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Two Selection Methods and Estimation of some Important Genetic Parameters in Broad Bean (*Vicia faba* L.)

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ABSTRACT

Two cycles of mass selection and individual plant selection methods for two generations of selfing with selection were practiced to obtain the best promising progenies, according to some important and economical characters of broad bean cultivar Aquadolce, during the three successive winter seasons of 2007/2008, 2008/2009 and 2009/2010, at the Experimental Station Farm (at Abies) of the Faculty of Agriculture, Alexandria University, Egypt. The obtained results indicated generally that 6 out of 11 studied characters were improved through the practiced mass selection method; while, favorable performances were obtained in all the studied characters but, with different magnitudes; with practiced individual plant selection with selfing and selection for two generations method. In most of the studied characters, the two values of Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV) differed in narrow. High broad sense heritability values were recorded for most studied characters; which, ranged from 80.19% for pod diameter to 99.83% for pods number per plant. The characters total yield per plant, pods number per plant, pod weight, branches number per plant and plant height showed high heritability estimates which associated with high genetic advance, indicating the presence of additive gene effects. The correlations between the following pairs of characters total yield with each of branches number per plant and pods number per plant; branches number per plant with pods number per plant and stem diameter with each of pod diameter and seeds number per pod were found positive and desirable for the objectives of selection in the present study. However, nods number to first pod set showed desirable negative correlation with number of branches per plant.

Key words: Broad bean, yield and its components, selection methods, heritability, correlation, variability, genetic advance

INTRODUCTION

Broad bean (*Vicia faba* L. 2n = 14) is considered one of the most important and popular vegetable crops belonging to the family Leguminosae, that is successfully grown in Egypt as well as in many other countries of the world. Broad bean is a nutritious component for the human feed, especially in developing countries, because of the richness of seeds in protein as well as in some of the important minerals and vitamins. The green seeds are consumed fresh, frozen or canned. In Egypt, it was noticed decrease of broad bean productivity and its fluctuation from one season to another, could be due to growing old local cultivars which are generally characterized by relatively low productive capacity with a noticeable deterioration in their quality characters. Moreover, the common grown local cultivars of broad bean were noticed to have great amounts of variability in most of their traits among the individual plants of the commercially grown population. However, it might be stated that no serious attempts have been so far made to purify and upgrade the productivity and acceptability of this crop; since, the growers seeds of broad bean are not usually produced by specialists; but, multiphicated by growers without any attention to perform rouging or put the isolation distance under consideration. So, improvement of productivity could be a basic objective of crop improvement programs. To achieve this goal, the breeders should choose effective program which facilitate the simultaneous improvement of yield and its components traits. Accordingly, improving production of broad bean can be achieve through purification of already established cultivars by both mass and individual plant selection programs. In this respect, some studies have been carried out on the effectiveness of different selection approaches for improvement of broad bean and faba bean characteristics by several investigators such as (Ragheb and El-Gamal, 1992; Abd-El-Kader-Helmy, 2001; Helaly, 2010) on broad bean (Shalaby *et al.*, 2001; El-Hosary and El-Badawy, 2003; Ahmed *et al.*, 2008; Abd-El-Haleem and Mohamed, 2011) on faba bean.

Success in crop breeding program is also depending up on the isolation of genetically superior genotypes based on the amount of variability present in the original population. Therefore, information on the variability existed in a group of populations of broad bean are essential. Some studies were conducted by El-Hosary *et al.* (1983), El-Hosary and El-Badawy (2003), El-Galaly (2003) and Abd-El-Haleem and Mohamed (2011) on variability magnitudes of faba bean. Moreover, a basic knowledge of interrelationships of certain plant characters with yield and their correlations among themselves is an important topic for breeder to improve a complex character such as yield. For this reason, Abd-El-Raheem and Ismail (1986), Bakheit and Mahdy (1987), Ulukan *et al.* (2003), Alan and Geren (2007), Alghamdi (2007), Ahmed *et al.* (2008) and Tadesse *et al.* (2011), determined the correlation coefficients among various characters of faba bean in their studies.

Genetic, environment and their interaction effects are of the most important factors that control on yield and yield components which are related to weather changes year by year. Also, genotype and environment interactions are important to decide a possible breeding method to improve cultivars with adequate adaptation to environments (Fox *et al.*, 1997). Therefore, estimation of heritability should be determined as minimal requirement in breeding strategy. Many studies were reported in this respect (El-Refaey, 1999; Kalia and Sood, 2004; Toker, 2004; Farage and Darwish, 2005; Alan and Geren, 2007; Alghamdi, 2007; Abd-El-Haleem and Mohamed, 2011). The utility of heritability increase when it is used to calculate genetic advances which indicate the degree of gain in the obtained character under a particular selection pressure. Thus, genetic advance considered another important selection parameter that aids breeders in a selection programe (Shukla *et al.*, 2004).

The present study was conducted to compare the efficiency of two selection methods; i.e., mass selection and individual plant selection; on the improvement of general performances of broad bean cultivar Aquadolce, in comparison with its original population and two commercially grown cultivars Aspany and Giza Blanka. Broad sense heritability percentages, phenotypic and genotypic coefficients of variation as well as genetic advance parameters were estimated for some growth and productivity characters. The phenotypic correlation coefficients among the different studied characters were also estimated.

MATERIALS AND METHODS

Experimental work: The present study was carried out during three successive winter seasons of 2007/2008, 2008/2009 and 2009/2010 at the Experimental Station Farm, Faculty of Agriculture, Alexandria University; at Abies, Alex, A.R.E. The basic plant material, in this study, was Aquadolce cultivar of broad bean. In the first season of 2007/2008, seeds of the original population of Aquadolce cultivar were sown in a field experiment on November 10, 2007. All agricultural practices such as fertilization, irrigation and pests control were performed as usually recommended for commercial broad bean production, whenever they were thought necessary. The measurements of the different studied characters, on individual plant basis, were recorded through the practiced procedures of the two selection methods; mass selection and individual plant selection. At the beginning flowering and pods setting (green matured pods) stages, the best twenty plants were primarily selected on the basis of the following desirable characters; i.e., shorter plant height, thicker stem diameter, more number of branches per plant, less number of nods to first pod set, less number of days to first pod set, long and wide pod, heavy pod weight, more number of pods per plant, more number of seeds per pod and high green pods yield per plant. At the end of pods maturity stage, the seeds of the first selfed progenies and the seeds of the first cycle of mass selection (C_1) as well as seeds of the original population were separately collected, extracted and stored to be used in the next cycle. Data of the various interested characters were recorded to be used for calculating the statistical parameters; i.e., range (R), mean ($\bar{X}$) and Coefficient of Variation (CV%). In the second season of 2008/2009, seeds of each of the first mass selection cycle progeny and the first selfed progenies of each selected plant were separately sown to initiate families; then, selection on the same forgoing basis, was also practiced within and between the selfed progenies of the individual selected plants to maintain the most promising plants of the second cycle of mass selection and the second selfed progenies. The number of the finally selected progenies from the second selfed progenies of the selected plants came down to be only seven populations of Aquadolce cultivar. In the third season of 2009/2010, field experiment was carried out to evaluate the efficiency of the second mass selection cycle (C_2) and the individual plant selection for two generations of selfing with selection on the variability and general performances of the studied characters. In this experiment, seeds of the Aquadolce cultivar as the original population (C_0), the second mass selection cycles' population (C_2) and those of the seven second selfed progenies of the individual plant selection ($S_{2\text{-}1}$, $S_{2\text{-}2}$, $S_{2\text{-}3}$, $S_{2\text{-}4}$, $S_{2\text{-}5}$, $S_{2\text{-}6}$ and $S_{2\text{-}7}$) as well as the two check cultivars Aspany and Giza Blanka were separately sown in a randomized complete block design with three replicates. Each plot was represented by three rows 4 m long and 0.60 m wide and 0.20 m between plants. All cultural practices such as fertilization, irrigation and plant protection against weeds, diseases and insects; were performed whenever they were necessary, as recommended for broad bean production in Egypt. The data were recorded and measured for all studied characters, as previously mentioned, to be used in the estimation of the different statistical and genetic parameters.

Statistical analysis and estimation of genetic parameters: The mean values of each character under the study were computed and subjected to analysis of variance, following the procedures described by Al-Rawi and Khalf-Allah (1980), using Co-Stat computer software program 2004.

Estimates of phenotypic and genotypic variances: Phenotypic and genotypic variances were calculated by the methods suggested by Allard (1960) as follows:

$$\sigma_p^2 = \sigma_g^2 + \sigma_e^2$$

$$\sigma_p^2 = MS_g - (MS_e)/r$$

Where:

σ_p^2 = Phenotypic variance
σ_g^2 = Genotypic variance
σ_e^2 = Environmental variance (error mean square)

Estimates of phenotypic coefficients of variation: The genotypic and phenotypic coefficients of variation (GCV and PCV) were estimated, according to the procedure outlined by Johnson *et al.* (1955) as follows:

$$PCV = \frac{\sqrt{\sigma_p^2}}{\bar{X}} \times 100$$

$$GCV = \frac{\sqrt{\sigma_g^2}}{\bar{X}} \times 100$$

Where:

$(\bar{X})$ = Grand mean

Estimates of broad sense heritability and the expected genetic advance: Broad sense heritability ($H^2_{b.s.}$%) and the expected genetic advance under selection, assuming the selection intensity of 5% were calculated as suggested by Allard (1960) as follows:

$$H^2_{b.s}(\%) = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

$$G_g = (k)\sigma_A (H^2_{b.s})$$

Where:

G_g = Expected genetic advance
K = Selection differential (2.06 at 5% selection intensity)
σ_A = Phenotypic standard deviation

Estimates of genetic advance as percent of mean: Genetic advance as percent of mean (GAM) was calculated using the following equation:

$$GAM = \frac{G_g}{\bar{X}} \times 100$$

RESULTS

Evaluation of the two selection methods mass selection and individual plant selection: The presented results in Table 1 show that the estimated values of the coefficients of variation of the 11 studied traits were found to be in the range from 8.64 to 49.75% in the original population (C_0) and from 7.55 to 30.83% in the first cycle of mass selection (C_1) for days number to first pod set and total yield per plant characters, respectively. While, in the second cycle of mass selection (C_2), the highest variability magnitude of all studied characters was reflected by branches number per plant (22.14%), followed by total yield per plant (19.83%). On the contrary, the characters pod diameter and days number to first pod set showed low variability magnitudes and their estimated CV% values were 5.47 and 6.92%, respectively. Generally, it was noticed that the variability magnitudes for all studied characters, in the first and in the second-cycle of mass selection, were found to be lower than those of their original population, as appeared from either of the detected ranges or the estimated coefficients of variation values (CV%). The estimated means of each studied character of the three populations; i.e., C_0, C_1 and C_2 in Table 1, reflected, generally, clear improvement in most studied characters after the first and the second selection cycles.

The obtained results, in Table 2, indicate that using the two cycles of mass selection was found to be highly efficient in increasing the means of the characters branches number per plant, pods number per plant and total yield per plant with about 12.33, 37.91 and 39.29; 17.87, 53.05, 26.30, 22.01, 42.20 and 329.79%, relative to those of the original population, Aspany and Giza Blancka cultivars, respectively. Meanwhile, such selection method was able to reduce the mean values of the plant height and days number to first pod set characters which were estimated by 11.81, 22.32, 22.27; 12.42, 9.20 and 12.05%, relative to those of the original population, Aspany and Giza Blancka cultivars. It was also noticed that the pod weight character was increased by 25.92 and 125.29%, relative to those of Aspany and Giza Blancka cultivars, respectively. Moreover, mass selection method increased pod length by 12.47 and 29.23%, relative to those of the original population and Giza Blancka cultivar. On the contrary, the other four characters; stem diameter, nods number to first pod set, pod diameter and seeds number per pod; did not reflect any significant improvement after the second cycle of mass selection. The advanced progenies, that exhibited favorable performances, according to the selection criteria in the present investigation, through

Table 1: Means ($\bar{X}$), ranges (R) and coefficients of variation (CV%) estimates for the various studied characters of the different populatious; i.e., original population (C_0), first (C_1) and second (C_2) cycles of mass selection; of Aquadolce broad bean

Populations	C_0			C_1			C_2		
Characters	($\bar{X}$)	R	CV (%)	($\bar{X}$)	R	CV (%)	($\bar{X}$)	R	CV (%)
Plant height (cm)	89.22	42.0-20.00	19.89	78.72	61.0-89.000	09.90	78.68	65.0-88.0	09.89
Stem diameter (cm)	01.22	00.5-02.20	16.12	01.26	01.0-01.600	12.57	01.30	01.1-01.6	10.26
Branches No. per plant	09.94	03.0-23.00	35.76	10.13	06.0-16.000	25.55	09.74	07.0-15.0	22.14
Nods No. to first pod set	03.79	02.0-08.00	21.85	03.66	02.0-05.000	16.45	03.79	03.0-05.0	14.13
Days No. to first pod set	64.09	46.0-75.00	08.64	04.49	48.0-64.000	07.55	59.74	48.0-64.0	06.92
Pod length (cm)	19.49	08.0-30.00	18.07	18.62	13.0-25.000	18.18	20.47	01.5-25.0	11.76
Pod diameter (cm)	02.06	01.1-03.00	11.78	02.09	1.70-2.300	08.68	02.17	01.8-02.3	05.47
Pod weight (g)	31.05	10.0-61.73	29.76	30.52	15.1-45.600	26.39	35.37	25.4-45.6	16.39
Seeds No. per pod	04.81	02.3-07.70	16.85	04.87	03.3-06.000	14.17	05.20	04.3-06.0	08.45
Pods No. per plant	30.57	08.0-100.0	45.61	40.63	35.0-57.000	15.12	41.63	35.0-57.0	14.66
Total yield per plant (kg)	00.92	00.09-2.96	49.75	01.24	00.6-02.200	30.83	01.58	01.1-02.2	19.83

Table 2: Mean performances of the nine evaluated populations of Aquadolce cultivar and the two check cultivars Aspany and Giza blanka for the various studied characters

Characters Genotypes	Plant height (cm)	Stem diameter (cm)	Branches No. per plant	Days No. to first pod set	Nods No. to first Pod set	Pod length (cm)	Pod diameter (cm)	Pod weight (g)	Seeds No. per pod	Pods No. per plant	Total yield (Kg)
S_{2-1}	67.30^{h}	1.30^{b-d}	08.60^{cd}	54.80^{f}	4.53^{a}	9.47^{ef}	1.95^{a}	35.49^{d}	5.20^{bc}	37.70^{e}	1.40^{cd}
S_{2-2}	72.81^{g}	1.58^{a}	08.40^{cd}	69.20^{a}	4.18^{ab}	23.88^{b}	2.12^{a}	43.98^{b}	5.67^{a-c}	55.41^{c}	2.24^{ab}
S_{2-3}	101.10^{c}	1.17^{d}	08.50^{cd}	54.14^{f}	4.10^{ab}	23.20^{b}	1.98a	32.27e	5.87^{ab}	67.52^{a}	1.99^{b}
S_{2-4}	98.49^{c}	1.55^{a}	08.07^{de}	48.49^{g}	3.37^{b}	22.62^{bc}	2.31^{a}	43.49^{b}	5.77^{ab}	32.97^{g}	1.41^{cd}
S_{2-5}	140.01^{a}	1.40^{a-c}	13.50^{a}	64.09^{cd}	2.28^{c}	17.67^{g}	1.99^{a}	41.14c	5.13^{bc}	67.63^{a}	2.18^{ab}
S_{2-6}	109.22^{b}	1.48^{ab}	10.43^{b}	62.53^{d}	4.27^{ab}	29.23^{a}	2.30^{a}	53.82^{a}	6.53^{a}	25.89^{h}	1.30^{cd}
S^{2-7}	94.32^{d}	1.30^{b-d}	12.33^{a}	57.78^{e}	3.92^{ab}	21.33^{cd}	2.15^{a}	36.35^{d}	5.67^{a-c}	63.66^{b}	2.470^{a}
C_2	78.68^{f}	1.30^{b-d}	09.75^{bc}	59.70^{e}	3.79^{ab}	20.47^{de}	2.17^{a}	35.37^{d}	5.20^{bc}	41.63^{d}	1.55^{c}
Original pop.	89.22^{e}	1.20^{cd}	08.68^{cd}	68.17^{a}	3.90^{ab}	18.20^{fg}	2.18^{a}	35.72^{d}	4.87^{c}	35.32^{f}	1.27^{cd}
Aspany	101.29^{c}	1.30^{b-d}	07.07^{e}	65.75^{bc}	4.77^{a}	20.60^{de}	1.93^{a}	28.09^{f}	5.53^{bc}	27.20^{h}	1.09^{d}
Giza blanka	101.22^{c}	1.40^{a-c}	07.00^{e}	67.88^{ab}	4.77^{a}	15.84^{h}	2.05^{a}	15.70^{g}	5.07^{bc}	32.96^{g}	0.47^{e}

Values having the same alphabetical letter (s) within each column, don't significantly differ from one another, using Duncan's multiple range test at 0.05 level of probability

Table 3: Estimates of variance components, genotypic coefficient of variation, phenotypic coefficient of variation, broad sense heritability, expected genetic advance and genetic advance as percent of mean for 11 characters in the evaluated genotypes of broad bean

Parameters Characters	σ^2_g	σ^2_p	GCV	PCV	$H^2_{b.s.}$ (%)	GA	GAM
Plant height (cm)	389.44	392.39	20.60	20.68	99.25	40.50	42.28
Stem diameter (cm)	0.01	0.02	08.53	07.66	62.79	00.59	43.98
Branches No. per plant	4.08	4.40	22.55	21.71	92.66	04.00	42.99
Nods No. to first pod set	89.78	90.85	15.49	15.59	98.83	19.40	31.73
Days No. to first pod set	0.39	0.60	15.82	19.43	66.28	01.05	26.32
Pod length (cm)	12.97	13.37	17.04	17.29	97.02	07.30	34.54
Pod diameter (cm)	0.25	0.31	23.54	26.30	80.19	00.06	02.66
Pod weight (g)	94.59	95.50	26.65	26.78	99.04	19.93	54.61
Seeds No. per pod	0.16	0.29	07.23	09.76	54.86	00.60	10.91
Pods No. per plant	259.93	260.36	36.35	36.38	99.83	33.18	74.81
Total yield per plant (kg)	0.33	0.36	36.60	37.95	93.04	01.14	72.19

σ^2_g: Genotypic variance, σ^2_p: Phenotypic variance, GCV: Genotypic coefficient of variation, PCV: Penotypic coefficient of variation, $H^2_{b.s.}$ (%): Heritability in broad sense, GA: Expected genetic advance, GAM: Genetic advance as percent of mean

practiced individual plant selection method, were found to be those of the line S_{2-1} for plant height; the line S_{2-3} for pods number per plant; the line S_{2-4} for days number to first pod set; the lines S_{2-7} and S_{2-2} for total yield per plant; the line S_{2-5} for branches number per plant, nods number to first pod set and pods number per plant and the line S_{2-6} for pod length, pod weight and seeds number per pod.

Estimates of phenotypic and genotypic coefficients of variation: The results in Table 3 illustrate that both phenotypic and genotypic coefficients of variation reflected high values which were estimated by more than 20% for the six characters plant height, branches number per plant, pod diameter, pod weight, pods number per plant and total yield per plant. Whereas, the three characters nods number to first pod set, days number to first pod set and pod length showed relatively moderate levels of phenotypic and genotypic coefficients of variation. On the other hand, low phenotypic and genotypic coefficients of variation values were reflected by the two characters stem diameter and seeds number per pod.

Estimates of heritability: High broad sense heritability values, in Table 3, were recorded for all studied characters which were found to be in the range of 80.19% for pod diameter character up to 99.83% for pods number per plant, with only three exceptions. These exceptions were noticed in the estimated values of broad sense heritability for the characters stem diameter, days number to first pod set and seeds number per pod; which were estimated by 62.79, 66.28 and 54.86%, respectively.

Estimates of expected genetic advance: The estimated values of the expected genetic advance as well as genetic advance, expressed as percentage of genotypes mean, for 11 characters of the evaluated broad bean genotypes are presented in Table 3. The estimates of expected genetic advance were found to be in the range from 0.06 for pod diameter to 40.50 for plant height. Generally, the results show that the expected genetic advance values were considered moderate to high for all characters, with the exception of the three characters stem diameter, pod diameter and seeds number per pod. Comparatively, high values of genetic advance were recorded for pods number per plant, followed by total yield per plant and pod weight. This indicates that selecting the top 5% of the genotypes could make an advance of 74.81% in pods number per plant, 72.19% in total yield per plant and 54.61% in pod weight. High heritability along with high genetic advance is an important factor for predicting the resultant effect for selecting the best individuals. In the present investigation, high heritability along with high genetic advance as percent of the mean were obtained for pods number per plant, total yield per plant, pod weight, branches number per plant and plant height. On the other hand, the two characters nods number to first pod set and pod length exhibited relatively moderate genetic advance; however, their heritability estimates were high.

Estimates of phenotypic correlation coefficients: The estimates of phenotypic correlation coefficient values show generally that 11 out of 55 possible relationships were found to be either significant or highly significant; whereas, the other phenotypic correlations (44 relationships) were found to have too small values to be significant at the used testing level (Table 4). Ten out of eleven significant or highly significant relationships were found to have a positive trend, whereas, the other one appeared to be a negative value. Highly significant and positive correlations were detected between the pairs of the characters; total yield per plant with each of branches number per plant and pods number per plant; seeds number per pod with each of days number to first pod set, pod length and pod diameter and pods number per plant with branches number per plant. Significant and positive correlations were also observed between the pairs of the characters; stem diameter with each of seeds number per pod and pod diameter; pod weight and pod diameter and plant height and branches number per plant. On the other hand, significant and negative correlation was detected between number of branches per plant and nods number to first pod set.

Table 4: Phenotypic correlation coefficients among different pairs of the studied characters in broad bean cultivar Aquadolce

Characters	Stem diameter (cm)	Branches No. per plant	Days No. to first pod set	Nods No. to first pod set	Pod length (cm)	Pod diameter (cm)	Pod weight (g)	Seeds No. per pod	Pods No. per plant	Total yield per plant (Kg)
Plant height (cm)	0.068	0.489*	0.099	-0.399	-0.049	0.037	0.117	0.117	0.231	0.068
Stem diameter (cm)		0.114	0.121	0.120	0.376	0.439*	0.357	0.456*	-0.119	0.135
Branches No. per plant			-0.017	-0.424*	0.115	0.219	-0.040	0.189	0.579**	0.673**
Nods No. to first pod set				0.247	-0.182	0.102	0.193	-0.045	-0.097	-0.146
Days No. to first pod set					0.217	0.419	0.091	0.547**	-0.343	-0.258
Pod length (cm)						0.393	0.107	0.717**	-0.072	0.295
Pod diameter (cm)							0.452*	0.714**	-0.041	0.158
Pod weight (g)								0.169	-0.133	-0.196
Seeds No. per pod									0.032	0.295
Pods No. per plant										0.830**

*Significant at 0.05 level of probability, **Highly significant at 0.01 level of probability

DISCUSSION

The forgoing results of the various studied characters clearly indicated that the used original population of Aquadols broad bean cultivar was characterized by great variability magnitudes for most studied traits. Such result suggested the presence of good chances for selection and improvement in these characters which meant that good genotypes could be derived through selection methods. The obtained results showed also that the detected ranges for the various studied characters in the original population were really wide which suggested, clearly, the high potentialities for improving such characters in broad bean. Similar results were obtained by El-Hosary *et al.* (1983). In the present study, the realized response to mass selection was found in the characters plant height, branches number per plant, days number to first pod set, pod length, pods number per plant and total yield per plant, suggesting that the practiced mass selection reflected high scope for improvement of these traits. Concerning practiced individual plant selection method, using selfing with selection for two generations, favorable performances were obtained in all the studied characters; but, with different magnitudes. The obtained results in this respect were confirmed by the findings of Ragheb and El-Gamal (1992) and Abd-El-Kader-Helmy (2001) when they applied individual plant selection on broad bean. In attempt to determine which the preferable selection method would facilitate improvement of broad bean yielding ability between mass selection and individual plant selection methods. According to the current investigation, individual plant selection came in the first followed by mass selection. It appears that individual plant selection method considered better than mass selection method in the case of broad bean breeding for higher yield and some yield components under this work condition.

The moderate to high values of phenotypic-and genotypic-coefficients of variation (PCV and GCV) for most characters indicated that most of these traits might be further improved through selection programs. For all characters under the study, PCV values were greater than GCV values, with the exception of the two characters branches number per plant and stem diameter. In this concern, Kalia and Pathania (2007) recorded similar results for all studied characters on faba bean. Moreover, in most cases, the two values differed in narrow, indicating that the variability due to the genetic constitution of the genotypes was more than variability exerted by environmental factors. This result was supported by Abd-El-Haleem and Mohamed (2011), when they estimated PCV and GCV values for yield and yield components of faba bean. Although the genotypic coefficient of variation revealed the extent of genotypic variability present in the genotypes for various traits, it does not provide full scope to assess the variation that is heritable. As stated by Burton and Devane (1952), the genotypic coefficient of variations along with heritability estimates provide reliable estimate of the amount of genotypic advance to be expected through phenotypic selection.

Even though heritability estimates provide the basis for selection on the phenotypic performance, the estimates of heritability and genetic advance should always be considered simultaneously as high heritability, will not always be associated with high genetic advance (Johnson *et al.*, 1955). The estimates of genetic advance help in understanding the type of gene action involved in the expression of various polygenic characters. High values of genetic advance are indicative of additive gene action; whereas, low values are indicative of non-additive gene action (Singh and Narayanan, 1993). Thus, the heritability estimates will be reliable if an accompanied by a high genetic advance. As stated by Panse (1957), high heritability associated with equally high genetic advance is chiefly due to additive gene effect but if the heritability is mainly due to dominance and epistasis, the genetic gain would be low. Hence, selection for these characters would prove quite effective since the characters seemed to be governed by additive gene action. The presence of high heritability and moderated genetic advance are the effects of equal contribution of additive and non-additive gene action (Shelby, 2000). In the present investigation, high heritability along with high genetic advance as percent of the mean were obtained for pods number per plant, total yield per plant, pod weight, branches number per plant and plant height. Similar results were also noticed in dry bean (Raffi and Nath, 2004). High GCV along with high heritability and genetic advance will provide better information than a single parameter (Sahao *et al.*, 1990). Hence, in this study, total yield per plant, pods number per plant and pod weight exhibited high genotypic coefficient of variation, high heritabihty together with high genetic advance, indicating that these characters would be very useful as a base for selection in broad bean improvement selection programs. The forgoing results concerning the phenotypic correlation coefficients among all possible pairs of the studied characters of Aquadolce cultivar of broad bean, illustrated generally that desirable positive and significant associations were detected between the characters; stem diameter with each of pod diameter and seeds number per pod; branches number per plant with each of pods number per plant and total yield per plant; pod length and seeds number per pod; pod diameter with each of pod weight and seeds number per pod and pods number per plant and total yield. Alan and Geren (2007) recorded positive and significant correlation between number of branches per plant and seeds number per pod of faba bean. Such results suggested generally that selection for increasing of these characters would lead spontaneously to increases on the other ones which agreed with the objectives of the present study. On the contrary, undesirable positive and significant relationships between the pairs of the characters; plant height and branches number per plant and days number to first pod set and seeds number per pod. Such result clearly indicated that attention should be given in breeding programs to individual characters having undesirable correlations. In the same manner, negative and significant correlation between branches number per plant and nods number to first pod set was fund to be undesirable.

CONCLUSION

Based on the high heritability and high genetic advance shown by the different characters, especially, pods number per plant, total yield per plant and pod weight, it could conclude that the determinate genetic effects of the phenotypic expression of these characters are fundamentally of additive type. For this reason, a high response should be achieved after selection cycles. It was concluded also that individual plant selection is a preferable method for improvement yielding ability in broad bean and is recommended for broad bean breeding. Further, branches number per plant and pods number per plant could be used as selection criteria for higher yield under this method.

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