

**DRY COMMON BEANS (*Phaseolus vulgaris* L.) RESPONSE TO MULTITRAIT SELECTION FOR HIGH TEMPERATURE TOLERANCE IN LATE SEASON**

(Received: 3.5. 2012)

By  
**H. H. Hamed and S. M. Ahmed**

*Horticultural Research Institute, Agricultural Research Center, Giza Egypt*

**ABSTRACT**

The main target of the current study was to investigate the response of Nebraska (dry seed bean cv.) to multitrait selection based on selection index under high temperature season and knowing the availability of growing this cultivar on late sowing date without losing in yield quality and quantity. The study was carried out during the period from 2009 to 2011 at Kaha Vegetable Research Farm (Kaluobia Governorate). Responses to multitrait selection were detected in three generations of selection as well as the mother population under high temperature season. The selection index based on the characteristics; viz., number of primary branches, number of pods per plant, first class seed weight per plant, total seed weight per plant, yield per plant and pod setting (%). In addition, studying the phenotypic and genotypic variability, released genetic gain, differential of multitrait selection, heritability, as well as phenotypic and genotypic correlations between the characteristics of plant growth, yield, yield components and proline content in fresh leaves. SDS protein gel electrophoresis was extracted from the seeds of the selected generation under high temperature season. Field experiment was conducted in two sowing dates, the common season was sown on mid-February and the high temperature season was sown on 30 March. Obtained results reflected that the multitrait selection based on selection index increased genetic variation within the population or variety which remained under the selection for a long period. That facilitated obtaining new lines which possessed tolerance to high temperature. The results indicated that the magnitude of the genetic variability persisted in this material was sufficient for providing rather substantial amount of improvement through the selection of superior progenies. Therefore, the multitrait selection based on selection indices under high temperature had clear effect on mean values of each studied trait and differed from those of the mother population.

Although the total seed weight per plant had a significant difference among the estimates of mean values between the third generation of multitrait selection under high temperature season and mother population (under common sowing season) (15.863 and 19.510 g, respectively); there was considerable improvement compared to the first generation of multitrait selection (9.149 g). Bearing in mind that these results were achieved only after two cycles of multitrait selection.

The genetic gain responses to multitrait selection after two cycles of multitrait selection under high temperature recorded processions for all traits. Besides, the multitrait selection based on selection indices under high temperature season had clear effects on the genetic and phenotypic coefficient collocation from generation to generation (concerning the sign or degree of significance). Moreover, the multitrait selection based on selection indices under the high temperature stressed common bean (Nebraska cv.) compared to proline content in mother population. The extracted protein from the affected seeds produced under high temperature showed some bands that could be used as a biochemical or genetic marker.

**Key words:** *dry common bean, genetic correlation, high temperature tolerance, multitrait selection, Phaseolus vulgaris, selection indices.*

**1. INTRODUCTION**

Common bean belongs to the legume family that is widely cultivated and represents one of the largest food components in Latin America and Africa. It is valued for its high content of protein and micronutrients such as iron and folic acid. It is

one of the most economically important crops and provides an income source for small holder farmers (Pachico, 1989). The winter season period in Egypt is extended as a result of climatic changes in the summer season beginning. The common bean sowing date for instance used to be

from mid-February to the beginning of March, but due to the previously mentioned reason the sowing date and growing season period were affected.

There are two solutions for this problem. The first depends on ending the winter season early which is not recommended by the commercial market and the farmers. The second depends on producing new lines or varieties that could be adapted to climate changes which is the main target of the current study. Some studies indicated that Africa's agriculture is negatively affected by climate changes (Pearce *et al.*, 1996; McCarthy *et al.*, 2001). In addition, some other studies mentioned that adaptation is one of the policy options for reducing the negative impact of climate changes (Adger *et al.*, 2003; Kurukulasuriya and Mendelsohn, 2006). Adaptation to climate changes refers to natural or artificial adjustment in response to actual or expected climatic stimuli or their effects, which moderates harm or exploits beneficial opportunities (IPCC, 2001). Common adaptation methods in agriculture include using of new crop varieties and livestock species that are better suited to dry conditions, irrigation, crop diversification, adoption of mixed crop and livestock farming systems, and changing planting dates (Bradshaw *et al.*, 2004; Kurukulasuriya and Mendelsohn 2006; Nhemachena and Hassan, 2007). Although, common bean is mainly self-pollinated, many authors reported out crossing or natural hybridization in both wild and cultivated populations. Ibarra-Perez *et al.* (1997) reported cross-pollination rates between 0 and 85%. Common bean grows well at temperatures ranging from 15 to 27°C and will withstand temperatures up to 29.5°C. High temperature (close to or higher than 35°C) and humidity during flowering and pod setting results in abortion of large numbers of blossoms and developing pods. High temperature episodes have a major effect on yield especially when coinciding with flowering (Wheeler *et al.*, 2000), whereas increases in temperature mean have an effect on crop duration (Nigam *et al.*, 1994). The impact of short periods of high temperature on grain setting is able to reduce the season end and the yield significantly. The maximum temperature is not the only important factor in evaluating the effect of high temperature on yield but also the sowing date has its influence. In addition, most of the annual crops are extremely sensitive to high temperature during the developmental stage specially flowering period. Selection for superior genotypes based on one or

few traits is not effective, where the selected genotype might show superiority for the selected traits only. Therefore, simultaneous selection of traits, which can be performed effectively by the use of selection indices, increases the opportunity of successfully breeding programs. The selection indices enable selection based on a complex of variables of economic interest. However, relative efficiency of different selection procedures depend on the relative rate of improvement, time and cost of the procedure. Studies comparing effects of different selection procedures are reported by El-Lowendey (2003), Soliman and El-Lawendey (2008), Kassem *et al.* (2008) and El-Lawendey *et al.* (2011), their results prove that the estimation of phenotypic and genotypic coefficient variation in F<sub>4</sub> was higher than in F<sub>3</sub> generation. This indicates that, the magnitude of the genetic variability persisted in these material was sufficient for providing rather substantial amounts of improvement through the selection of superior progenies, the results were reported by Meena *et al.* (2001). Selection for two or more traits are different from single-trait selection. The genotype can be partitioned into parts representing different traits that can then be combined in several ways for selection. It is possible that the permanent and temporary changes of genetic variance and correlation are different of the various multiple-trait selection methods (Bennett and Swiger, 1980). The change in permanent genetic correlation following selection for two characteristics was not a surprise since pleiotropic gene frequencies were expected to change at rates different from independent gene frequencies. Rasmuson (1964) suggested that there might be differences among multiple-trait selection methods in the rate of change in permanent genetic correlation. The rate of change per unit of genetic response does not appear to be different when a large number of unlinked pleiotropic genes with small additive effects are the cause of genetic correlation. In any breeding program, selection is a dual-purpose task: selection for varieties and selection for parents. The requirement for a new variety is that it meets the minimum criterion for all essential breeding objectives while having superior package of traits, as measured by the selection index. Failure to meet the minimum criterion for any breeding objective will lead to the failure of the variety. This is where independent culling and index selection must be applied. In contrast, the requirement for a parent is that it is outstanding in one or more of the breeding objectives; a higher selection index is

desirable but not essential. The most appropriate strategy for selecting superior parents may be "independent selection" as opposed to "independent culling". Therefore, in all breeding programs and at any breeding stages, the selection scheme should consist of three strategies, explicitly or implicitly: (i) independent selection (ii) independent culling, and (iii) index selection, and in that order (Yan and Fregeau-Reid, 2008).

This investigation aimed to the obtainment of dry common bean line that can adapt to high temperature season using the multitrait selection based on selection index. This new cultivar can be grown in late sowing date without severe decreasing in the yield quality and quantity.

**2. MATERIALS AND METHODS**

This study was carried out at Kaha Vegetable Research Farm (Kaluobia Governorate, Egypt) during the period from 2009 to 2011. The soil type of the experimental site is classified as a clay soil. One genotype, Nebraska (a common grown variety for dry seed yield) was used. Seeds were obtained from the Vegetable Seed Production Unit, Vegetable Research Departments, Dokki, Giza, Egypt. Yield performance was compared in two sowing dates in the same field environment, *i.e.*, the common sowing date and the high

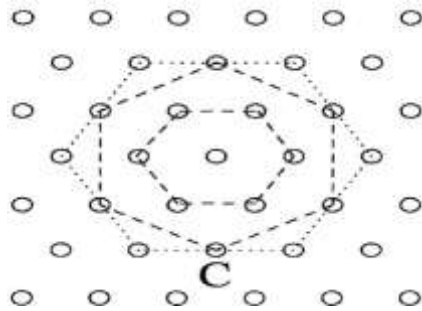
temperature in late season. The field experiment was conducted under common sowing season (C) was sown on mid-February 2011 (mother population) and under high temperature in late season (H) on 30 March 2009, 2010 and 2011 (the first generation of multitrait selection (S<sub>0</sub>), the second generation of multitrait selection (S<sub>1</sub>), and the third generation of multitrait selection (S<sub>2</sub>), respectively). Selection for high temperature late season tolerance was following two sowing dates, the common sowing season (C) as a control and the high temperature late season (H). The two seasons were assigned according to the maximum and minimum temperatures that affecting common beans growth and yield determined by Porch, 2006. Maximum, minimum and average temperatures and relative humidity in Table (1) were obtained from the Central Laboratory for Agricultural Climate (CLAC), Dokki, Giza. Seeds were sown in the field directly. Each ridge was 60 cm wide, 3.4 m long and 15 cm plant spacing. Data were recorded on the number of primary branches per plant, plant height, number of pods per plant, number of seeds per plant, first class seed weight per plant (was graded by using thieves of 7.33 mm), total seed weight per plant and pod setting (was calculated as the number of setting pods divided by the total number of pods).

**Table (1): Average temperature and relative humidity of field trials in Kaha Vegetable Research Farm, Kaha Kaluobia Governorate, Egypt for evaluation of the high temperature in late season response in common bean genotype during 2009, 2010 and 2011.**

Month	Temperature (C°)			Relative humidity (%)
	Average	Maximum	Minimum	
January	13.4	19.3C <sup>a</sup>	7.6	81
February	14.2	20.6C	14.2	78
March	16.4	23.2C	16.4	71
April	20.5	27.5H <sup>b</sup>	20.5	67
May	23.8	31.6H	23.8	64
June	26.4	35.9H	26.4	70
July	27.3	34.4H	27.3	77
August	27.4	34.0H	27.4	79
September	25.8	32.3H	25.8	78
October	23.6	30.3H	23.6	79
November	19.5	25.4C	19.5	72
December	14.9	20.8C	14.9	81

<sup>a</sup>: C = common season. <sup>b</sup>: H = high temperature in late season.

**2.1. Experimental design and statistical analysis:** the collected data between the mother population and the third generation of multitrait selection which was grown in 2011 were analyzed statistically using Fisher's analysis of variance technique. ANOVA and Duncan's multiple range test were employed to compare the difference among the treatment means at 5% level of probability. All computations were performed using the Minitab software (Minitab Inc., state college, PA, USA). Eight experimental units per generation, the experimental unit was consisted of one grid, one grid was contained of 19 plants (1 central plant + 18). Population was consisted of 152 plants (8 x 19) in one generation (Fig. 1), according to Bos and Caligari (1995). The highest eight selection index plants were selected through all the selecting generations.



**Fig. (1):** A regular triangular pattern of plant positions within experimental unit. Each plant in its turn is considered as a candidate and compared to the plants occurring alongside three (grid C) surrounding aureoles.

The breeder may divide the selection field into parts such that growing conditions within each of the so-called grids are more uniform than across the whole field. This procedure is called grid selection (Bos and Caligari, 1995). Separated analysis of variance was performed (Sokal and Rohlf, 1981).

ANOVA Table: Formulas

Source Variation	of	DF	SS	MS	F <sub>3</sub>	Expected MS
$\bar{Y} - \bar{Y}$ Among group (genetic lines)(grids)		a - 1	SS <sub>1</sub>	$\frac{SS_1}{(a - 1)}$	$\frac{MS \text{ groups}}{MS \text{ within}}$	$\frac{\sum \alpha^2}{a - 1}$
$Y - \bar{Y}$ Within group (error) (within genetic lines)		a (n-1)	SS <sub>2</sub>	$\frac{SS_2}{a (n-1)}$		
$\bar{Y} - \bar{Y}$ Total		an - 1	SS <sub>3</sub>			

**2.1.1. Estimation of selection index**

The formula used for estimating selection index was  $b = P^{-1}GV$  (Singh and Singh, 1994); where b is the column vector used to estimate the relative weights,  $P^{-1}$  is the inverse of phenotypic variance and covariance matrix, G is the genotypic variance and covariance matrix and V is the column vector of economic weights for the various characters under selection.

**2.1.2. Estimation of phenotypic, genotypic and environmental variation**

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

$$MSV - MSE$$

Where, genotypic variance ( $\sigma_g^2$ ) =  $\frac{MSV - MSE}{r \text{ or } n_0}$

Where, MSV and MSE are mean sum of squares due to populations (varieties or treatments) and error, respectively. Environmental variance ( $\sigma_e^2$ ) is equal to mean sum of squares for error (MSE). Phenotypic variance ( $\sigma_p^2$ ) is comprised of ( $\sigma_g^2$ ) plus ( $\sigma_e^2$ ); in addition, r = number of replications (in case of equal sample size) (Singh and Singh, 1994); while,  $N_0$  = average sample size (in case of unequal sizes) (Sokal and Rohlf, 1981). The phenotypic and genotypic coefficient of variation were estimated using the formula developed by Burton (1952).

$$\text{Phenotypic coefficient of variation} = \frac{\sqrt{V_{ph}}}{\bar{x}} \times 100$$

$$\text{Genotypic coefficient of variation} = \frac{\sqrt{V_g}}{\bar{x}} \times 100$$

Whereas  $\sqrt{V_{ph}}$  = Phenotypic standard deviation.

$\sqrt{V_g}$  = Genotypic standard deviation.

$\bar{x}$  = Genotypic means.

**2.1.3. Estimation of broad-sense heritability**

The formula used for estimating broad-sense heritability was  $h^2 = \sigma_g^2 / \sigma_p^2$  (Allard, 1960); where  $\sigma_g^2$  is the genetic and  $\sigma_p^2$  is the phenotypic variance.

**2.1.4. Estimation of released genetic gain (observed selection response)**

The formula used for estimating the genetic gain was  $R = (X_p - X_0)$  (Singh and Chaudhary, 1977); where R is the genetic gain and  $(X_p - X_0)$  is the difference between the progeny mean of selected individuals ( $X_p$ ) and the base population ( $X_0$ ).

**2.1.5. Estimation of selection differential:** Selection differential refers to the difference in

mean of the selected individuals ( $\bar{X}_s$ ) from that of

the base population ( $\bar{x}_0$ ). Symbolically  $S = \bar{x}_s - \bar{x}_0$  (Singh and Chaudhary, 1977).

**2.1.6. Estimation of relative efficiency for selection indices:** The relative efficiency of each index was computed by the ratio of genetic advance (gain) of the indices based on morphological characters to direct selection (Al-Rawi and Ahmed, 1984).

**2.1.7. Estimation of coefficient of correlation**

The used formula for estimating genotypic, phenotypic and environmental coefficients of correlation was  $r = Cov_{XY} / (\text{var}_x \cdot \text{var}_Y)^{1/2}$  (Falconer, 1989); where  $Cov_{XY}$  is genetic, phenotypic or environmental covariance between characters X and Y and  $\text{var}_x$  is genetic, phenotypic or environmental variance for character X and  $\text{var}_Y$  is genetic, phenotypic or environmental variance for character Y.

**2.2. Determination of proline content in fresh leaves**

Free proline was extracted from 0.5 g of fresh leaves in 3% (w/v) aqueous sulphosalicylic acid and determined by ninhydrin reagent (Bates *et al.*, 1973).

**2.3. SDS PAGE electrophoresis technique**

The SDS PAGE gel electrophoresis was used in protein band separation. The technique was composed of stacking gel that was prepared according to Laemmli method (Fahmy and Abou El-Nasr, 1998). The gel scanning was done on photo scanner and the data were integrated using the scanner software. The similarity in indices between the different treatments were calculated according to Kulczynski equation (Khafagi, 1995).

$$\text{Similarity \%} = \frac{1}{2} [(S/(S+U)) + (S/(S+V))] * 100$$

Where:  
S = number of bands found in both A and B columns

U = number of bands found in column A not in B

V = number of bands found in column B not in A

**3. RESULTS AND DISCUSSION**

**3.1. Genetic parameters of yield and its components in common bean genotype (Nebraska cv) through three generations of multitrait selection index under high temperature in late season were studied.**

Results in Table (2) revealed that mean values of the third generation of multitrait selection ( $S_2$ ) in respect to the characters of plant height (33.350 cm), number of pods per plant (16.446), number of seeds per plant (36.640), the first class seed weight per plant (8.730 g), total seed weight per

plant (15.863 g) and pod setting (43.970%) were higher than those of the first generation of multitrait selection ( $S_0$ ) for the same traits (32.140 cm, 11.196, 20.655, 5.482 g, 9.149 g, and 36.270%, respectively). While, the mean number of primary branches for ( $S_2$ ) (2.946) was lower than that of ( $S_0$ ) (6.220). All the previously mentioned results are consistent with breeder's objectives. There was a significant difference among the estimated mean values between the third generation of multitrait selection ( $S_2$ ) and the mother population (MP) for the characters number of primary branches (2.946 and 5.386, respectively), the plant height (33.350 and 47.750cm, respectively), the number of pods per plant (16.446 and 15.107, respectively), the first class seed weight per plant (8.730 and 14.562gm, respectively), the total seed weight per plant (15.863 and 19.510gm, respectively), and the pod setting (43.970% and 50.300%, respectively). Despite the significant difference among the estimates of mean values between the third generation of multitrait selection ( $S_2$ ) and the mother population (MP), remarkable increase in mean values through the generations of multitrait selection based on selection index indicated a requirement for more selected generations.

Results of phenotypic variance and phenotypic coefficient variance values in the third generation of multitrait selection ( $S_2$ ) of each studied traits differed from those of the mother population through the three generations of multitrait selection. The results revealed that there was an increase in phenotypic coefficient variance of the third generation of multitrait selection ( $S_2$ ) compared to the first generation of multitrait selection ( $S_0$ ) for the characters number of primary branches (26.590 and 14.340, respectively), plant height (14.470 and 12.440 cm, respectively). The results indicated that there was a decrease in phenotypic coefficient variance of the third generation of multitrait selection ( $S_2$ ) compared to the first generation of multitrait selection ( $S_0$ ) for the characters number of seeds per plant (45.160 and 52.460, respectively), the first class seed weight per plant (62.570 and 67.210 gm, respectively), total seed weight per plant (47.030 and 55.210 gm, respectively), and pod setting (%) (38.420 and 42.630 %, respectively). These results are in accordance with the breeding objectives. The results indicated that there was an increase in phenotypic coefficient variance of the third generation of multitrait selection ( $S_2$ ) compared to the mother population (MP) for all the studied traits.

**Table (2): Genetic parameters of yield and its components in common bean genotype through three generations of multitrait selection based on selection index under high temperature in late season.**

Parameters of genetics <sup>1</sup>	Trait <sup>2</sup>						
	NPB	PH (cm)	NP	NS	FCSW (g)	TSW (g)	PS (%)
<b>S<sub>0</sub></b>							
Mean	6.220	32.140	11.196	20.655	5.482	9.149	36.270
SE Mean	0.069	0.308	0.344	0.836	0.284	0.390	1.190
StDev	0.891	3.997	4.456	10.835	3.684	5.052	15.470
Genetic variance	-0.223	37.397	-6.457	-17.021	5.059	-0.751	-16.329
Environmental variance	0.818	15.560	20.090	112.992	13.235	24.619	234.303
Phenotypic variance	0.595	52.957	13.633	95.971	18.294	23.868	217.974
Phenotypic C V %	14.340	12.440	39.800	52.460	67.210	55.210	42.630
Genetic C V %	13.530	9.423	17.437	12.044	33.506	12.462	6.788
<b>S<sub>1</sub></b>							
Mean	3.088	35.604	12.000	25.480	5.550	10.780	39.700
SE Mean	0.096	0.384	0.451	1.390	0.409	0.606	1.200
StDev	0.898	4.977	5.848	18.010	5.301	7.857	15.530
Genetic variance	0.026	6.079	147.915	1030.520	50.388	169.828	1.517
Environmental variance	0.673	22.109	29.613	238.820	20.309	45.189	231.360
Phenotypic variance	0.699	28.188	177.528	1269.340	70.697	215.017	232.877
Phenotypic C V %	29.140	13.980	48.740	70.700	95.520	72.880	39.11
Genetic C V %	15.930	5.401	35.593	27.234	58.794	41.014	3.424
<b>S<sub>2</sub></b>							
Mean	2.946 <sup>b</sup>	33.350 <sup>b</sup>	16.446 <sup>b</sup>	36.640 <sup>a</sup>	8.730 <sup>b</sup>	15.863 <sup>b</sup>	43.970 <sup>b</sup>
SE Mean	0.060	0.375	0.493	1.280	0.421	0.576	1.300
StDev	0.783	4.858	6.391	16.550	5.462	7.640	16.900
Genetic variance	-0.157	1.021	47.905	292.430	-7.436	30.663	436.410
Environmental variance	0.477	19.376	30.339	223.310	22.562	43.617	258.790
Phenotypic variance	0.320	20.397	78.244	515.740	15.126	74.280	695.200
Phenotypic C V %	26.590	14.570	38.86	45.160	62.570	47.030	38.420
Genetic C V %	26.170	3.692	19.592	13.823	23.167	18.168	12.731
<b>MP</b>							
Mean	5.386 <sup>a</sup>	47.750 <sup>a</sup>	15.107 <sup>a</sup>	37.760 <sup>a</sup>	14.562 <sup>a</sup>	19.510 <sup>a</sup>	50.300 <sup>a</sup>
SE Mean	0.054	0.218	0.444	1.200	0.516	0.631	1.270
StDev	0.700	2.830	5.756	15.560	6.683	8.182	16.440
Genetic variance	-0.165	5.012	-10.466	211.470	34.724	59.021	463.200
Environmental variance	0.502	6.392	31.493	243.303	44.920	67.263	261.190
Phenotypic variance	0.337	11.404	21.027	454.773	79.644	126.284	724.390
Phenotypic coefvar %	13.000	5.930	38.100	41.210	45.890	41.940	32.680
Genetic coefvar %	14.501	3.838	14.582	12.369	20.417	17.400	11.296

<sup>1</sup>: SE Mean = Standard error mean; StDev = Standard deviation; Phenotypic coefvar = Phenotypic coefficient variance; S<sub>0</sub> = The first generation of multitrait selection; S<sub>1</sub> = The second generation of multitrait selection; S<sub>2</sub> = The third generation of multitrait selection; MP = Mother population. <sup>2</sup>: NPB = Number of primary branches; PH = Plant height; NP = Number of pods per plant; NS = Number of seeds per plant; FCSW = The first class seed weight per plant; TSW = Total seed weight per plant; PS = Pod setting (%). Any means within rows followed by the same letter are not statistically different at 5% level (Duncan's multiple test).

Data of genetic variance and genetic coefficient variance values in the third generation of multitrait selection (S<sub>2</sub>) of each studied trait differed from those of the mother population through the three generations of multitrait selection. The results revealed an increase in genetic coefficient variance of the third generation of multitrait selection (S<sub>2</sub>) compared to the first generation of multitrait selection (S<sub>0</sub>) for the characters number of primary branches (26.170 and 13.530, respectively), number of pods per plant (19.592 and 17.437, respectively), number of

seeds per plant (13.823 and 12.044, respectively), total seed weight per plant (18.168 and 12.462 gm, respectively) and pod setting (%) (12.731 and 6.788 %, respectively). The results indicated a reduction in genetic coefficient variance of the third generation of multitrait selection (S<sub>2</sub>) compared to the first generation of multitrait selection (S<sub>0</sub>) for the characters plant height (3.692 and 9.423, respectively) and the first class seed weight per plant (23.167 and 33.506, respectively).

The results revealed an increase in genetic

coefficient variance of the third generation of multitrait selection ( $S_2$ ) compared to the mother population (MP) for all the studied traits except for plant height. These results agree with those of Bennett and Swiger (1980) who reported that selection for two or more traits is different from single-trait selection. The genotype can be partitioned into parts representing different traits that can be combined in several ways for selection. It is possible that the permanent and temporary changes of genetic variance and correlation are different for the various multiple-trait selection methods. A permanent effect of selection aimed to increase the means of one or more multi locus traits with additive genetic variances is an increase in the frequency of favourable alleles. Gene frequency changes may alter genetic variance and correlations, meanwhile, gene frequency changes from short-term selection for multi-locus traits are usually considered to be small and have a little effect on genetic variance and correlation. Moreover, El-Lawendey and El-Dahan (2012) mentioned that the phenotypic coefficient variation was generally higher than the genetic coefficient variation for all the studied traits, but in many cases, the values of phenotypic coefficient variation and genetic coefficient variation differed only slightly. Also, the estimates of phenotypic coefficient variance and genetic coefficient variance in  $F_4$  for most traits were higher than those of  $F_3$  generation. This indicates that, the magnitude of the genetic variability persisted in this material was sufficient for providing rather substantial amounts of improvement through the selection for superior progenies.

Equations presented in Table (3) showed that construction of selection indices using the discriminating function technique was helpful in discriminating desirable genotypes on the basis of their phenotypic performance as mentioned by Singh and Singh (1994). The indices were constructed on the basis of the characters; number of primary branches, number of pods per plant, first class seed weight per plant, total seed weight per plant and pod setting (%). These previous characteristics agree with those reported by Amankwa and Michaels (1997) and Salehi *et al.* (2008). The results showed that the highest value of selection efficiency occurred in the selected third generation indices made the third generation of selection.

Table (4) shows the data after two-cycles of multitrait selection ( $S_0-S_2$ ) illustrating that all traits showed high realized genetic gain values as compared with the first cycle of multitrait selection ( $S_0-S_1$ ), where the positive values indicate the occurrence of increases in the positive direction for the character. While, the negative values reflect decreases or changes in the negative direction for the character. The results revealed an increase in realized genetic gain of the third-cycle of multitrait selection ( $S_0-S_2$ ) compared to the first cycle of multitrait selection ( $S_0-S_1$ ) for the characters number of primary branches (-3.274 and 3.137, respectively), number of pods per plant (5.250 and 0.804, respectively), first class seed weight per plant (3.248 and 0.068, respectively, total seed weight per plant (6.718 and 1.613 gm, respectively) and pod setting (%) (7.700 and 3.430 %, respectively). These results are in accordance with breeding objectives. Data indicated that there was an increase in the mean values of the selected plants due to the selection index of the third cycle of multitrait selection ( $S_0-S_2$ ) compared to the first cycles of multitrait selection ( $S_0-S_1$ ) for the characters number of pods per plant (29.900 and 23.300, respectively), first class seed weight per plant (21.814 and 14.906, respectively), total seed weight per plant (33.100 and 23.196 gm, respectively) and pod setting (%) (77.187 and 68.569 %, respectively). The results are in harmony with the breeder's objectives.

The results revealed an increase in differential of multitrait selection based on selection index of the third cycle of multitrait selection ( $S_0-S_2$ ) compared to the first cycles of multitrait selection ( $S_0-S_1$ ) for the characters number of primary branches (1.954 and 1.780, respectively), number of pods per plant (13.454 and 12.104, respectively) first class seed weight per plant (13.084 and 9.424 gm, respectively), total seed weight pre plant (17.237 and 14.047 gm, respectively) and pod setting (%) (33.217 and 32.299 %, respectively).

The results showed an increase in heritability values for the third cycle of multitrait selection based on selection index compared to the first cycle of multitrait selection ( $S_0-S_1$ ) for the characters number of pods per plant (0.612 and -0.474, respectively), total seed weight per plant (0.413 and -0.031 gm, respectively) and pod setting (%) (0.628 and - 0.075 %, respectively). A similar trend was obtained by de Silva *et al.*

**Table (3): Values of selection indices and their relative efficiency for common bean genotype through three generations of multitrait selection under high temperature in late season.**

Generation of selection <sup>1</sup>	Selection indices <sup>2</sup>	Relative efficiency (%)
S0	0.374X <sub>1</sub> +0.363X <sub>2</sub> +0.586X <sub>3</sub> +0.512X <sub>4</sub> +0.568X <sub>5</sub>	22.043
S1	0.037X <sub>1</sub> +0.059X <sub>2</sub> +0.065X <sub>3</sub> +0.145X <sub>4</sub> +1.416X <sub>5</sub>	40.770
S2	0.491X <sub>1</sub> +0.496X <sub>2</sub> +0.486X <sub>3</sub> +0.498X <sub>4</sub> +0.492X <sub>5</sub>	81.283

<sup>1</sup>: S<sub>0</sub> = The first generation of multitrait selection; S<sub>1</sub> = The second generation of multitrait selection; S<sub>2</sub> = The third generation of multitrait selection; MP = Mother population. <sup>2</sup>: X<sub>1</sub> = Number of primary branches; X<sub>2</sub> = Number of pods per plant; X<sub>3</sub> = The first class seed weight per plant; X<sub>4</sub> = Total seed weight per plant; X<sub>5</sub> = Pod setting (%).

**Table (4): Estimate of the genetic gain of common bean genotype based on selection index combining five traits of agronomic interest through three generations of multitrait selection under high temperature in late season.**

CS <sup>a</sup>	Trait <sup>b</sup>	Δ <sub>RG</sub>	Δ <sub>RG</sub> (%)	X <sub>Si</sub>	Δ <sub>Si</sub>	h <sup>2</sup>
S <sub>0</sub> - S <sub>1</sub>	NPB	-3.137	-101.00	8.000	1.780	-0.375
	NP	0.804	6.700	23.300	12.104	-0.474
	FCSW	0.068	1.225	14.906	9.424	0.277
	TSW	1.631	15.130	23.196	14.047	-0.031
	PS	3.430	8.640	68.569	32.299	-0.075
S <sub>1</sub> - S <sub>2</sub>	NPB	-0.137	-4.650	5.300	2.217	0.037
	NP	4.446	27.034	28.900	16.900	0.833
	FCSW	3.180	36.426	21.597	16.047	0.713
	TSW	5.083	32.043	34.525	23.745	0.790
	PS	4.270	9.711	74.475	34.775	0.007
S <sub>0</sub> - S <sub>2</sub>	NPB	-3.274	-111.00	4.900	1.954	-0.491 (-0.491) <sup>c</sup>
	NP	5.250	31.923	29.900	13.454	0.612 (-0.498) <sup>c</sup>
	FCSW	3.248	37.205	21.814	13.084	-0.492 (0.436) <sup>c</sup>
	TSW	6.718	42.325	33.100	17.237	0.413 (-0.491) <sup>c</sup>
	PS	7.700	17.512	77.187	33.217	0.628 (-0.491) <sup>c</sup>

<sup>a</sup>: CS = Cycle of multitrait selection; (S<sub>0</sub> - S<sub>1</sub>) = The first cycle of multitrait selection; (S<sub>1</sub> - S<sub>2</sub>) = The second cycle of multitrait selection; (S<sub>0</sub> - S<sub>2</sub>) = The third cycle of multitrait selection. <sup>b</sup>: NPB = Number of primary branches; NP = Number of pods per plant; FCSW = The first class seed weight per plant; TSW = Total seed weight per plant; PS = Pod setting (%). <sup>c</sup>: Broad - sense heritability of mother population.

(2008) who mentioned that the selection for one trait only can rise undesirable changes of other important traits due to the association among them. In this context, the chances of success in an improvement program can be increased by simultaneous selection of a set of important traits in a crop. In addition, Lerner (2002) reported that there is a function of genes in providing a basis for the development of the trait within the individual, hence, heritability describes something about a population and nothing about an individual. Accordingly, the selected generations were obtained from individual plants under different conditions. Negative heritability can be assumed to be zero (Gabriele, and Wehner, 2007 and Sabu

*et al.*, 2009) but should be reported in order to contribute to the accumulation of knowledge which may be properly interpreted (Gabriele and Wehner, 2007). Galal and Karam (1984) reported that when heritability is equal to zero the trait would be kept under selection for a long time, which requires following other ways of selection instead of phenotypic or mass selection. Breeders must achieve an increasing in additive genetic variation and prevent its decreasing. Nakano *et al.* (1998), Nakano *et al.* (2000), Suzuki *et al.* (2001) and Tsukaguchi *et al.* (2003) reported that high temperature in the summer is causing a drastic reduction in common bean yield. Moreover, higher pod set in branches, which vary with the



cultivar and temperature, plays an important role in achieving a higher harvest index in the heat-tolerant compared to the heat-sensitive cultivars. In addition, Porch (2006) indicated that it is possible to identify superior genotypes for heat tolerance based on their stress indices. In this evaluation of heat tolerance indices, stress tolerance indices and the geometric mean, although correlated, were found to be effective stress indices for the selection of genotypes with good yield potential under stress and low-stress conditions.

**3.2.** Phenotypic, genetic and environmental correlations in common bean genotype through three generations of multitrait selection based on selection index under high temperature in late season among all pairs were studied.

Data in Table (5) revealed the presence of high positive and significant genetic correlation between total seed weight per plant and each of plant height in the first generation of multitrait selection and the mother population (0.881 and 0.377, respectively). Also, total seed weight per plant reflected a high positive and the significant genetic correlation coefficient with the number of pods per plant in the second generation of multitrait selection (0.931). Besides, total seed weight per plant showed an increased positive and significant genetic correlation with the first class seed weight per plant in both the first and the third generations of multitrait selection (0.394 and 0.694, respectively). Moreover, total seed weight per plant appeared to have high positive and significant genetic correlation with pod setting in both the second and the third generation of multitrait selection (0.766 and 0.325, respectively). On the other hand, total seed weight per plant showed highly negative and significant genetic correlation coefficient with number of pods per plant in both first generation of multitrait selection and mother population (-0.911 and -0.412, respectively). Also, total seed weight per plant involved high negative and significant genetic correlation coefficient with number of primary branches in the first generation of multitrait selection (-0.577). In addition, total seed weight per plant showed highly negative and significant correlation with plant height in the third generation of multitrait selection (-0.423).

Data in Table (5) revealed the presence of high positive and significant phenotypic correlation coefficient between total seed weight per plant and plant height in both first and third generations of multitrait selection and mother population (0.566, 0.427, and 0.338, respectively). Besides, positive

significant phenotypic correlation coefficient was found between total seed weight per plant and number of pods per plant in all generations of multitrait selection and mother population (0.764, 0.224, 0.860 and 0.414, respectively). Also, total seed weight per plant showed increased positive and significant phenotypic correlation coefficient with pod setting in all generations of multitrait selection (0.340, 0.905 and 0.358, respectively). Breeders are concerned with genetic correlations under some circumstances, because it may be more effective to conduct indirect selection for grain yield or stress tolerance *via* selection for a correlated trait than to select directly. Estimates of genetic correlation between traits or between the same traits measured in different environments are useful in determining the predictive power of a screen or selection environment. These results agree with those of Bennett and Swiger (1980) who reported that selection for two or more traits is different from a single trait selection. The genotype can be partitioned into parts representing different traits that could be combined in several ways for selection. It is possible that the permanent and temporary changes of genetic variance and correlation are different for the various multiple trait selection methods. Moreover, the effect of increasing selection intensity and heritability was generally to intensify the changes in genetic variances and correlation. In addition, the changes in permanent genetic correlation followed by selection for two traits were not surprising since pleiotropic gene frequencies were expected to change at rates different from independent gene frequencies (Rasmuson, 1964). Correlation between characters seriously complicate the measurement of phenotypic selection because selection on particular trait produces not only a direct effect on the distribution of that trait in a population but also produces indirect effects on the distribution of correlated characters (Land and Arnold, 1983). Phenotypic correlation in a genetically heterogeneous population depends on both genetic and environmental correlation which might have very different values, even values of opposite signs (Toms *et al.*, 1994). The results of genetic and phenotypic correlations of common bean in mother population were almost similar to results obtained by Amankwa and Michaels (1997). The relationship between phenotypic and genetic correlations in plants is poorly understood (Waitt and Levin, 1998).

**3.3.** Proline content, SDS protein electrophoresis and similarity of common bean genotype through

**Table (5): Phenotypic, genetic and environmental correlations in common bean genotype through three generations of multitrait selection based on selection index under high temperature in late season among all pairs of the studied traits.**

Trait i with j	Generation of Selection <sup>1</sup>	$r_{gij}$	$r_{eij}$	$r_{pij}$
<b>Number of primary branches (i)</b>				
<b>Plant height</b>	S <sub>0</sub>	-0.081	0.231**	0.105
	S <sub>1</sub>	-0.124	0.171	0.137
	S <sub>2</sub>	-0.370**	0.156	0.127
	MP	-0.185	0.282**	0.172
<b>Number of pods per plant</b>	S <sub>0</sub>	-0.177	0.199	0.208
	S <sub>1</sub>	-0.095	0.137	0.038
	S <sub>2</sub>	-0.057	0.126	0.065
	MP	-0.126	0.126	0.126
<b>Number of seeds per plant</b>	S <sub>0</sub>	-0.118	0.085	0.078
	S <sub>1</sub>	-0.022	0.044	0.015
	S <sub>2</sub>	-0.023	0.046	0.025
	MP	-0.025	0.045	0.028
<b>First class seed weight per plant</b>	S <sub>0</sub>	-0.240	0.246	0.168
	S <sub>1</sub>	-0.161	0.155	0.056
	S <sub>2</sub>	-0.145	0.145	0.146
	MP	-0.053	0.102	0.069
<b>Total seed weight per plant</b>	S <sub>0</sub>	-0.577**	0.183	0.155
	S <sub>1</sub>	-0.062	0.102	0.035
	S <sub>2</sub>	-0.073	0.105	0.065
	MP	-0.045	0.085	0.054
<b>Pod setting</b>	S <sub>0</sub>	-0.122	0.059	0.052
	S <sub>1</sub>	-0.257**	0.054	0.049
	S <sub>2</sub>	-0.019	0.043	0.022
	MP	-0.019	0.044	0.022
<b>Plant height (i)</b>				
<b>Number of pods per plant</b>	S <sub>0</sub>	0.912**	0.885**	0.977**
	S <sub>1</sub>	-0.179	0.824**	0.222**
	S <sub>2</sub>	-0.523**	0.779**	0.381**
	MP	+0.706**	0.443**	0.736**
<b>Number of seeds per plant</b>	S <sub>0</sub>	+0.763**	0.370**	0.771**
	S <sub>1</sub>	-0.077	0.290**	0.080
	S <sub>2</sub>	-0.185	0.288**	0.154
	MP	0.203*	0.161	0.180
<b>First class seed weight per plant</b>	S <sub>0</sub>	0.961**	0.982**	0.808**
	S <sub>1</sub>	-0.369**	0.990**	0.325**
	S <sub>2</sub>	0.327**	0.925**	0.752**
	MP	0.464**	0.377**	0.415**
<b>Total seed weight per plant</b>	S <sub>0</sub>	0.881**	0.791**	0.566**
	S <sub>1</sub>	-0.197	0.672**	0.191
	S <sub>2</sub>	-0.423**	0.653**	0.427**
	MP	0.377**	0.307**	0.338**
<b>Pod setting</b>	S <sub>0</sub>	0.887**	0.259**	0.488**
	S <sub>1</sub>	-0.777**	0.308**	0.205**
	S <sub>2</sub>	-0.082	0.273**	0.148
	MP	0.095	0.157	0.121

Cont. Table (5)				
Trait i with j	Generation of selection <sup>1</sup>	$r_{gij}$	$r_{eij}$	$r_{pij}$
<b>Number of pods per plant (i)</b>				
<b>Number of seeds per plant</b>	S <sub>0</sub>	-0.617**	0.424**	0.380**
	S <sub>1</sub>	0.052	0.222*	0.082
	S <sub>2</sub>	0.267*	0.362**	0.306**
	MP	-0.219*	0.361**	0.218*
<b>First class seed weight per plant</b>	S <sub>0</sub>	-0.874**	0.833**	0.885**
	S <sub>1</sub>	0.527**	0.829**	0.587**
	S <sub>2</sub>	0.712**	0.754**	0.756**
	MP	-0.527**	0.837**	0.523**
<b>Total seed weight per plant</b>	S <sub>0</sub>	-0.911**	0.908**	0.764**
	S <sub>1</sub>	0.159	0.508**	0.224*
	S <sub>2</sub>	0.931**	0.822**	0.860**
	MP	-0.412**	0.686**	0.414**
<b>Pod setting</b>	S <sub>0</sub>	-0.607**	0.293*	0.254*
	S <sub>1</sub>	0.716**	0.358**	0.898**
	S <sub>2</sub>	0.421**	0.339**	0.390**
	MP	-0.133	0.345**	0.178
<b>Number of seeds per plant (i)</b>				
<b>First class seed weight per plant</b>	S <sub>0</sub>	-0.602**	0.909**	0.798**
	S <sub>1</sub>	0.451**	0.911**	0.578**
	S <sub>2</sub>	0.884**	0.751**	0.830**
	MP	-0.120	0.454**	0.195
<b>Total seed weight per plant</b>	S <sub>0</sub>	0.028	0.076	0.086
	S <sub>1</sub>	0.009	0.050	0.017
	S <sub>2</sub>	0.154	0.130	0.140
	MP	-0.012	0.033	0.012
<b>Pod setting</b>	S <sub>0</sub>	-0.962**	0.698**	0.675**
	S <sub>1</sub>	0.852**	0.091	0.912**
	S <sub>2</sub>	0.944**	0.930	0.937
	MP	0.870**	0.963**	0.897**
<b>First class seed weight per plant (i)</b>				
<b>Total seed weight per plant</b>	S <sub>0</sub>	0.394**	0.143	0.161
	S <sub>1</sub>	-0.009	0.124	0.024
	S <sub>2</sub>	0.694**	0.244	0.541
	MP	-0.035	0.087	0.032
<b>Pod setting</b>	S <sub>0</sub>	0.684**	0.237*	0.307**
	S <sub>1</sub>	0.820**	0.295*	0.515**
	S <sub>2</sub>	-0.126	0.296*	0.151
	MP	0.328**	0.416**	0.361**
<b>Total seed weight per plant (i)</b>				
<b>Pod setting</b>	S <sub>0</sub>	-0.055	0.326**	0.340**
	S <sub>1</sub>	0.766**	0.440**	0.905**
	S <sub>2</sub>	0.325**	0.411**	0.358**
	MP	-0.010	0.054	0.018

<sup>1</sup> S<sub>0</sub> = The first generation of multitrait selection; S<sub>1</sub> = The second generation of multitrait selection; S<sub>2</sub> = The third generation of multitrait selection; MP = Mother population;  $r_{gij}$  = Genetic correlation;  $r_{eij}$  = Environmental correlation;  $r_{pij}$  = Phenotypic correlation.  
\*, \*\* significant at 5% and 1% respectively.

three generations of multitrait selection based on selection index under high temperature in late season:

Results in Table (6) showed significant elevation in proline content that was extracted from fresh leaves in high temperature stressed common bean (Nebraska cv) compared to proline content in mother population (0.360, 0.356, 0.357 and 0.274 µg/g fresh mass, respectively). Similar results were obtained by Nogesh and Devraj (2008), Wahid and Close (2007), and Ashraf and Foolad (2007) on French beans and sugarcane.

Generation of selection <sup>1</sup>	Mean
S0	0.360 <sup>a</sup>
S1	0.356 <sup>a</sup>
S2	0.357 <sup>a</sup>
MP	0.274 <sup>b</sup>

<sup>1</sup>:S<sub>0</sub> = The first generation of multitrait selection; S<sub>1</sub> = The second generation of multitrait selection; S<sub>2</sub> = The third generation of multitrait selection; MP = Mother population. Any means within rows followed by the same letter are not statistically different at 5% level (Duncan's multiple test).

Electrophoretic SDS protein patterns were shown in Table (7). The total number of protein bands obtained by scanning the gel of seed proteins of the four generations of multitrait selection under high temperature in late season were 17 distinguished bands that varied from generation to another. The number of these bands ranged from 7 to 11 bands in the generation of multitrait selection under high temperature in late season. The highest number of seed protein band (11 bands) was found in the second generation of multitrait selection, and the lowest number; (7 bands) was recorded in the third generation of multitrait selection. Only two bands namely 11 and 12 were found in all generations. Band number 4 was found only in seed protein of the mother population and both first and second generations of multitrait selection. Bands number 3 and 10 were found only in seed protein of the mother population and both the first and the third generations of multitrait selection. The band number 14 was found only in seed protein of the mother population and both second and third generations of multitrait selection under high

temperature in late season. Also, bands number 6 and 9 were found only in seed protein of both first and second generations of multitrait selection. Bands number 13 and 16 were found only in seed protein of mother population, second and third generations of multitrait selection under high temperature in late season. In addition, bands number 15 and 17 were found only in seed protein of both second and third generations of multitrait selection under high temperature in late season. While, band number 2 was found only in seed protein of first generation of multitrait selection. Also, band number 5 was found only in seed protein of mother population. Band number 7 was found only in seed protein of mother population. Meanwhile, band number 8 was found only in seed protein of second generation of multitrait selection under high temperature in late season. Some specific bands (band 15 and 17) of the examined seed protein of the generation of multitrait selection showed relation to tolerance for high temperature in late season. This might be used as a biochemical genetic marker for this character (high temperature tolerance).

The results in Table (8) represent the values of the similarity indices among the four seed proteins of the generations of multitrait selection under high temperature in late season. The results indicated that the highest similarity was between

Band number	Generation of selection <sup>1</sup>			
	MP	S <sub>0</sub>	S <sub>1</sub>	S <sub>2</sub>
1	-	-	-	-
2	-	+	-	-
3	+	+	-	+
4	+	+	+	-
5	+	-	-	-
6	-	+	+	-
7	+	-	-	-
8	-	-	+	-
9	-	+	+	-
10	+	+	-	+
11	+	+	+	+
12	+	+	+	+
13	+	-	+	-
14	+	-	+	+
15	-	-	+	+
16	+	-	+	-
17	-	-	+	+

<sup>1</sup>:S<sub>0</sub> = The first generation of multitrait selection; S<sub>1</sub> = The second generation of multitrait selection; S<sub>2</sub> = The third generation of multitrait selection; MP = Mother population.

the mother population and the third generation of multitrait selection (60.417%). The lowest similarity was between the first generation of multitrait selection and the third generation of multitrait selection (53.571%). These results agree with those of Nogesh and Devraj (2008) who reported that SDS-PAGE patterns of stressed French bean also showed intensification of few protein bands and appearance of at least five new bands. Interestingly, the SDS-PAGE patterns of salt and temperature stress differed significantly, indicating the involvement of different controllers.

**Table (8): The percentages of similarity between the protein bands resulted from the generation of multitrait selection of dry common bean genotype.**

Generation of selection <sup>1</sup>	MP	S0	S1	S2
MP	-			
S0	59.027	-		
S1	57.273	53.977	-	
S2	60.714	53.571	58.442	-

<sup>1</sup>:S<sub>0</sub> = The first generation of multitrait selection; S<sub>1</sub> = The second generation of multitrait selection; S<sub>2</sub> = The third generation of multitrait selection; MP = Mother population.

**Conclusion**

It could be concluded that (i) the multitrait selection based on selection indices increased the genetic variation within the population or variety which remained under the selection for a long time. That helped in obtaining new tolerated strains to high temperature in late season. That indicates to the magnitude of the genetic variability persisted in this material that was sufficient for providing rather substantial amount of improvement through the selection of superior progenies. Therefore, the results showed that multitrait selection based on selection indices under high temperature in late season had clear effects on mean values of each studied traits and differed from that of mother population. Although, the total seed weight per plant had a significant difference among the estimates of mean values between the third generation of multitrait selection under high temperature in late season and mother population (15.863 and 19.510gm, respectively), but there was considerable improvement compared to the first generation (9.149gm). These results are in accordance with breeding objectives. (ii) the genetic gain responses to multitrait selection after two cycles of multitrait selection under high temperature in late season recorded

processions for all traits. Besides, the multitrait selection based on selection indices under high temperature in late season had clear effects on genetic and phenotypic coefficient correlation from generation to generation (concerning the sign or degree of significance). (iii) moreover, the multitrait selection based on selection indices showed elevation in proline content that was significantly observed in high temperature stressed common bean (Nebraska cv) compared to proline content in mother population. (iv) the separated protein from the affected seed by high temperature in late season showed some bands that can be used as biochemical or genetic marker.

**4. REFERENCES**

Adger W.N., Huq S., Brown K., Conway D. and Hulme M. (2003). Adaptation to climate change in the developing world. Progress in development studies. 3: 179 – 195.

Allard R.W. (1960). Principles of Plant Breeding. John Wiley and Sons Inc. New York, London. 471 P.

Al-Rawi K.M. and Ahmed A.A. (1984). Evaluation of the relative efficiencies of several selection indices for predicting yield performance in upland cotton (*Gossypium hirsutum* L.). Iraqi J. Agric. Sci. (Zanco). 2: 15 – 27.

Amankwa G.A. and Michaels T.E. (1997). Genetic variances, heritabilities and genetic correlations of grain yield, harvest index and yield components for common bean (*Phaseolus vulgaris* L.) in sole crop and in maize-bean intercrop. Canadian Journal of Plant Science. 77: 533-538.

Ashraf M. and Foolad M.R. (2007). Roles of glycine betaine and proline in improving plant abiotic stress resistance. Environ. Exptl. Bot. 59: 206-216.

Bates L.S., Waldern R.P. and Teare I.D. (1973). Rapid determination of free proline for water stress studies. Plant and Soil. 39: 205 – 207.

Bennett G.L. and Swiger L.A. (1980). Genetic variance and correlation after selection for two traits by index, independent culling levels and extreme selection. Genetics. 94: 763 – 775.

Bos I. and Caligari P. (1995). Selection Methods in Plant Breeding. 1<sup>st</sup> Edition, Chapman and Hall Ltd. London. 347 pp.

Bradshaw B., Dolan H. and Smit B. (2004). Form-level adaptation to climatic variability and

- change: crop diversification in the Canadian prairies. *Climatic change*. 67: 119-141.
- Burton G.W. (1952). Quantitative inheritance in grasses. *Proc. 6th Int. Grassland Cong.* 11 : 277-283.
- De Silva F.F., Pereira M.G., Ramos H.C.C., Junior P.C.D., Periera T.N.S, Gabriel A.P.C., Viana A.P. and Ferregueti G.A. (2008). Selection and estimation of the genetic gain in segregating generations of papaya (*Carica papaya* L.). *Crop Breeding and Applied Biotechnology*. 8: 1 - 8.
- El-Lawendey M.M. (2003). Effect of some selection procedures on lint yield and seed characters improvement in cotton. Ph.D Thesis, Fac. Agric., Moshtohor, Zagazig University, Egypt.
- El-Lawendey M.M. and El-Dahan M.A.A. (2012). Comparison between direct and indirect selection and two indices in segregating population of cotton (*Gossypium barbadense* L.). *J. Agric. Res., Kafer El-Sheikh Univ.* 38 (1): 38 -53.
- El-Lawendey M.M., El-Mansy Y.M. and El-Dahan M.A.A. (2011). Economic values effects on genetic gains of lint cotton yield and its components using selection indices. *Minufiya J. Agric. Res.* 36 (6): 1649 – 1668.
- Fahmy E.M. and Abou El-Nasr N.M. (1998). Physical and biochemical genetic identification of some selected Almond tress. *Arab. Univ. J. Agric. Sci., Ain Shams Univ., Cairo.* 6 (2): 481 - 508.
- Falconer D.S. (1989). *Introduction to Quantitative Genetics*. 3<sup>rd</sup> Edition, Longman. pp. 188 - 192.
- Gabriele G. and Wehner T.C. (2007). Heritability and genetic variance estimates for fruit weight in watermelon. *Hort Science*. 42(6): 1332 – 1336.
- Galal E.S.E. and Karam H. (1984). *Animal Breeding*. 4<sup>th</sup> Edition. Dar-El-Maaref Publishers, Egypt 216 P. (in Arabic).
- Ibarra-Perez F., Bohman E. and Saines G. (1997). Estimation of out crossing rate in common bean. *Crop Science*. 37: 60 - 65.
- IPCC (Intergovernmental Panel on Climate Change). (2001). *Climate change: the scientific basis*. <http://www.ipcc.Ch>
- Kassem M., Sary G.A., El-Okkia A. F. and El-Lawendey M.M. (2008). Comparison of the efficient of the different selection procedures in three population of Egyptian cottons (*Gossypium barbadense* L.). *Egypt. J. Agric. Res.* 86(2): 623 – 629.
- Khafagi A.A.F. (1995). The taxonomic significance of seed protein in some fabaceae species in Egypt. *Annals Agric. Sci., Ain Shams Univ., Cairo.* 40(1): 1-10.
- Kurukulasuriya P. and Mendelsohn R. (2006). A Ricardian analysis of the impact of climate change on African crop land. CEEPA Discussion paper No. 8. Centre for Environmental Economics and Policy in Africa. Pretoria, South Africa: University of Pretoria.
- Lande R. and Arnold S.J. (1983). The measurement of selection on correlated characters. *Evolution*. 37(6): 1210 - 1226.
- Lerner R.M. (2002). *Concepts and Theories of Human Development*. 3<sup>rd</sup> Edition, Lawrence Erlbaum-Associates, Inc, 648 P.
- McCarthy J, Cabziani O.F., Leary N.A., Dokken D. J. and White C. (2001). *Climate change 2001: Impacts, adaptation, and vulnerability*. Contribution of working group II to the third assessment report of the Intergovernmental panel on climate change. Cambridge: Cambridge university press.
- Meena R.A., Mishra M.N. and Dani R.G. (2001). Genetic variability and correlation for seed-quality parameters in upland cotton (*Gossypium hirsutum* L.). *Indian J. Agric. Sci.* 71(6): 417 – 420.
- Nakano H., Kobayashi M.K. and Terauchi T. (1998). Sensetive stages to heat stress in pod setting of common bean (*Phaseolus vulgaris* L.). *Japanese Journal of Tropical Agriculture*. 42: 72 - 84.
- Nakano H., Kobayashi M.K. and Terauchi T. (2000). Heat acclimation and de-acclimation for pod setting in heat-tolerant varieties of common bean (*Phaseolus vulgaris* L.). *Japanese Journal of Tropical Agriculture*. 44: 123 - 129.
- Nhemachena C. and Hassan R. (2007). Micro-level analysis of farmers' adaptation to climate change in southern Africa. IFPRI Discussion on paper N. 00714. International Food Policy Research Institute, Washington,DC. <http://www.ifpri.org/publication/micro-level-analysis-farmers-adaptation-climate-change-southern-africa-0>
- Nigam S.N., Rao R.C.N., Wynne J.C., Williams J.H., Fitzner M. and Nagabhushanam G.V.S. (1994). Effect and interaction of temperature and photoperiod on growth and

- partitioning in 3 groundnut (*Arachis hypogaea* L.) genotypes. *Ann Appl. Biol.* 125: 541 - 552.
- Nogesh B.R. and Devraj V.R. (2008). High temperature and salt stress response in French bean (*Phaseolus vulgaris*). *Australian Journal of Crop Science.* 2 (2): 40 – 48.
- Pachico D. (1989). Trends in world common bean production. In: Schwatz, H. F. and Pastor – Corrales, M. A. editors. *Bean production problems in the Tropics.* CIAT, Cali, Colombia. 1-8. Available from: <http://cropgenebank.sgrp.Cigar.Org/linex.Php?option=com.content&view=article&id=270&itemid=397>
- Pearce D.W., Cline W.R., Achanta A.N., Fankhauser S., Pachauri R.K., Tol R.S.J., and Vellinga P. (1996). The social costs of climate change: greenhouse damage and the benefits of control. In: *Economic and Social Dimensions of Climate Change, Equity and Social Considerations.* Contribution of Working Group III to the Second Assessment Report of the Intergovernmental Panel on Climate Change [Bruce, J.P., H. Lee, and E.F. Haites (eds.)]. Cambridge University Press, Cambridge, United Kingdom and New York, NY, USA, pp. 179-224.
- Porch T.G. (2006). Application of stress indices for heat tolerance screening of common bean. *J. Agronomy & Crop Science.* 192: 390-394.
- Rasmuson M. (1964). Combined selection for two bristle characters in *Drosophilla*. *Hereditas.* 51: 231 – 256.
- Sabu K.K., Abdullah M.Z., Lim L.S. and Wicknesswari R. (2009). Analysis of heritability and environmental variances in rice cross. *Agronomy Research.* 7: 97– 102.
- Salehi M., Tajik M. and Ebadi A.G. (2008). The study of relationship between different traits in common bean (*Phaseolus vulgaris* L.) with multivariate statistical methods. *American Eurasian J. Agric. & Environ Sci.* 3(6): 806 – 809.
- Singh R.K. and Chaudhary B.D.(1997). *Biometrical Methods in Quantitative Genetics Analysis.* 1<sup>st</sup> Edition, Kalyani Publishers, India. 288 P.
- Singh R.K. and Singh P.K. (1994). *A Manual on Genetics and Plant Breeding Experimental Techniques.* 1<sup>st</sup> Edition, Kalyani Publishers India. 134 P.
- Sokal R.R. and Rohlf F.J. (1981). *Biometry: The Principles and Practice of Statistics in Biological Research.* 2<sup>nd</sup> Edition, Freeman Ltd. USA. pp. 221-281.
- Soliman Y.A. and El-Lawendey M.M. (2008). Relative efficacy of selection indices for improving lint yield in two intraspecific cotton crosses. *Egypt. J. Agric. Res.* 86 (1): 207 – 222.
- Suzuki K., Tsukaguchi T., Takeda H. and Egawa Y. (2001). Decrease of pollen stain ability of green bean at high temperatures and relationship to heat tolerance. *Journal of the American Society for Horticultural Science.* 126: 571 - 574.
- Toms E.M., Kearsley M.J. and Cornish M.A. (1994). Correlated response to selection during seleging. *Heredity.* 73: 641- 649.
- Tsukaguchi T., Kawamitsu Y., Takeda H., Suzuki K. and Egawa Y. (2003). Water status of flower buds and leaves as affected by high temperature in heat-tolerant and heat-sensitive cultivars of snap bean (*Phaseolus vulgaris* L.). *Plant Production Science.* 6: 24 - 27.
- Wahid A. and Close T.J. (2007). Expression of dehydrins under heat stress and their relationship with water relations of sugarcane leaves. *Biol. Plant.* 51: 104 - 109.
- Waitt D.E. and Levin D.A. (1998). Genetic and phenotypic correlations in plants: a botanical test of cheverud's Conjecture. *Heredity.* 80: 310 - 319.
- Wheeler T.R., Craufurd P.Q, Ellis R.H., Porter J.R. and Prasad P.V.V. (2000). Temperature variability and the annual yield of crops. *Agric. Ecosyst. Environ.* 82: 159 - 167.
- Yan W. and Fregeau-Reid J. (2008). Breeding line selection based on multiple traits. *Crop Science.* 48 (2): 417 – 423.

## إستجابة الفاصوليا الجافة للإنتخاب لصفات متعددة لتحمل الحرارة المرتفعة في موسم الزراعة المتأخر

حامد حسن حامد - سيد محمود أحمد

معهد بحوث البساتين- مركز البحوث الزراعية - الجيزة - مصر

### ملخص

أجريت هذه الدراسة في ثلاثة مواسم زراعية بمزرعة بحوث الخضر بمدينة قها – محافظة القليوبية خلال أعوام 2009 و2010 و 2011 لدراسة إستجابة الفاصوليا الجافة (صنف نبراسكا) للإنتخاب لصفات متعددة لتحمل الحرارة المرتفعة. أستخدمت طريقة "دليل الإنتخاب" للتحسين على مدى ثلاث أجيال من الإنتخاب. زرعت هذه الأجيال في موعد متأخر ( 30 مارس) ثم تمت مقارنة النتائج بين الجيل الثالث للإنتخاب والعشيرة الأم التي زرعت في ميعاد الزراعة التقليدي (15 فبراير). أعتد دليل الإنتخاب على خمس صفات هامة للفاصوليا وهي عدد الأفرع للنبات، وزن وعدد القرون الكلية للنبات، وزن بذور الدرجة الأولى للنبات، وزن المحصول الكلي على النبات، النسبة المئوية لعقد القرون بالإضافة إلى تأثير هذه الصفات مجتمعة على صفة المحصول الكلي للنبات ومدى تأثيرها على الإستجابة الملحوظة للإنتخاب لصفات متعددة. كذلك تمت دراسة أثر الإنتخاب لصفات متعددة لتحمل الحرارة المرتفعة في الفاصوليا الجافة على التباين الوراثي والمظهرى خلال الأجيال الإنتخابية بالإضافة إلى دراسة التغيرات في الإرتباط الوراثي والمظهرى خلال الأجيال الثلاثة الإنتخابية. كذلك تمت دراسة التغيرات الحادثة في تقدير كل من المكافئ الوراثي والعائد الوراثي الحقيقي للإنتخاب والفارق الإنتخابي خلال الأجيال الإنتخابية الثلاثة لصفة التحمل للحرارة المرتفعة. أظهرت النتائج استجابة ملحوظة للإنتخاب لصفات متعددة لتحمل الحرارة المرتفعة في الفاصوليا الجافة (صنف نبراسكا) وذلك بعد دورتين من الإنتخاب حدث تقدم ملحوظ على مستوى متوسطات الصفات المختلفة للعشيرة في الإتجاه الذى يحقق أهداف المربي. وبالرغم أن هذه المتوسطات تقل بنسب معنوية إذا ما قورنت بالعشيرة الأم مع الأخذ في الإعتبار أن ذلك فقط بداية برنامج الإنتخاب وأن هناك زيادة ملحوظة خلال الدورتين الإنتخابيتين. ثبت من النتائج أن الإنتخاب لصفات متعددة اعتمادا على دليل الإنتخاب لعدة صفات هامة لمحصول الفاصوليا الجافة له القدرة على زيادة التباين الوراثي داخل عشيرة او صنف ظل لمدة طويلة بحالة من الاستقرار الوراثي بما يعطى مجالا خصبا للإنتخاب لصفات الإجهاد البيئي مثل التحمل لدرجة الحرارة المرتفعة. كذلك وجد إختلافات وتذبذب في علاقات الإرتباط الوراثي والمظهرى بين الصفات المختلفة للعشيرة تحت الإنتخاب لصفات متعددة لتحمل الحرارة المرتفعة، على مستوى الإشارة والمعنوية، خلال دورتين إنتخابيتين وتعزى هذه الإختلافات لقدرة تلك الطريقة الإنتخابية على إحداث تباين وراثي داخل العشائر التى ظلت تحت الإنتخاب لمدة طويلة. أيضا ظهرت زيادة معنوية في نسبة البرولين في العشيرة المنتخبة لصفة التحمل للحرارة المرتفعة مقارنة بالعشيرة الأم. كذلك وجد أختلاف على مستوى بروتينات البذور بل كانت هناك بروتينات مميزة (معلمة) للعشيرة المحتملة للحرارة عنها في العشيرة الأم التي تزرع في ميعاد الزراعة التقليدي. عموما أظهرت النتائج أن إستخدام الإنتخاب لصفات متعددة على اساس دليل الإنتخاب قد أدى إلى تحسن ملحوظ في عشيرة الصنف نبراسكا من حيث درجة التحمل للحرارة المرتفعة و زيادة متوسط العشيرة للمحصول الكلي للنبات من البذور الجافة وزنا وعددا. كذلك أثبتت النتائج أن الإنتخاب لصفات متعددة والمعتمد على دليل الإنتخاب له القدرة على إحداث تباينات وراثية في العشائر التى ظلت تحت الإنتخاب لمدة طويلة.

المجلة العلمية لكلية الزراعة – جامعة القاهرة – المجلد (63) العدد الثالث ( يوليو 2012): 299-314.