

Genetic and Phenotypic Correlations Between the Yield and Its Components For Three Genotypes of Broad Bean, As Affected By Humic Acid and Iron and Zinc Elements and It's Partitioning into Direct and Indirect Effects

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Abstract: *Three genotypes of broad bean (local, Spanish, LOZ DE OTO and Italian FAVA DE ORTO) were planted at the Research Station of the Faculty of Agriculture, University of Kirkuk in Al-Sayada through the winter agricultural season (2018-2019), at three levels of humic acid (0, 12 and 24 mg.L⁻¹) and four levels of iron and zinc (0, 80 Fe, 60 Zn, and 60 Zn + 80 Fe) mg.L⁻¹), carried out as factorial experiment using randomized complete block design with three replications, to evaluate the traits: dry seed yield per plant and some of its components from other traits (plant height, number of branches per plant, number of nodes on the main stem, number of pods per plant, pod length, 100 seeds weight, number of seeds per pod), and analysis of the genetic and phenotypic path coefficient between the yield and its components. The results showed that the Italian genotype was significantly surpassed others for most number of traits, including the dry seed yield per plant, followed by the local genotype. It turns out that 20.25, 9.5, 12, 10 and 13.5 mg.L⁻¹ of humic acid gave the highest means of plant height, number of nodes on the main stem, number of pods per plant, 100 seeds weight, and dry seeds yield per plant respectively, and the treatment Zn 60 mg.L⁻¹ gave the highest yield of dry seeds per plant with a non-significant difference from the control treatment. The results of path coefficient analysis showed that the highest direct and indirect effects through other traits genetically were for the traits 100 seeds weight, and pod length, but phenotypically, the direct effects were positive and high for five traits: number of branches per plant, number of nodes, number of pods per plant, pod length and 100 seeds weight, and the indirect effects of the traits number of pods per plant, 100 seeds weight and pod length through other traits being the best, therefore, these three traits can be relied upon as a selection criteria in breeding programs for higher dry seed yield.*

Keywords: *Broad bean, Phenotypic variance, Heritability, Correlation, Path analysis*

Introduction:

Vicia faba L. is a winter crop of the legume family. Its seeds contain a high percentage of protein (25-40%), in addition to carbohydrates, which sometimes reach 56% in most varieties, as well as mineral elements, fibers and vitamins, and the importance of this crop, like other leguminous crops, comes in its ability to improve soil qualities through its contribution in fixing atmospheric nitrogen in the soil by means of root nodule bacteria in symbiosis with rhizobium bacteria, so it is included in the crop succession to improve soil conditions (Carmen *et al.*, 2005). A lot of researchers have been interested in this crop for the purpose of obtaining its dry seeds that are included in the human diet and in some cases are animal fodder (Altafi *et al.*, 2013). China is one of the most producing and

consuming countries of the crop, as its production is estimated at about 2.7 million tons per year, followed by Ethiopia, which produces about 9% of the crop, and then Egypt, which produces about 262 thousand tons of the crop per year (Belitz, 2009). In Iraq, the production of the crop was estimated at 49.9 thousand tons (The Central Statistical Organization and Information Technology, 2016).

The process of developing new varieties of the crop characterized by high production and good quality qualities is one of the most basic goals that plant breeders strive for. It is possible to improve crop productivity by using the available genetic resources and by learning about the nature and importance of the genetic differences present in the population. Estimating genetic differences is a precondition for planning an appropriate method of breeding. An accurate view of the importance of genetic differences in crop species is also of prime importance in that it provides a basic basis for an effective selection process. In order to practice an effective selection process, defining the traits of the outcome is desirable. The correlations between traits represent a measure of the strength of the relationship between them, and their knowledge between the different traits is important in plant breeding. If there are two positively correlated traits, one of them can be indirectly improved by improving the other. The correlation coefficient is useful if indirect selection of the secondary trait is to be used to improve the primary trait is useful (Hussain *et al.*, 2010). Estimation of the correlation coefficient is essential for the development of selective index, and for the purpose of creating meaning for correlation, Wright (1921) developed a pathway analysis method which was used to develop criteria for selecting complex traits in many crop species (Dewey and Lu, 1958, Diz *et al.*, 1994, Kang *et al.*, 1983). This analysis provides an effective means by estimating the direct and indirect causes of the associations (Kale *et al.*, 2007). The method of analyzing the path coefficient in broad bean has been adopted by many researchers. From a previous study, Berhe *et al.* (1998) note that path analyses showed that number of seeds per plant and 100-seed weight were the major direct contributors to seed yield per plant. Ulukan *et al.* (2003) indicated the direct and indirect effects of plant height, pod length, first pod height, pod number per plant and grain number per pod upon biological yield. It has shown by Alghamd (2007) that significant positive correlations were detected between faba bean seed yield and each of number of pods per plant, number of seeds per plant, seed weight per plant and biological yield. Badolay *et al.*, (2009) reported that the seed yield per plant exhibited positive and significant correlation with pod length, plant height, branches per plant, pods per plant and hundred seed weight. Tadesse *et al.* (2011) find out that number of pods per plants, number of seeds per pod, thousand seed weight and plant height had significant association with seed yield per plot. Sharifi (2014) suggested that attention should be paid to some of characters such as pod length, hundred seed weight, number of pods per plant and number of stems per plant for augmentation of seed yield, and these traits could be used as selection criteria in faba bean breeding programs. From their study, Tofiq *et al.* (2016) reported that the trait first node height showed maximum direct effect value in seed yield at the first and third season, while number of pods/plant showed maximum direct effect value in seed yield at the second season.

The aim of the current study is to evaluate the yield traits and some of its components for three genotypes of broad bean at levels of humic acid, iron and zinc elements, and to partitioning the genetic and phenotypic correlations of yield with some of its components from other traits into direct and indirect effects to benefit from that in the future in adopting an efficient selection program to find new varieties by diagnosing the most influential traits on yield (Mustafa *et al.*, 2020).

Materials and Methods:

This study was conducted at the Agricultural Research and Experimental Station of the Faculty of Agriculture, University of Kirkuk in the Sayada location for the winter agricultural season (2018-2019). The study included three factors, the first three genotypes of broad bean (local, Spanish, LOZ DE OTO and Italian FAVA DE ORTO), the second factor, three levels of humic acid (0, 12 and 24 mg. L⁻¹), and the third factor, four levels of iron and zinc (0, 80 Fe, 60 Zn, and 60 Zn + 80 Fe) mg.L⁻¹, carried out as a factorial experiment using a randomized complete block design with three replications. The land was prepared for cultivation with two vertical plowing, then the soil was softened well, and then the triple superphosphate fertilizer was added to the soil before planting at a rate of 25 kg. ha⁻¹. Each experimental unit contained 4 lines 2 m long, at a distance of 0.70 m between the lines and 0.20 m between plants within a single line. The treatment combinations were randomly

distributed to the experimental units, which were separated from each other by a distance of 0.70 m. The seeds were planted on 22 October 2018 by placing two seeds in each hole, and after germination of the seeds, the thinning process was carried out to one seed. The weeds were controlled manually four times during the growing season, and irrigation was performed according to the plant's need. The harvest took place on 30 April 2019. Data were recorded on the traits: plant height (cm), number of branches per plant (NBP), number of nodes on the main stem (NNS), number of pods.Plant⁻¹ (NPP), pod length (cm) (PL), 100 seeds weight (g) (100SW), number of seeds per Pod⁻¹ (NSP) and single plant yield from dry seeds (gm) (PY). The data of studied traits were statistically analyzed according to the method of the experimental design used, and the differences between the means of the levels of the three factors were tested by Duncan's multiple range test method, with the adoption of the trend analysis method between levels of humic acid as it was a levels of a quantitative factor, where the sum of the squares of this factor was divided into the two relationships, linear (first degree) and quadratic (second degree) to learn the nature of the traits response to this acid (Al-Zubaidy and Al-Falahy, 2016). The phenotypic and genotype variances (σ^2P and σ^2G respectively), and the phenotypic and genotype covariances ($\sigma P_x P_y$ and $\sigma G_x G_y$ respectively) were estimated through the relationship between the estimated and expected mean square in the variance and covariance analysis table, and then the genetic (r_G) and phenotypic (r_P) correlations between the studied traits were estimated from the following equations (Al-Zubaidy and Al-Jubbory, 2016) ((AL-Samarraie,*et al*,2019)).

$$r_G = \sigma G_x G_y / [\sqrt{(\sigma^2 G_x)(\sigma^2 G_y)}] ; r_P = \sigma P_x P_y / [\sqrt{(\sigma^2 P_x)(\sigma^2 P_y)}]$$

Then the broad sense heritability (H_{BS}) were estimated in the manner indicated by Demir and Turgut (1999) from the equation:

$$H_{BS} = \sigma_g / \sigma_{ph} = \sigma_g / (\sigma_g + \sigma_{gH} / H + \sigma_{gI} / I + \sigma_{gHI} / HI + \sigma_e / Hlr)$$

Where σ_g total genetic variance, σ_{ph} phenotypic variation, σ_{gH} variance of genotypes with humic acid interaction, σ_{gI} variance of genotypes with elements treatments interaction, σ_{gHI} variance of genotypes with both humic acid and elements interaction, σ_e environmental variance, (H) number humic acid levels, (I) number of elements levels and (r) number of replicates, as well as the expected genetic advance in the next generation as a percentage of the trait mean was estimated. The path coefficient analysis established by Wright (1921) was used to partition the genetic and phenotypic correlation coefficients between the yield and its components into direct and indirect effects, in the manner explained by Dewey and Lu (1959) and then provided in detail by Al-Rawi (1987) to test the model that included seven independent variables: PH (X_1), NBP (X_2), NNS (X_3), NPP (X_4), PL (X_5), 100SW (X_6) and NSP (X_7), as shown in figure (1). The direct effects (phenotypic and genetic) were estimated using correlation matrix as follows: $P_{iy} = R^{-1} r$, As: P_{iy} = direct effects vector, R^{-1} = Inverse of the correlation coefficients matrix between all possible pairs of traits and r = vector of correlation coefficients between grain yield and and other traits. Then by following the path shown in Figure (1), the indirect effects (genetic and phenotypic) were estimated.

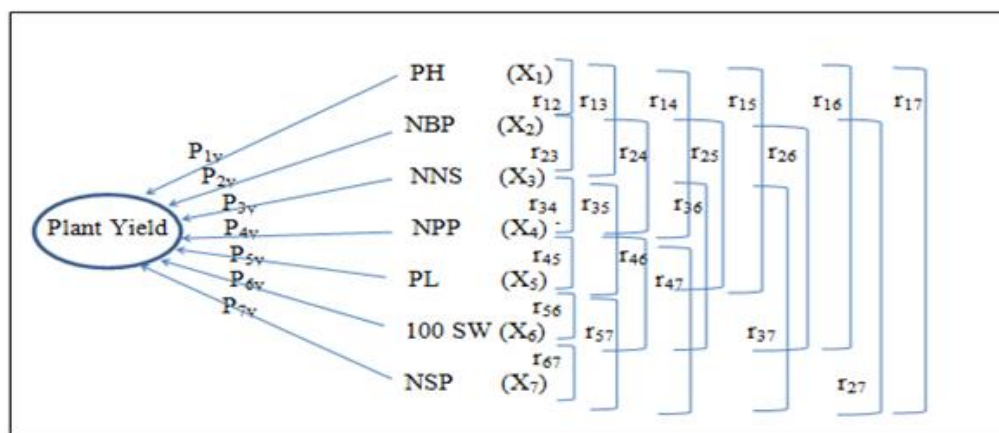


Figure 1: Diagram of path way relationship for PH (X_1), NBP (X_2), NNP (X_3), NPP (X_4), PL (X_5), 100 SW (X_6) and NSP (X_7) affecting the plant yield (PY) (y).

The importance of the direct and indirect effects was determined according to the grading mentioned by Al-Zubaidy and Al-Jaboury (2016) as follows (from 0,00 - 0.09 neglected), (from 0.10 - 0.19 few), (from 0.20 - 0.29) moderate, (from 0,30 - 0,99) high and (more than 1,00) very high. The available programs SAS, Minitab and Microsoft Office excel (2003) were used in the implementation of all statistical and genetic procedures.

Results and discussion:

The results of the analysis of variance of data of broad bean genotypes planted at three levels of humic acid and four levels of iron an zink elements for seed yield and some other traits shown in Table (1). It is noticed from it that the mean square of genotypes, humic acid, elements and all type of intractios between the three factors was significant at a 1% probability level for all studied traits, except NSP in case of genotypes (significant at 5% probability level), NSP in case of humic acid and NBP and NSP in case of elements (was not significant). These results related to the variations in genotypes and other factors in their studies are consistent with the findings of Balcha and Tigabu (2015), Tofiq, *et al* (2016) and Goa and ambata (2017). The results of the significant interaction of genotypes with each of humic acid and elements or both indicate that the behavior of the genotypes towards the studied traits differs in the presence of both factors. The mean square data from analysis of variance of all traits under and the covariance analysis between them were used to estimate the

Table 1: Analysis of variance results for studied traits of broad bean.

Source	df	Traits							
		PH	NBP	NNS	NPP	PL	100SW	NSP	PY
Reps.	2	237.95	46.485	49.467	65.84	48.57	0.0007	10.119	189.35
genotype s	2	2539.8* *	24.860* *	9.423**	26.57* *	29.44* *	0.012* *	0.502*	658.2* *
Humic	2	386.26* *	8.618**	39.544* *	18.48* *	13.85* *	0.004* *	0.067	346.3* *
Linear	(1)	648.0**	0.347	28.827* *	0.700	2.836* *	0.002* *	0.120	87.94* *
Quadratic	(1)	124.52* *	16.889* *	50.460* *	36.26* *	24.85* *	0.005* *	0.014	604.6* *
Elements	3	3505.8* *	24.806* *	32.408* *	24.39* *	21.44* *	0.010* *	4.842* *	571.1* *
V x H	4	408.05* *	1.313* *	1.984**	16.82* *	1.164	0.004* *	0.838* *	274.8* *
V x E	6	523.93* *	3.644**	5.597**	8.658* *	3.166* *	0.001* *	1.432* *	402.6* *
H x E	6	360.26* *	3.633**	6.396**	9.138* *	2.141* *	0.002* *	0.712* *	159.9* *
V x H x E	12	448.05* *	3.757**	6.231**	10.53* *	14.86* *	0.006* *	1.537* *	261.9* *
Error	70	13.916	0.453	0.397	0.720	0.50 9	0.0000 5	0.146	4.682

- (***) and (*) significant at 1% and 5% respectively.

phenotypic and genotypic variances and covariance's for these traits, and these components were used in the estimation of genetic and phenotypic correlations, as shown in Table 7. Table (2) shows the means of genotypes for the different traits as an average of humic acid and elements levels, and it is noticed through the results of the Duncan multiple range test that there are significant differences between them for all the traits. The highest means for the traits PH, NBP, NNS, NPP, PL, 100SW, NSP and PY were 152.42, 4.464, 17.067, 16.125, 19.055, 0.742, 4.857 and 72.284 in genotypes Italy (i), local (i), Espain, local (ii), Italy (ii), local (iii), Italy (iii) and Italy (iv) Respectively, while the lowest means were 136.58, 6.844, 16.050, 14.425, 17.343, 0.709, 4.631 and 63.738 in genotypes Espain (i), Espain (ii), local (i), Espain (iii) local (ii) Espain (iv), local (iii) and Espain (v)

respectively, and it is clear that Italy genotype gave distinct results for the most number of traits, including PY, followed by local genotypes, and these results indicate the possibility of benefiting from these two genotypes in breeding by future crossbreeding programs to transfer the desired traits to local one which adapted to environmental conditions, as well as in developing new varieties of broad bean. In previous studies, other researchers obtained significant differences between the means of genotypes for PY and other traits, including, Alghamd (2007), Badolay *et al.*, (2009), Sharifi (2014), Balcha and Tigabu (2015), Tofiq, *et al* (2016) and Goa and

Table 2: Means of genotypes for studied traits of broad bean.

genotypes	traits							
	PH	NBP	NNS	NPP	PL	100SW	NSP	PY
local	149.36 b	4.464 a	16.050 c	16.125 a	17.343 c	0.742 a	4.631 b	67.738 b
Espain	136.58 c	6.844 c	17.067 a	14.425 c	18.704b	0.709 b	4.684 ab	63.738 c
Italy	152.42 a	7.978 b	16.658 b	15.058 b	19.055 a	0.739 a	4.857 a	72.284 a
Mean	146.12	7.762	16.592	15.203	18.367	0.730	4.724	67.920

- The values followed by the same letter for each trait are not significantly different.

ambata (2017). Table (3) shows the means of the humic acid levels as an average of the genotypes and the levels of iron and zinc, from which it is noticed that the level 12 mg. L⁻¹ gave the highest means for PH, NNS, NPP, 100SW and PY, with a significant difference from the other two levels, while the non-acid treatment was surpassed by highest PH and SL, and no significant differences were found between the three levels for NSP trait. It is noted that PY at the level of 12 mg. L⁻¹ was higher than at 0 and 24 mg. L⁻¹ by 9.401% and 5.811%, respectively. When conducting a trend analysis for humic acid levels as levels of a quantitative factor and for the purpose of determining

Table 3: Means of humic acid levels for studied traits of broad bean.

Humic acid	traits							
	PH	NBP	NNS	NPP	PL	100SW	NSP	PY
0	142.36 b	8.111 a	16.739 b	14.892 b	18.905 a	0.731 b	4.691 a	65.142 c
12	147.64 a	7.203 b	17.558 a	16.022 a	17.689 c	0.740 a	4.708 a	71.266 a
24	146.36 a	7.972 a	15.478 c	14.694 b	18.508 b	0.720 c	4.773 a	67.352 b
Mean	146.12	7.762	16.592	15.203	18.367	0.730	4.724	67.920

- The values followed by the same letter for each trait are not significantly different.

the nature of the response of the traits to it, and determining the best response of each trait and the best level of the acid, it is noticed from Table (1) that the mean square of the second degree relationship (quadrature) was highly significant for PH, NBP, NNS, NPP, PL, 100SW and PY, an indication that they govern the relationship between acid levels and these traits, while an appropriate relationship with the NSP trait was not clear due to the insignificance of the mean squares of linear and quadratic relationships, and Figures (2-8) show response curves of PH, NBP, NNS, NPP, PL, 100 SW and PY to humic acid levels. It is noticed from Figures (2, 4, 5, 7 and 8) that the mean of the traits PH, NNS, NPP, 100SW and PY increase with increasing humic acid level and to a certain limit after it begins to decrease, while Figures (3 and 6) show a decrease in NBP and PL, respectively, with an increase in humic acid from zero to 12.5 and 13 mg. L⁻¹ for the two traits respectively, then the relationship is reflected by increase the values of these two traits at the higher levels of acid, but these increases do not rise to what was given by the no-acid addition treatment, meaning that the best mean for the two traits respectively is 8.111 branches and 18.905 cm when not adding humic acid. To determine the best response of the traits: PH, NNS, NPP 100SW and PY at the best levels of humic acid, two lines are drawn from the highest top in the curves shown in Figures (2, 4, 5, 7 and 8), the first is horizontal to cross the vertical axis and determine the best response of the trait, and the second is vertical to cross the horizontal axis and determines the best level of humic acid. Based on that, it becomes clear from the results presented in Table (4) that the best means of PH, NNS, NPP, 100SW and PY were 148.70, 17.6, 16.0, 0.741 and 71.5 at the best levels of humic acid, which are: 20.25, 9.5, 12, 10 and 13.5 mg. L⁻¹ respectively. The same table shows the regression equations of the second degree (quadratic) that this study reached, through which it is possible to predict the values of these five traits at any level of humic acid that is assumed.

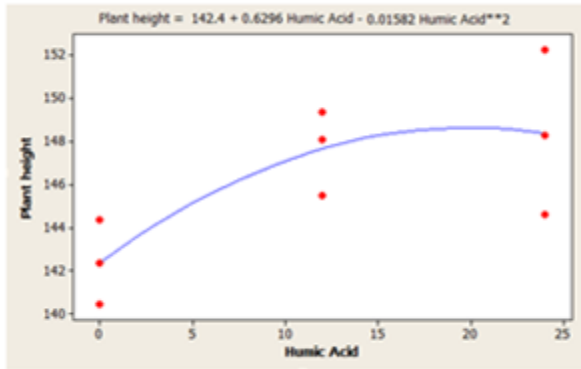


Figure 2: Response of PH to humic acid

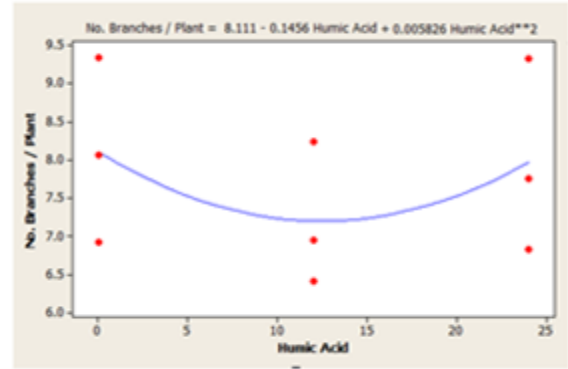


Figure 3: Response of NBP to humic acid

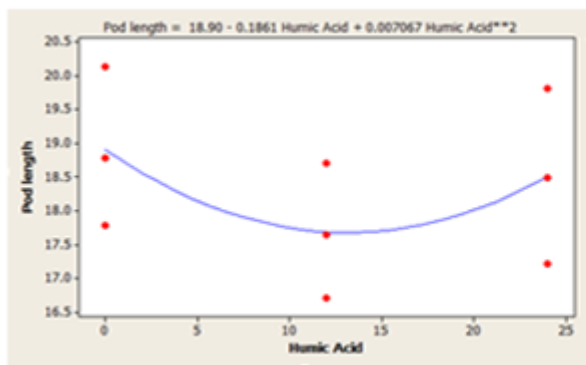


Figure 4: Response of NNS to humic acid

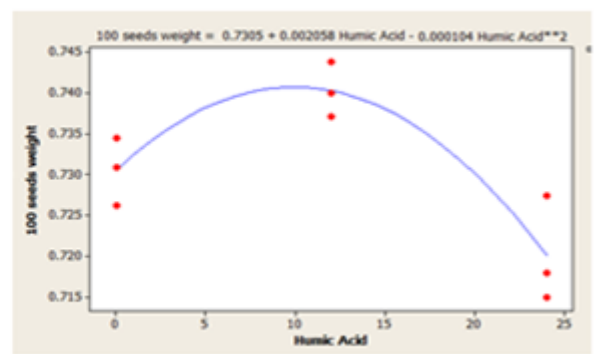


Figure 5: Response of NPP to humic acid

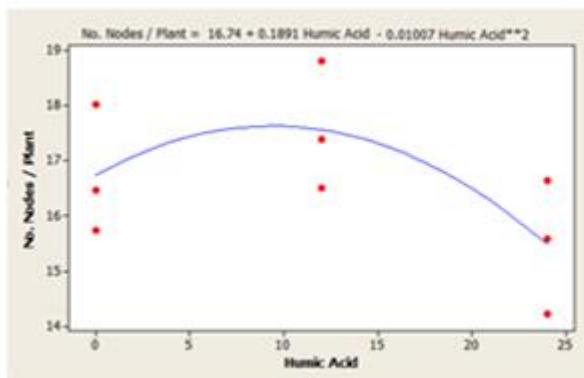


Figure 6: Response of PL to humic acid

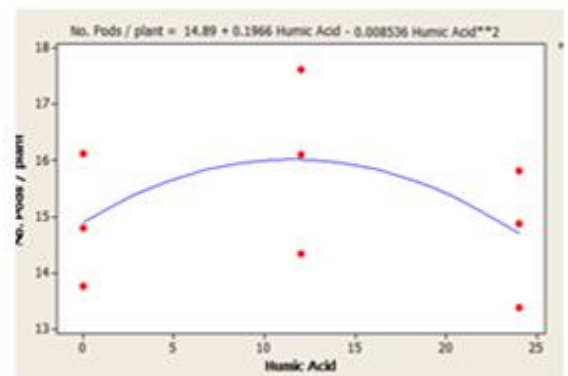


Figure 7: Response of 100SW to humic acid

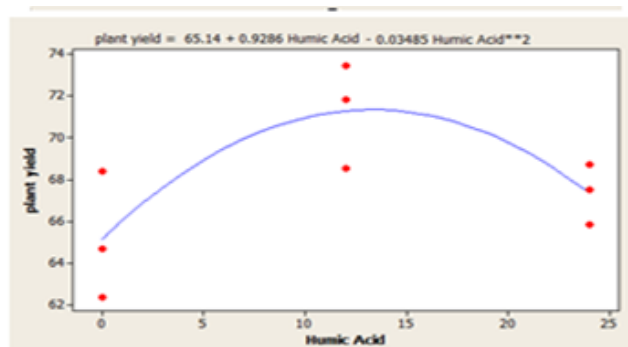


Figure 8: Response of PY to humic acid

Table 4: The best regression equation between humic acid rates and studied traits of broad bean.

Traits	Degree of equation	Surpassed response value	Best humic acid rate	Prediction equation
PH	Quadratic	148.70	20.25	$PH = 142.4 + 0.629 H - 0.015 H^2$
NBP	Quadratic	8.111	0	$NBP = 8.111 - 0.146 H + 0.005 H^2$
NNS	Quadratic	17.6	9.5	$NNS = 16.74 + 0.1189 H - 0.0101 H^2$
NPP	Quadratic	16.0	12	$NPP = 14.89 + 0.197 H - 0.009 H^2$
PL	Quadratic	18.905	0	$PL = 18.9 - 0.186 H + 0.007 H^2$
100SW	Quadratic	0.741	10	$100SW = 0.731 + 0.002 H - 0.0001 H^2$
NSP	----	----	----	-----
PY	Quadratic	71.5	13.5	$PY = 65.14 + 0.929 H - 0.035 H^2$

The means of the treatment levels with iron and zinc are shown in Table (5), and it is noticed that the treatment Fe 80 mg.L⁻¹ surpassed by highest means for the traits PH, NNS and NPP, with a significant difference than all other treatments, and also gave the highest mean for 100SW with a non-significant difference from the two treatments (non Add any element and Zn 60 mg.L⁻¹). The treatment Zn 60 mg.L⁻¹ gave the highest seed yield per plant with a non-significant difference with the case of no elements. The control treatment (no addition of elements) gave the highest number of branches per plant and longer pods. These results indicate the ineffectiveness of using each of the two elements or a mixture of them. Table (6) shows the estimates of the components of the phenotypic variance (genetic, environmental, and interactions of genotypes with any of the other two factors or both). These components were used to estimate the values of broad sense heritability and expected genetic advance from selection in the next generation. It is noticed that the values of broad sense heritability ranged from 9.21% for NSP trait and 75.77% for NBP trait, and it appeared to be high for PH, NBP and PL traits, moderate for NNS, NPP, 100 SW and PY traits, while it was low for NSP. As for the expected genetic advance as a percentage of the mean of each trait, it was moderate for NBP and equal 16.251%, and low for all other traits, and ranged from 1.125% for NSP

Table 5: Means of elements (iron and zink) for studied traits of broad bean.

elements	traits							
	PH	NBP	NNS	NPP	PL	100SW	NSP	PY
0	148.111b	8.437a	17.259b	15.437b	19.167a	0.739a	4.783b	70.888a
Fe (80)	158.48a	8.274ab	17.704a	16.263a	18.052b	0.742a	4.802b	67.009b
Zn (60)	147.00b	7.985b	16.111c	15.144b	18.998a	0.739a	5.165a	71.976a
Fe +Zn	130.89c	6.352c	15.293d	13.967c	17.252c	0.701b	4.146c	61.807c
Mean	146.12	7.762	16.592	15.203	18.367	0.730	4.724	67.920

- The values followed by the same letter for each trait are not significantly different.

Table 6: Genetic parameters for studied traits of broad bean.

parameters	traits							
	PH	NBP	NNS	NPP	PL	100SW	NSP	PY
ϕg	70.164	0.678	0.251	0.718	0.803	0.00032	0.0099	18.154
ϕgH	10.948	0.024	0.044	0.447	0.018	0.00011	0.0192	7.504
ϕgI	14.167	0.089	0.144	0.221	0.074	3.45E-05	0.0357	11.053
ϕgHI	12.059	0.092	0.162	0.272	0.399	0.00018	0.0386	7.148
ϕE	0.387	0.013	0.011	0.020	0.014	1.46E-06	0.0041	0.130
ϕP	107.725	0.895	0.612	1.678	1.308	0.0006	0.108	43.989
heritability	0.6513	0.7577	0.4095	0.4279	0.6141	0.5023	0.0921	0.413
GA	11.898	1.262	0.564	0.976	1.236	0.022	0.053	4.817
GA%	8.143	16.251	3.399	6.417	6.731	3.048	1.125	7.093

and 8.143 for PH. Table (7) shows the genetic and phenotypic correlation coefficients between the pairs of traits, and it is noticed that both types of correlations were close in strength and direction in most cases, and that the genetic correlations are more in values than the phenotypic in most of them. It is evident that the seed yield per plant has a positive, significant correlation (genetically and phenotypically) with the traits PH, NBP, 100SW, NSP and genetically with the NPP and PL and genetically negative with NNS, indicating that all the traits are genetically correlated with the seed yield, and the phenotypic negative correlation of the seed yield with NPP and the positive with NNS and PL to did not reach significant the limit. On the other hand, no significant correlation relationships (whether negative or positive) were shown genetically for PH trait with PL, NBP with NSP, and phenotypically for PH trait with PL and NSP and NBP with NSP and PL with 100SW and 100SW with NSP. This independent association of the different traits with the seed yield trait is generally beneficial to the crop breeder, because if strong selection is practiced for any of these

Table (7): Genetic correlations (above) and phenotypic (below) between the plant yield of broad bean and some of its components.

	PH	NBP	NNS	NPP	PL	100SW	NSP	PY
PH	1	0.898**	-0.704**	0.669**	-0.148	0.977**	0.552**	0.936**
NBP	0.568**	1	-0.968**	0.954**	-0.596**	0.981**	-0.013	0.664**
NNS	-0.418**	-0.423**	1	-1.033**	0.843**	-0.856**	0.420**	-0.379**
NPP	0.457**	0.575**	-0.528**	1	-0.863**	0.832**	1.685**	0.338**
PL	-0.041	-0.473**	0.414**	-0.409**	1	-0.375**	0.964**	0.233*
100SW	0.440**	0.452**	-0.437**	0.436**	-0.112	1	0.277*	0.822**
NSP	0.069	0.142	0.268*	0.736**	0.285*	0.089	1	0.906**
PY	0.437**	0.387**	0.019	-0.018	0.148	0.646**	0.270*	1

- (***) and (*) significant at 1% and 5% respectively.

mentioned traits in the early generations, there is less possibility of excluding offspring with good yield if they are negatively correlated. In order to determine the traits most influencing the seed yield for use in breeding programs to select the higher yield, the genetic and phenotypic correlation coefficients of the yield with other traits were divided into direct and indirect effects through the adoption of the pathway analysis technique. It is noted from the results of the genetic pathway analysis (Table 8) that the direct effect of the PH trait on the seed yield was high positive, while the indirect effect through 100SW was high positive and through other traits (negative or positive) was not important. The direct effect of NBP on the seed yield was negative and not important, and the indirect effect through PH and 100 SW was positive high and through PL negative medium, while it was not important through other traits. The direct genetic effect of NNS was shown as positive not important in the seed yield trait, and the indirect effect was high negative through PH and 100 SW and high positive through PL, while the remainder effects through other traits were not important. The direct effect of NPP on the seed yield was positive, not important, while the indirect effect of the trait was high positive through PH and 100 SW, negative through PL and not important through the remainder traits. The direct effect of PL trait on the seed yield appeared high positive (0.4506), and its indirect effects were not important through all other traits except for 100SW where it was negative and moderate in its value (-0.2429). The trait 100SW had a positive and high direct effect on the seed yield (0.6485), and its indirect effect was positive, high through PH, and negatively low through PL. Finally, the direct genetic effect of the NSP trait on the yield was positive, not important, while its indirect effect was positive high through PL, moderate through PH, and little through 100SW, and it was not important through other traits. From the results of the phenotypic pathway analysis presented in Table (9), it is noticed that the direct effect of PH on the seed yield was negative, unimportant, and its indirect effect was high positive through NPP and negative through NNS, and it was positive moderate through the two traits NBP and SW100 and negative not important through PL and NSP. For the trait NBP, the direct effect was positive high and amounted to 0.4311, its indirect effect was high positive through NPP and negative through NNS and PL

Table (8): Genetic path analysis for traits affecting plant yield of broad bean.

Traits	PH	NBP	NNS	NPP	PL	100SW	NSP	r_{iy}
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PH	(0.4744)	-0.0607	-0.0457	0.0003	-0.0667	0.6336	0.0004	0.936**
NBP	0.4259	(-0.0676)	-0.0629	0.0004	-0.2684	0.6360	0.0000	0.664**
NNS	-0.3338	0.0655	(0.0649)	-0.0004	0.3799	-0.5549	0.0003	-0.379**
NPP	0.3172	-0.0645	-0.0670	(0.0004)	-0.3889	0.5393	0.0012	0.338**
PL	-0.0703	0.0403	0.0547	-0.0004	(0.4506)	-0.2429	0.0007	0.233*
100SW	0.4635	-0.0663	-0.0555	0.0003	-0.1688	(0.6485)	0.0002	0.822**
NSP	0.2621	0.0009	0.0273	0.0007	0.4345	0.1793	(0.0007)	0.906**

- (**) significant at 1% and.

Table (9): Phenotypic path analysis for traits affecting plant yield of broad bean.

Traits	PH	NBP	NNS	NPP	PL	100SW	NSP	r _{iy}
PH	(-0.0069)	0.2450	-0.3594	0.3679	-0.0259	0.2751	-0.0595	0.437**
NBP	-0.0039	(0.4311)	-0.3636	0.4626	-0.3013	0.2828	-0.1204	0.387**
NNS	0.0029	-0.1823	(0.8601)	-0.4248	0.2636	-0.2731	-0.2276	0.019
NPP	0.0029	0.2477	-0.4539	(0.8049)	-0.2605	0.2727	-0.6258	-0.018
PL	-0.0032	-0.2038	0.3557	-0.3289	(0.6374)	-0.0699	-0.2426	0.148
100SW	-0.0031	0.1949	-0.3758	0.3511	-0.0713	(0.6252)	-0.0753	0.646**
NSP	-0.0005	0.0611	0.2302	0.5924	0.1818	0.0554	(-0.8503)	0.270*

- (**) significant at 1% and.

traits, positive moderate through 100SW and negative and low through NSP, and not important through PH. The NNS trait showed a positive high direct effect on seed yield (0.8601), while the indirect effect was negative, high through NPP, moderate through 100SW and NSP, and it was low through NBP, while it was positive moderate through PL and not important through PH. The NPP trait showed a positive and high direct effect of 0.8049, and a positive moderate indirect effect through NBP and 100SW and not important through PH, while the indirect effect was negative high through NNS and NSP, and moderate through PL. The PL trait showed positive and high direct effect on seed yield, positive high indirect effect through NNS, negative high through NPP, moderate through NBP and NSP, and not important through PH and 100SW. The 100SW trait had a positive and high direct effect on seed yield (0.6252), and a positive high indirect effect through NPP and low through NBP, while the indirect effect was negative high through NNS and not important through the remainder traits. Finally, the value of the correlation coefficient of NSP trait with seed yield was positive and significant at the probability level of 5% (0.270*), and when partitioned, it appeared that the direct effect of the trait was negative and high and reached -0.8503, while the indirect effect was positive high through NPP and moderate through NNS and low through PL and not important through NBP and 100SW, and it was negative and not important through PH.

It is concluded from the foregoing that the highest direct and indirect effects through other traits genetically were for the traits 100SW first and PL second, but phenotypically, the direct effects were positive and high for five traits: NBP, NNS, NPP, PL and 100SW, and the indirect effects of the traits NPP, 100SW and PL through other traits being the best, therefore, these three traits can be relied upon as a selection criteria for higher seed yield in breeding programs. From previous studies, (Berhe *et al.*, 1998). reported that path analysis showed that number of seeds per plant and 100-seed weight were the major direct contributors to seed yield per plant, Ulukan *et al.*(2003) indicated the direct and indirect effects of plant height, pod length, pod number per plant and grain number per pod upon biological yield. In the other study, Tadesse *et al.* (2011) pointed out that number of pod per plants, seed per pod, 1000 seed weight and plant height had high positive direct effect on seed yield per plot. Sharifi (2017) stated that path coefficient analysis indicated that number of pod per plant, pod length, and 100 seed weight had the highest positive direct effects on dry seed yield in studied faba bean genotypes, and reported that attention should be paid to traits such as pod length, 100 seed weight, number of pods per plant and number of stems per plant for augmentation of seed yield and these traits could be used as selection criteria in faba bean breeding programs.

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