant and ١٠٠-seed

weight, when the selection criteria was number of pods/plant (PP), seed index (SI) and seed yield/plant (SYP).

INTRODUCTION

Faba bean *(Vicia faba L.)* is an important source of protein for human and animal nutrition. Moreover, as other seed legumes, faba bean provides nitrogen fixation and has a major role in crop rotations in many regions of the world (Alan and Ceren, ٢٠٠٥). In case of crop rotation, faba bean legume improves soil fertility and reduces weeds, diseases and pests (Mwanam wenge et al.,١٩٨٨).

The total cultivated area and yield for dry seed of faba bean in Egypt is ٧٧٣١١ hectare (١٨٤٠٠٠ Fadden) produced ٢٣٣٥٢٣ tones (F.A.O ٢٠١٠). In Egypt, there is little possibility of increasing the cultivated area, therefore it is important to obtained higher-yielding varieties through breeding programs. Plant breeders are continuously searching for more effective and efficient selection procedure for crop improvement. Numerous procedures have been proposed but only a few valid comparisons have been made between alternative procedures. Pedigree and early generation seed yield testing methods are described in most plant breeding texts. These breeding procedures take advantage of the rapid fixation of favorable alleles through selection (Shalaby et al., ٢٠٠١, Yamani ٢٠٠٣ and Ahmed et al., ٢٠٠٨). The objective of this work was to study, the efficiency of pedigree selection for number of pods/plant, ١٠٠-seed weight and seed yield improving seed yield and its components in two populations of faba bean.

MATERIALS AND METHODS

The present investigation was carried out at Faculty of Agriculture, Al-Azhar University Experimental Farm (Assiut Branch) during the period of ٢٠٠٨/٢٠٠٩, ٢٠٠٩/٢٠١٠ and ٢٠١٠/٢٠١١ growing seasons. The main objective of this study was to compare the relative efficiency of two selection procedures i.e. pedigree and bulk selection for improving seed yield and its components in faba bean *(Vicia faba L).* The breeding material used in this study was ١٢٠٠ $F_{٣}$- families traced back to random $F_{٢}$ plants from two crosses Giza٤٢٩xMisr١ (population I) and (P١XP٢) (population II) the parents (P١XP٢) were obtained from legume crops selection, Field Crops Research Institute, Agriculture Research Center, Giza. Egypt. While, Assiut ٢١٥: a breeding line in the ninth generation, provided by prof. Dr. E. A. Waly, Horticultural Dep. Faculty of Agriculture Assiut University.

Experiments Layout:

In ٢٠٠٨/٢٠٠٩ season, ١٢٠٠ individual $F_{٣}$ plants of the two populations were grown in a breeding nursery in non – replicated rows of ٣ meters long ٦٠cm between rows and ٢٠cm between hills. A total of ١٨٠ plants were selected for three characters, number of pods/plant, seed index and seed yield/plant

In the ٢٠٠٩/٢٠١٠ growing season, the ١٨٠ F٤ plants which were selected from each population with the original parents, $F_{٤}$- bulk random sample (a mixture of equal number of seed from each plant) grown in a randomized complete block design of three replications. Each plot was single rows ٣m long, ٦٠cm apart and ٢٠cm between hills. The beast ٢٧ plants from the beast ١٨٠ families of both populations for each of the selection criteria i.e number of pods/plant, seed index and seed yield/plant were saved to give the $F_{٥}$ families

In ٢٠١٠/٢٠١١ season, ٢٧ $F_{٤}$ families which were selected from each of selection criteria as well as $F_{٥}$ bulk sample, with the parents and the two checks cultivars Giza ٤٠ (chek١) and Giza ٦٧٤ (chek٢) were sown at ٢٠$^{th.}$ of October in a randomized complete block design with three replications. Each family was single row ٣m long, ٦٠cm between rows and ٢٠cm between hills. Recommended cultural practices for faba bean production were adopted throughout the growing seasons. The following traits were measured on ten random plants from each family, parent, bulk, and chick, days to maturity, plant height, number of branches/plant, number of pods/plant, ١٠٠-seed weight and seed yield/plant.

Statistical Analysis:

For each season, estimates of phenotypic and genotypic variance, as well as heritability estimates were calculated from E.M.S of variance components of the selected families as presented in table (٢)

Table ١: The analysis of variance and expected mean squares.

Source of variance	D.F	M.S	E.M.S
Replications	r-١	$M_٣$	$\boldsymbol{\sigma^{٢}e+g\sigma^{٢}\, r}$
Genotypes	g-١	$M_٢$	$\boldsymbol{\sigma^{٢}e+r\sigma^{٢}g}$
Error	(r-١)(g-١)	$M_١$	$\boldsymbol{\sigma^{٢}e}$

Where: r and g = number of replications and genotypes, respectively.

$\sigma^{٢}e$ and $\sigma^{٢}g$ = error variance and genetic variance, respectively.

The phenotypic ($\sigma^{٢}p$) and genotypic ($\sigma^{٢}g$) variance as given by Al-Jibouri et al., (١٩٥٨)

Heritability the broad sense was estimated from the analysis of variance.

The genotypic variance $\sigma^{٢}g = M_٢ - M_١/r$

The phenotypic variance $\sigma^{٢}p = \sigma^{٢}g+\sigma^{٢}e/r$

Heritability in broad sense "H" = $(\sigma^{٢}g/\sigma^{٢}p)$ x١٠٠.

The phenotypic (p.c.v%) and genotypic (g.c.v%) coefficient of variability were calculated as $(\sigma p/ \bar{x})١٠٠$ and $(\sigma g/\bar{x})١٠٠$ respectively.

Correlations among studied attributes:

The statistical analysis was carried out as illustrated by Steel and Torrie (١٩٨٠), Phenotypic and genotypic correlations coefficients were calculated as described by Johnson et al. (١٩٥٥), as follows:

Phenotypic correlation $rp_{xy} = Covp_{xy} / (\sigma p_{xy}.\ \sigma p_{xy})$ and genotypic correlation $rg_{xy} = Covg_{xy}/ (\sigma g_{x}.\ \sigma g_{y})$.

RESULTS AND DISCUSSION

Two cycles of pedigree selection were achieved in two faba bean populations *(Vicia faba L)* stemmed from a crosses between Giza٤٢٩/Misr١ (population I) and Giza٤٢٩/Assiut ٢١٥ (population II) in the $F_{٣}$, $F_{٤}$ and $F_{٥}$ generations. Direct pedigree selection for number of pods/plant, seed index and seed yield/plant were applied.

Description of the base population ($F_{٣}$ generation).

Means and variance of the characteristics of the individual plants in the $F_{٣}$ generation of the two populations are presented in Table (٢) the two base populations used in this study consisted of ١٢٠٠ $F_{٣}$ families for each population traced beck to random sample from $F_{٢}$ single plants originated from the crossing of Giza٤٢٩/Misr١ and Giza٤٢٩/Assiut ٢١٥. All traits in the $F_{٣}$ generation showed wide rang of variability in both populations. Days to maturity ranged from ١٣٥.٥ to ١٧٢.٣ with an average ١٧٠ days and $\sigma^{٢}$ph ٩٥٠.٥٠ and C.V% ١٨.٢٠٪ in population I. As well as it ranged from١٣٤.٦ to ١٧٥.٢ days with an average of ١٧١.٣ days and $\sigma^{٢}$ph ١١٥٢.٤٨ and C.V% ١٩.٨٢٪ in population II. With respect to number of pod/plant, it was ranged from ٤.٠ to ٣.٦ with an average of ٣.٧ and $\sigma^{٢}$ph ٠.٢٧ as well as C.V% ١٣.٩٣٪ in population I. But, it was ranged from ٤.٥ to ٣.٨ with an average of ٤.٠ and $\sigma^{٢}$ph ٠.٢٤ as well as C.V% ١٢.١٦٪ in population II. The plant height was ranged from ١٢٣.٤ to ١٤٦.٤ with an average of ١٤٣.٢ gm as well as $\sigma^{٢}$ph ٦٥٧.١٢ and C.V% ١٧.٩٪ in population I. While, it was ranged from ١٢٥.٣ to ١٤٥.٤ with an average of ١٤٠.٤ gm as well as $\sigma^{٢}$ph ٧١١.٤٨ and C.V% ١٩٪ in population II. The number of pods/plant wee ranged from ٥٠.٢ to ٣٦.٤ with an average of ٤٠.٨٢ and $\sigma^{٢}$ph ٥٨.٠٨ and C.V% ١٨.٦٧% in population I. But, it was ranged from ٤٣.٤ to ٣٣.٨ with an average of ٣٩.٩ and $\sigma^{٢}$ph ٣٤.٦٨ and C.V% ١٤.٨٢٪ in population II. Seed index was ranged from ٣٩.٣ to ٥٩.٤ with an average of ٥٣.٦ gm as well as $\sigma^{٢}$ph ٧٥ and C.V% ١٦.٢٪ in population I. But, average of seed index ranged from ٦٠.٨ to ٤٩.٢ with an average of ٥٥.٢ gm as well as $\sigma^{٢}$ph ١٠٨ and C.V% ١٨.٨٤٪ in population II. Seed yield/plant was ranged from ٦٥.٣ to ٨٥ .٦ gm with an average of ٧٩.١ gm. In addition $\sigma^{٢}$ph ١٤٧ and C.V% ١٥.٣٪ in population I. But, it was ranged from ٨٤.١ to ٦٦.٩ gm with an average of ٧٥.٦ gm. In addition $\sigma^{٢}$ph ١٦٤.٢٨ and C.V% ١٧٪ in population II. The pedigree selection was practiced on the two population of faba bean for three traits, i.e. number of pods/plant, seed index and seed yield/plant.

Pedigree selection

The pedigree selection was practiced on the two populations of faba bean for three traits,i.e. number of pods/plant, ١٠٠- seed weight and seed yield.

Selection for number of pods/plant

The analysis of variance for the selected families for three selection criterion along with the parents, the bulk population and the check cultivars Giza ٤٠ and Giza ٦٧٤ for the six studied traits in cycle ١ ($F_{٤}$ generation) and cycle ٢ ($F_{٥}$ generation) of the two populations are shown in Table (٣). The analysis of variance revealed highly significant difference (Table٣) among families for number of pods/plant and all other studied traits in the two cycle of selection in the two populations. Mean of the selected families, parents, bulk sample and check cultivar as wells genotypic (GCV) and phenotypic (PCV) coefficients of variability are presented in Table ٤, ٥ and ٦. The over all mean of selected families after two cycle of pedigree selection for number of pods/plant in two populations were ranged from ٤٧.٢٠ and ٤٧.٣٠ in cycle ١ to ٥٦.٠٠ and ٥٦.٩٠ in cycle ٢. Also, the bulk sample ranged was from ٤٥.٣٠ and ٤٢.٨٠ to ٥١.٤ and ٥٦.٧ in population I and II respectively. Pedigree selection for number of pods/plant in population I reduced the genotypic coefficient of variability from ٤.٥ after the first cycle to ٣.٥ after the two cycles of selection for number of pods/plant and from ٤.٥ in cycle ١ to ٣.٩ in cycle ٢ in seed yield/plant. The same trend was observed in population II. These data were in agreement with those obtained by Shalaby et al. (٢٠٠١) and Yamani (٢٠٠٣). The broad sense heritability after the two cycle of selection were high for number of pods/plant (٨٧.٦ and ٨٧.٤), day to maturity (٨٥.١ and ٨٩.٤), plant height (٩٥.٩ and ٩٨.٤), number of branches/plant (٨٩.٦ and ٨٨.١), seed index (٨٥.١ and ٨٩.٤) and seed yield/plant (٨٨.٧ and ٩٥.٣) for population I and II, respectively. These data were in agreement with those obtained by EI-Shazly (١٩٩٣) and Haridy ٢٠٠٩. The results of the phenotypic and genotypic correlations indicated high positive correlations between numbers of pods/plant and seed yield/plant in populations I and II. However the correlations between days to maturity and seed yield/plant was negative in both populations. These data were in agreement with those obtained by Antoun et al. (١٩٩١), Abdelmula et al. (٢٠٠٤) and Alghmadi (٢٠٠٧).

Table ٢: Means, phenotypic variance ($\sigma^{٢}$ph) and expected genetic advance (ΔG) of base population) $F_{٣}$ for days to maturity, Plant height, number of branches/plant, number of pods/plant, seed index and seed yield/plant for populations I and II.

Item	days to maturity	Plant height	No. of branches/ plant	No. of pods/plant	Seed index	Seed yield/plant
$F_{٣}$- Population I. Means ±S.E.	١٦٩.٩٩ ± ٠.٨٩	١٤٣.٢٢ ± ٠.٧٤	٣.٧٣ ± ٠.٠١٥	٤٠.٨٢ ± ٠.٢٢	٥٣.٥٥ ± ٠.٢٥	٧٩.٠٦ ± ٠.٣٥
Max.	١٧٢.٣٣	١٤٦.٣٥	٣.٩٩	٥٠.١٦	٥٩.٣٦	٨٥.٥٧
Min.	١٣٥.٥٥	١٢٣.٤٤	٣.٥٥	٣٦.٣٥	٣٩.٣٣	٦٥.٣٢
$\sigma^{٢}ph$	٩٥٠.٥٢	٦٥٧.١٢	٠.٢٧	٥٨.٠٨	٧٥.٠٠	١٤٧
CV%	١٨.١٤٪	١٧.٩٠٪	١٣.٩٣٪	١٨.٦٧٪	١٦.١٧٪	١٥.٣٤٪
ΔG	٢.٥٥	١.٩٤	٠.١٨	٢.٦٨	١.٨٢	٣.٨٩
$F^{٣}$- Population II. Means ±S.E	١٧١.٣٠ ± ٠.٩٨	١٤٠.٣٧ ± ٠.٧٧	٣.٩٩ ± ٠.٠١٤	٣٩.٩٤ ± ٠.١٧	٥٥.١٧ ± ٠.٣٠	٧٥.٥٩ ± ٠.٣٧
Max.	١٧٥.٢٢	١٤٥.٤٣	٤.٤٤	٤٣.٤٣	٦٠.٧٧	٨٤.٠٩
Min.	١٣٤.٥٦	١٢٥.٢٨	٣.٧٥	٣٣.٧٨	٤٩.٢٢	٦٦.٨٩
$\sigma^{٢}ph$	١١٥٢.٤٨	٧١١.٤٨	٠.٢٤	٣٤.٦٨	١٠٨	١٦٤.٢٨
CV%	١٩.٨٢٪	١٩.٠٠٪	١٢.١٦٪	١٤.٨٢٪	١٨.٨٤%	١٦.٩٦٪
ΔG	٢.١٢	٢.١٦	٠.١٠	٣.١٩	٢.٣٧	٦.٨٤
Parents: Giza ٤٢٩	١٥٠.٨٨	١٣٥.٩٠	٥.٢٠	٥٢.٩٨	٤٩.٥٥	٩٠.٩٤
Parents: Misr ١	١٦١.٢٠	١٥٤.٤٠	٤.٠٠	٤٥.١١	٦٥.٤٤	٥٤.٣٢
Parents: Assiut ٢١٥	١٦٨.٢٠	١٥١.١١	٤.٥١	٥٠.٠٩	٥٥.٥٥	٧٦.٢١

Table ٤: Means, phenotypic (PCV %) and genotypic (GCV %) coefficients of variability, heritability in broad-sense (H.B.S). In the two cycle of pedigree selection for the three selection criteria for populations I and II.

Items		Selection criteria					
Items		No. of pods/plant		Seed index		Seed yield/plant	
		(C١)F٤	(C٢)F٥	(C١)F٤	(C٢)F٥	(C١)F٤	(C٢)F٥
Days to maturity							
Pop I	P١	١٦٠.٠٠	١٥٩.٢٢	١٦٠.١٠	١٥٩.٥٢	١٦٠.٠٠	١٥٩.٣٢
	P٢	١٤٩.٩٠	١٤٥.٠٠	١٤٩.٩٢	١٤٥.٠٢	١٤٩.٩٠	١٤٥.٠٩
	Bulk	١٦٦.٣٥	١٥٣.١٣	١٦٦.٣٠	١٥٣.١٦	١٦٦.٣٩	١٥٣.٢٢
	Check ١(G.٤٠)	-	١٤٦.٥٠	-	١٤٦.٣٤	-	١٤٦.٤٨
	Check ٢(G.٦٧٤)	-	١٦٤.٤٣	-	١٦٤.٤٥	-	١٦٤.١٩
	Selected families	١٦٥.١٠	١٥٧.٨٨	١٦٤.١٠	١٥٧.٦٦	١٦٤.١٠	١٥٧.٠٠
	PCV %	٣.٦٩	٣.٠٩	٣.٢٤	٢.٩٧	٣.٣٢	٢.٨٩
	GCV %	٣.٣٣	٢.٨٥	٣.٠٢	٢.٨٢	٣.١٤	٢.٧٤
	H.B.S %	٨١.٢٨	٨٥.٠٩	٨٦.٨٩	٨٩.٩٢	٨٩.٣٢	٨٩.٨٧
Pop II	P١	١٦٧.٧٧	١٦٦.٤٠	١٦٧.٥٧	١٦٦.٤٩	١٦٧.٧٤	١٦٦.٨٠
	P٢	١٥٠.١٤	١٤٥.٢٠	١٥٠.٢٢	١٤٥.٢٥	١٥٠.١٥	١٤٥.٧٧
	Bulk	١٦٥.١٠	١٥٨.٩٩	١٦٥.٠٠	١٥٨.١٦	١٦٥.٣٥	١٥٨.٠٩
	Check ١(G.٤٠)	-	١٤٦.٧٧	-	١٤٦.٨٢	-	١٤٦.٠٩
	Check ٢(G.٦٧٤)	-	١٦٤.٥٥	-	١٦٣.٩٨	-	١٦٤.٠٣
	Selected families	١٦٥.٦٥	١٥٧.٢٤	١٦٧.٧٧	١٥٩.٧٨	١٦٥.٤٤	١٥٧.٦٧
	PCV %	٤.٥	٣.٨٦	٣.٢٨	٢.٩٧	٢	١.٦٩
	GCV %	٤.٢٢	٣.٦٥	٣.١٣	٢.٨٥	١.٨١	١.٥٣
	H.B.S %	٨٧.٨٥	٨٩.٤	٩٠.٨٨	٩٢.٢٣	٨١.٧١	٨٢.٤
Plant height							
Pop I	P١	١٥٥.٤٠	١٥٦.٧٣	١٥٥.٤٢	١٥٦.٧٦	١٥٥.٣٠	١٥٦.٥٠
	P٢	١٣٦.٠٠	١٣٦.٩٢	١٣٦.٢٢	١٣٦.٨٢	١٣٦.٠٧	١٣٦.٧٢
	Bulk	١٤٧.٨٠	١٥٠.١٠	١٤٧.٨٨	١٥٠.١٦	١٤٧.٨٥	١٥٠.١٤
	Check ١(G.٤٠)	-	١٣٧.١٥	-	١٣٧.٩١	-	١٣٧.٤٦
	Check ٢(G.٦٧٤)	-	١٥٤.٨٩	-	١٥٤.٢٥	-	١٥٦.١٢
	Selected families	١٤٥.٢٣	١٤٩.٢٢	١٤٤.٣٥	١٤٧.٠٥	١٤٧.٢٣	١٥١.٢٤
	PCV %	٤.٨٥	٣.٩٦	٦.٨٩	٦.٠٤	٤.١٧	٢.٩٦
	GCV %	٤.٤٥	٣.٨٨	٦.٧٥	٥.٩٥	٣.٩٦	٢.٨٨
	H.B.S %	٨٤.٣٨	٩٥.٩٢	٩٥.٩	٩٦.٩	٩٠.٣٦	٩٤.٥٤
Pop II	P١	١٥٤.٠٠	١٥٧.١٠	١٥٤.٠٧	١٥٧.٦٠	١٥٤.٤٠	١٥٧.٦٠
	P٢	١٣٦.٩٠	١٣٦.٩٩	١٣٦.٢٤	١٣٦.٦٧	١٣٦.٩٥	١٣٦.٣٣
	Bulk	١٤٢.٩٠	١٤٦.٠٠	١٤٢.٩١	١٤٦.٥٤	١٤٢.٩٠	١٤٦.٦٦
	Check ١(G.٤٠)	-	١٣٧.٥٥	-	١٣٨.٣٦	-	١٣٨.٠٩
	Check ٢(G.٦٧٤)	-	١٥٥.٠٩	-	١٥٥.٢١	-	١٥٥.٤٦
	Selected families	١٤٣.١٢	١٤٧.٠٣	١٤٥.٠٣	١٥١.٠٣	١٤٤.٤٥	١٥٥.١٨
	PCV %	٨.٩٦	٧.٠٥	٥.٨٤	٣.٨٧	٥.٨٨	٤.٩٨
	GCV %	٨.٨٨	٦.٩٩	٥.٥٦	٣.٧٣	٥.٧٣	٣.٠٥
	H.B.S %	٩٨.٢١	٩٨.٣٩	٩٠.٦٨	٩٢.٨٢	٩٤.٨٤	٩٦.٣٥

		Seed yield/plant		Seed index		Seed yield/plant	
		(C١)F٤	(C٢)F٥	(C١)F٤	(C٢)F٥	(C١)F٤	(C٢)F٥
Number of branches/plant							
	P١	٤.٣٠	٤.٥٠	٤.٣٣	٤.٥٤	٤.٤٤٠	٤.٥٦
	P٢	٥.٦٠	٥.٧٠	٥.٦٢	٥.٥٧	٥.٦٧	٥.٧٥
	Bulk	٣.٨٠	٤.١٠	٣.٨٣	٤.٤٠	٣.٧٧	٤.٩٣
Pop I	Check ١(G.٤٠)	-	٤.٠٢	[illegible]	[illegible]	-	٤.٣٣
	Check ٢(G.٦٧٤)	-	٥.٥	-	٥.١٦	-	٥.٠٨
	Selected families	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
	PCV %	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
	GCV %	٥٥	[illegible]	٤٨.٤٢	٤٤.٧٥	٥٩.٩٥	٥٥.٧٨
	H.B.S %	٨٧.٢١	٨٩.٥٨	٩٠.٦١	٩٢.٠٩	٩٠.٠٢	٩١
	P١	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
	P٢	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
Pop II	Bulk	٤.٠٠	٤.١٠	٤.٠٥	٤.١٢	٤.٠٩	٤.١٥
	Check ١(G.٤٠)	-	٥.٠٤	-	٥.٥٩	-	٥.٤٤
	Check ٢(G.٦٧٤)	-	٥.٢٣	-	٥.١١	-	٥.٢٦
	Selected families	٤.١١	٤.٣٥	٤.٣٥	٥.٠٠	٤.٤٠	٥.٧٢
	PCV %	٤٥.٤١	٤٤.٧٣	٥٩.٠٦	٥٥.٨١	٥٣.٤	٥٠.٩٨
	GCV %	٤٢.٥٥	٤١.٩٩	٥٥.١٨	٥٢.٢٦	٥٠.٢٢	٤٦.٦٥
	H.B.S %	٨٧.٧٥	٨٨.١٢	٨٧.٢٧	٨٧.٧١	٨٨.٤٧	٩١.٤٤
No. of pods/plant							
Pop I	P١	٤٧.٠٠	٤٩.٣٠	٤٧.٠٨	٤٩.٣٥	٤٧.٢٢	٤٩.٣٩
	P٢	٥٥.٣٠	٥٨.٩٠	٥٥.٢٥	٥٨.٩٨	٥٥.٣٧	٥٨.٧٨
	Bulk	٤٥.٣٠	٥١.٤٠	٤٥.٢٧	٥١.٤٥	٤٥.٣٦	٥١.٤٣
	Check ١(G.٤٠)	-	٦٥.٠٤	-	٦٥.٥١	-	٦٥.٢١
	Check ٢(G.٦٧٤)	-	٧٥.٢١	-	٧٥.٢٥	-	٧٥.٣٥
	Selected families	٤٧.٢٠	٥٥.٩٧	٤٧.٠٠	٥٥.٩٧	٤٨.٢١	٥٥.٩٧
	PCV %	٤.٨٥	٣.٦٩	٦.٠٥	٥.٨٧	٧.٦٢	٥.٨٤
	GCV %	٤.٤٥	٣.٤٥	٥.٦٦	٥.٥٥	٧.١١	٥.٥٦
	H.B.S %	٨٤.٣٩	٨٧.٥٦	٨٧.٦٦	٨٩.٥٥	٨٧.٠٦	٩٠.٦٧
Pop II	P١	٥٢.٠٠	٥٥.٩٠	٥٣.٢٢	٥٥.٧٥	٥٢.٨٧	٥٥.٧٠
	P٢	٥٦.٠٠	٥٩.٠٠	٥٥.٤٤	٥٩.٠٦	٥٦.٧٦	٥٩.٢٨
	Bulk	٤٢.٨٠	٥٦.٧٠	٤٢.٨٧	٥٦.٧٦	٤٢.٥٥	٥٦.٤٦
	Check ١(G.٤٠)	-	٦٥.٠٢	-	٦٥.٠٠	-	٦٥.١٤
	Check ٢(G.٦٧٤)	-	٧٦.٤٤	-	٧٦.١٩	-	٧٦.٠٨
	Selected families	٤٧.٢٧	٥٦.٨٧	٤٧.٩٧	٥٧.٦٥	٤٨.٣٣	٥٧.٧٥
	PCV %	٧.٥٧	٦.٤	٥.٠٤	٣.٩٨	٨.٥	٦.٧٧
	GCV %	٦.٦٦	٥.٩٨	٤.٧١	٣.٧٣	٧.٧٨	٦.٤٥
	H.B.S %	٧٧.٤٣	٨٧.٣٦	٨٧.٢٤	٨٧.٧٩	٨٣.٨٦	٩٠.٧٦

Table ٥: Means, phenotypic (PCV %) and genotypic (GCV %) coefficients of variability, heritability in broad-sense (H.B.S). In the two cycle of pedigree selection for the three selection criteria for populations I and II .

Pop I	**Bulk**	٥٩.٣٠	٦٥.٩٠	٥٨.٣٠	٦٤.٩٥	٥٩.٢٩	٦٣.٩٠
	Check ١(G.٤٠)	-	٧٠.١١	-	٧٠.٠١	-	٧٠.١٨
	Check ٢(G.٦٧٤)	-	٥٧.٩٨	-	٥٨.٠٩	-	٥٨.٢٥
	Selected families	٥٨.٦٦	٦٥.٠٠	٥٨.١١	٦٤.٠٠	٥٧.٩٩	٦٣.٢٠
	PCV %	٣.٦٩	٣.٠٩	٣.٢٤	٢.٩٧	٣.٣٢	٢.٨٩
	GCV %	٣.٣٣	٢.٨٥	٣.٠٢	٢.٨٢	٣.١٤	٢.٧٤
	H.B.S %	٨١.٢٥	٨٥.١٢	٨٦.٩٢	٨٩.٨٨	٨٩.٣٢	٨٩.٨١
Pop II	**P١**	٦٨.٥٠	٧٥.٩٠	٦٧.٥٦	٧٤.٩٣	٦٧.٥٩	٧٥.٤٤
	P٢	٥٥.٤٥	٦٣.٣٠	٥٥.٧٨	٦٢.٣٥	٥٤.٩٥	٦٣.٣٧
	Bulk	٦٠.٦٢	٦٥.٦٧	٦١.٦٠	٦٣.٦٠	٦١.٦٠	٦٥.٦٩
	Check ١(G.٤٠)	-	٧٠.٨٨	-	٧٠.٧٥	-	٧٠.٦٤
	Check ٢(G.٦٧٤)	-	٥٨.٣٣	-	٥٨.٤٢	-	٥٨.٣٣
	Selected families	٦٠.٢٢	٦٧.٠٠	٥٩.٢١	٦٥.٢٢	٥٩.٤٥	٦٤.٨٥
	PCV %	٤.٥	٣.٨٦	٣.٢٨	٣.١٧	٣.٦٩	٢.٩٤
	GCV %	٤.٢٢	٣.٦٥	٣.١٣	٣.٠٢	٣.٢٥	٢.٧٧
	H.B.S %	٨٧.٨٥	٨٩.٣٩	٩٠.٩٢	٩١.٠١	٧٧.٦٢	٨٩.٠٥
Seed yield/plant							
Pop I	**P١**	٦٧.٥	٧٨.٩	٦٧.٥	٧٨.٩	٦٧.٥	٧٨.٩
	P٢	٩٩.٧٠	١٢٢.٢١	٩٩.٢٧	١٢٢.١٣	٩٩.٧٤	١٢٢.١٦
	Bulk	٧٢.٥٠	٩٧.٢٠	٧٢.٥٧	٩٧.٢٨	٧١.٥٠	٩٦.٢٥
	Check ١(G.٤٠)	-	٨٧.٢٢	-	٨٧.١٢	-	٨٧.٠٥
	Check ٢(G.٦٧٤)	-	١٠٥.٣٣	-	١٠٥.٢٥	-	١٠٧.١٢
	Selected families	٩٠.٢٣	١٠٦.٤٤	٩٠.٥٥	١٠٧.٦٦	٩١.٢٥	١٠٨.٤٩
	PCV %	٤.٨٤	٣.٩٦	٦.٨٩	٦.٠٤	٤.١٧	٢.٩٦
	GCV %	٤.٤٥	٣.٨٨	٦.٧٥	٥.٩٥	٣.٩٦	٢.٨٨
	H.B.S %	٨٤.٣٧	٩٥.٩١	٩٥.٩	٩٧	٩٠.٣٦	٩٤.٥١
Pop II	**P١**	٨٨.٧٠	٩١.٠٠	٨٨.٢٢	٩٢.٠٠	٨٨.٣٥	٩١.٥٥
	P٢	٩٩.٧٠	١٢٢.١٢	٩٩.١٦	١٢٠.٦٢	٩٨.٧٥	١٢٣.٤٤
	Bulk	٧٧.١٠	٩٦.٥٠	٧٥.١٠	٩٢.٢٨	٧٣.١٣	٩٢.١٩
	Check ١(G.٤٠)	-	٨٧.٤٥	-	٨٧.٦٧	-	٨٧.٩٩
	Check ٢(G.٦٧٤)	-	١٠٤.٠٩	-	١٠٩.١١	-	١٠٩.٠٤
	Selected families	٩٠.٩٣	١٠٥.٣٤	٩٢.١١	١١٠.٨٠	٩٠.٩٣	١٠٩.٢٠
	PCV %	٩.١٢	٧.١٦	٦.٣٦	٤.١٤	٦.١٨	٥.١٦
	GCV %	٩٨.٢١	٩٨.٣٩	٩٠.٦٨	٩٢.٨٣	٩٤.٨٤	٩٦.٣٥
	H.B.S %	٩٨.٢١	٩٨.٣٩	٩٠.٦٨	٩٢.٨٣	٩٤.٨٤	٩٦.٣٥

Table ٦: Means, phenotypic (PCV %) and genotypic (GCV %) coefficients of variability, heritability in broad-sense (H.B.S). In the two cycle of pedigree selection for the three selection criteria for populations I and II.

Table ٧: Phenotypic (rp) and genotypic (rg) correlation coefficients between seed yield/plant and each of other traits for populations I and populations II of $F_{٥}$ generations when selection was based on number of pods/plant (PP), seed index(SI) and seed yield/plant (SYP) in faba bean.

Characters		No. of pods/plant		Seed index		Seed yield/plant	
		Pop. I	Pop. II	Pop. I	Pop. II	Pop. I	Pop. II
		seed yield/plant					
days to maturity	rp	-٠.٥٢	-٠.٥٧	-٠.٥٥	-٠.٥٣	-٠.٥٢	-٠.٣٤
	rg	-٠.٤٣	-٠.٥١	-٠.٥١	-٠.٤٢	-٠.٤٤	-٠.٢٥
Plant height	rp	٠.٤٦	٠.٣٥	٠.٣٠	٠.٤٩	٠.٣٥	٠.٦٩
	rg	٠.٢٩	٠.٢٠	٠.٢٦	٠.٤٣	٠.٣٣	٠.٤٤
No. of branches/ plant	rp	٠.٣٥	٠.٦٩	٠.٥٩	٠.٤٤	٠.٤٩	٠.٥٥
	rg	٠.١٩	٠.٥٥	٠.٤٧	٠.٣٩	٠.٣٤	٠.٣٨
No. of pods/plant	rp	٠.٥٦	٠.٧٥	٠.٥٥	٠.٥٨	٠.٥٦	٠.٧٩
	rg	٠.٦٧	٠.٦٠	٠.٤١	٠.٤٧	٠.٤٩	٠.٧٧
Seed index	rp	٠.٥٦	٠.٦٢	٠.٤٤	٠.٣٦	٠.٤٦	٠.٤٣
	rg	٠.٤٦	٠.٥٥	٠.٣٠	٠.٢٥	٠.٤٠	٠.٣٥

Selection for seed index.

The analysis of variance for selected families for three selection criterion along with the parents, the bulk population and the check cultivars Giza ٤٠ and Giza ٦٧٤ for the six studied traits in cycle ١ ($F_{٤}$ generation) and cycle ٢ ($F_{٥}$ generation) of the two population are shown in Table (٣). The analysis of variance revealed highly significant difference (Table٣) among families for seed index and all other studied in the two cycle of selection in the two populations. Mean of the selected families, parents, bulk sample and checks cultivar as wells genotypic (GCV) and phenotypic (PCV) coefficients of variability are presented in Table ٤, ٥ and ٦. The over all means of selected families after two cycle of pedigree selection for seed index in two populations ranged from ٥٨.٧ and ٦٠.٢ in cycle one to ٦٥.٠ and ٦٧.٠ in cycle two. Also, the bulk sample ranged from ٥٩.٣٠ and ٦٠.٦ to ٦٥.٩ and ٦٥.٧ in population I and II respectively. These data were in agreement with those obtained by Abo-Elwafa and Bakheit (١٩٩٩b) and Nageeb (٢٠٠٢). Pedigree selection for seed index in population I reduced the genotypic coefficient of variability from ٣.٠٢ after the first cycle to ٢.٨٣ after the two cycle of selection for seed index and from ٦.٨ in cycle ١ to ٦.٠ in cycle two in seed yield/plant. The same trend was observed in population II. The broad sense heritability after the two cycle of selection were high for seed yield/plant (٩٧.٠ and ٩٢.٨), day to maturity (٨٩.٩ and ٩٢.٢), number of pods/plant (٨٩.٦ and ٨٧.٨), number of branches/plant (٩٢.١ and ٨٧.٧), seed index (٨٩.٩ and ٩١.٠) and plant height (٩٦.٩ and ٩٢.٨) for population I and II, respectively. These data were in agreement with those obtained by Bakheit and Mahdy (١٩٨٨a), Katiyar and Singh (١٩٩٠) and Bakheit (١٩٩٢). The results of the phenotypic and genotypic correlations indicated high positive correlations between numbers of pods/plant and seed yield/plant in populations I and II. While the correlations between days to maturity and seed yield/plant was negative in both populations. These data were in agreement with those obtained by Abd-Allah (١٩٩١), El-Shazly (١٩٩٣), Abo-Elezz (٢٠٠٥) and Alan and Geren (٢٠٠٧).

Selection for seed yield /plant.

The results indicated highly significant differences among genotypes (selected families, parents, bulk population and check cultivars) in the population I and II. Means of the selected families, parents, bulk sample and check cultivar Giza ٤٠ and Giza ٦٧٤, in addition to heritability in broad sense, genotypic (GCV) and phenotypic (PCV) coefficients of variability for all studied traits when selection was based on seed yield/plant are presented in Table ٤.٥ and ٦. The average seed yield of the selected families of populations I and II increased from ١٤٧.٢٠ and ١٤٤.٥٠ in F٤ generation (cycle ١) to ١٥١.٢٠ and ١٥٥.٢٠ gm/plant in F٥ generation (cycle ٢), respectively. These data were in agreement with those obtained by

Mahmoud (٢٠٠١) and Lithy and Abdel-Aal (٢٠٠٤). The average seed yield/plant for the bulk populations was ٧١.٥٠ and ٩٦.٣ gm/plant for population I and ٧٣.١٠ and ٩٢.٢٠ gm/plant for population II in $F_٤$ and $F_٥$ generations, respectively. The results indicated that pedigree selection decreased the genetic variability measured as genotypic coefficients of variability of the selection criterion and other studied traits of the two cycle of selection in both populations (Tables ٤, ٥ and ٦). Falconer (١٩٨٩) stated that selection reduces genotypic variance of the following generation. Heritability estimate of family means increase with the increase in homozygosity (from cycle ١ to cycle ٢) in all studied traits. Also, heritability in broad sense after two cycle of selection were high for all studied traits in populations I and II. The results showed that direct selection for seed yield/plant which is the main goal in the all breeding programs, increased it by ١٢.٧ and ١٨.٤٪ from the bulk sample after two cycles of selection in populations I and II respectively. Such increased accompanied with increased in number of pods/plant (٩.٠ and ٢.٣٪) the effect of pedigree selection on phenotypic and genotypic correlations after two cycle in the two populations are presented in Table (٧). The genotypic and phenotypic correlations between seed yield/plant and each of plant height, number of branches/plant, number of pods/plant and seed index were moderate and positive in populations I and II. While the correlation between seed yield and day to maturity was negative in both populations. These data were in agreement with those obtained by Abo-Elwafa et al (١٩٨٧), Bakheit and Mahdy (١٩٨٨a), Bakheit and Mahdy (١٩٨٨b), Katiyar and Singh (١٩٩٠) and Tadaesse et al. (٢٠١١).

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الاستجابة للانتخاب للمحصول ومكوناته في الفول البلدي

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أجرى هذا البحث في ثلاثة مواسم زراعيه هي من ٢٠٠٨/٢٠٠٩، ٢٠٠٩/٢٠١٠ و ٢٠١٠/٢٠١١ في مزرعة تجارب كلية الزراعة- جامعة الأزهر - فرع أسيوط في ثلاث تجارب الأولى الانتخاب لعدد القرون والثانية الانتخاب لوزن ١٠٠بذرة والثالثة الانتخاب لمحصول النبات وكان الهدف من هذا البحث : تقدير الاستجابة المباشرة لدورتين للانتخاب المنسب للتبكير وكذلك المحصول و تقدير الارتباط المظهري والوراثي.

الصفات التي تم دراستها هي :- عدد الأيام حتى٩٠ % نضج، طول النبات (سم) ، عدد الأفرع / النبات، عدد القرون / النبات،وزن١٠٠بذره ومحصول البذور للنبات (جم) .

استخدمت في هذه الدراسة عشيرتين من الفول البلدي كالتالي:-

العشيرة الأولى : (مصر ١x جيزة٤٢٩) والعشيرة الثانية: (اسيوط٢١٥x جيزة٤٢٩)

أهم النتائج المتحصل عليها يمكن عرضها كالتالي :-

أظهر تحليل التباين وجود اختلافات عالية معنوية بين العائلات المنتخبة لصفة محصول البذور للنبات (جم) في كل من العشيرتين مما يدل على أن الانتخاب داخل العشيرتين يكون فعالا . وفى العشيرة الأولى كان متوسط محصول البذور لنبات العائلات المنتخبة يتراوح ١٠٠.٣ و١١٦.٨ (جم) للجيل الثالث والرابع في التجربة الأولى و يتراوح ١٠١.١ و١١٧ (جم) للجيل الثالث والرابع في التجربة الثانية و يتراوح ٩٩.٧٢ و١١٩.٤ (جم) للجيل الثالث والرابع في التجربة الثالثة وكلن في العشيرة الثانية يتراوح ٩٧.٢ و١١٥.١ (جم) للجيل الثالث والرابع في التجربة الأولى و يتراوح ٩٩.٥٢ و١١٨.٩ (جم) للجيل الثالث والرابع في التجربة الثانية و يتراوح ١٠٠.٩ و١١٦ (جم) للجيل الثالث والرابع في التجربة الثالثة حيث تفوقت العائلات المنتخبة على العشيرة المجمعة قي الجيل الثالث والرابع في الثلاث تجارب في كل من العشيرتين. وكذلك أظهر تقدير الارتباط المظهري والوراثي بين المحصول و الصفات المذكورة أنة كان ارتباط موجب ماعدا صفة ميعاد النضج في الثلاث تجارب في العشيرتين.