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Genetic performance of Faba Bean genotypes in Iraq

Maan Mohammed Salih[1] and Kamal Benyamin Esho[2]

[1]Field Crops Department College of Agriculture Talafer University, **Iraq**
[2]Department of Horticulture and landscape Design, College of Agriculture and forestry Mosul University, **Iraq**

***Correspondence:** kamalesho@uomosul.edu.iq **Received 20-04-2020, Revised: 02-09-2020, Accepted: 10-09-2020 e-Published: 20-09-2020**

The study was carried out in the vegetable research field, department of horticulture and landscape design, college of agriculture and forestry, university of Mosul, during growing season 2018/2019. The aim was to study the genetic parameters and evaluate the 24 genotypes which were introduced to Iraq from ICARDA center along with the local genotype. The genotypes were planting in a randomized complete block design with three replicates. The results of the analysis showed that tested genotypes of faba bean differed significantly for most of the studied traits. The genotypic (O'^2g) and phenotypic (O'^2g) variations were high for the biological yield and seed yield ton/hectare, and the 100 seeds weight. The heritability in broad sense ($H^2_{b.s}$) was higher for all traits and it ranged between 61.575- 91.721%). The result indicated that total seeds yield per area showed a positive significant correlation in phenotypic and genotypic with the number of days for flowering, seeds maturity, number of pods per plant, number of seeds per plant and 100 seeds weight. The path coefficient analysis showed highest positive direct effects on the yield kg/hectare with the biological yield and harvest index attributes of 0.938 and 0.301 respectively.

Keywords: Faba bean, Genetic parameter, Seed yield , Genotypic variation . Heritability. Path analysis.

INTRODUCTION

Faba bean, horse bean or broad bean belonging to the genus Vicia , *Vicia faba* L. is one of the crops of the legume family (Fabaceae) , Smýkal et al., 2014) . Which is considered an important vegetable because its pods and dry seeds contain nutrients that are considered important for human consumption on a high percentage of protein ranging between 23-37 %, and addition to vitamins and other nutrients, as well as, containing quantities of sugary and starchy materials (Matlob et al., 1980; Diaz et al., 2006 and Alghamdi, 2009). The total area cultivated from it in the word reached 2.4 million hectares in 2014 (FAOSTAT, 2015). The faba crop caused to maintain fertility soil, it also caused to supply the soil with nitrogen when mixing the crop with soil for its bacterial nodules formed on the roots of plant (Kor and Ghani, 2001). The introduced method is a major source for plant breeders to obtain breeding material in order to obtain new genotypes and estimated them to evaluated their performance compared with local varieties and extent for their adaptation to local conditions to achieve genetic improvement which is one of the aims plant breeders seek when the available genetic information on these genotypes is not to the extent it is sufficient to determine the most promising genotypes with desired quantities of high production quantity and quality (Al-kummer, 1999) .The genotypes in faba bean variation within themselves in many phenotypic characteristics in terms of the growth and the dates of flowering , ripeness , color and shape of pods and leaves , and in the traits of seed , yield and its components (Qobayili and Khoury , 2005 , and Karadavut et al., 2010) . Many researchers have found through their studies that the yield in beans which is affected by

many factors , depends on genetic variation and that genetic analysis is important to give information about the traits being studied (Kalia et al., 2003 ; Mostafa , 2007 ; Alabade and Al-kummer , 2010 and Kumar and Kaushik , 2020). The inheritance ratio of any quality traits determines the best method for breeding programs (Allard, 1960). Thus, the information on the heritability ration for each trait and knowledge of the interrelation between the yield and those traits are necessary for the selection steps because of the influence of the trait of the high yield effected by environment because it is the outcome of number of related traits . So the direct selection for yield that is note effective compared with the selection based on other traits. Several researchers have found through their evaluation of faba genotypes there are variations between the genotypes in the characteristics of vegetative growth represented by the length of the plant , number of branches per plant , the number of pods per plant , number of seeds per pod and 100 seeds weight , in addition to the differences in the biological yield and seeds yield (ton/hectare) (Alan and Geren , 2007 ; Alghamdi , 2007 ; Abdel El-Zaher , 2007 and El-Shal and El-Sayed ,2019) . Inheritance plays an important role in selective the appropriate method of education and improving the quantitative traits in order to increase the yield as on the basis of which the selection program is done , especially if its value is high . Lush (1943) indicated that the heritability is the measure for the genetic distance among the parents and the hybrids and determine the phenotypic and genotypic correlation among the bare of different traits, this various often contribute to efficient program planning and evaluation. Abdel Sattar and El-Mouhamady (2012) when studying the evaluation of faba genotypes , the heritability ratio in the broad sense ($H^2_{b.s.}$) was 0.57 for the plant height , 0.91 for the seeds yield per plant , and the weight of 100 seeds . Solieman and Ragheb (2014) founded that the rate of heritability in the broad sense ($H^2_{b.s.}$) exceeded of 80.10 for pod diameter and 99.83% for the number of pods per plant , and it was higher also for both plant height , pod weight , total yield and increased the ration genetic advance of these traits . Al-Shamma (2014) found that the values of variations differed between the studied traits genotypic (O'^2g) and phenotypic (O'^2p) variation were greater than the environmental variance (O'^2e) for most traits , as for the rate of heritability in broad sense , it reached the highest value in most of the traits for the FI and F2 generations after the mutations , the values of heritability in broad sense varied among the studied traits , The highest heritability rate was in most of the studied traits in the first matant generation M1 due to the high values of genotypic variation (O'^2g) and the lowest values in the percentage of protein and the yield , while in the second mutant generation M2 the highest heritability rate was in most of the studied characteristics due to the high genotypic variation (O'^2g) and low environmental variation (O'^2e) and lowest values in number of seeds per pod. Sharifi, (2014) indicated in his study for some genotypes of faba , that the genotypes differed significantly among them in most of the traits under the studied and there is a positive significant correlation between the seeds yield and the length and diameter of the seed and the weight of 100 seeds , and the path coefficient analysis between the traits number of pods per plant and number of stems per plant , the pod length , and the ratio of length of seed to the diameter and weight of 100 seeds have a direct positive significantly effect on the seeds dried yield of the genotypes . High heritability was observed for most of the characters except for number of branches, number of pods per plant and pod width. A direct and indirect effect of yield components on seed yield per plant was also observed (Sheelamary and Shivani, 2015). Singh et al., (2015) when they studying to evaluate 25 genotypes line of faba , found that the genotypes differed significantly in each of traits represented by date of flowering , number of lateral branches per plant , plant height , number of pods per plant and weight of 100 seeds , as the indicated that the rate of heritability in the broad sense was high for plant height , number of lateral branches per plant , number of pods per plant and total seeds yield per area . Tadele et al., (2019) indicated that faba plant genotypes differ significantly between them in the traits of vegetative growth and pod and the coefficient of genotypic (GCV) and phenotypic (PCV) variation was high for the trait of 100 seeds weight , the heritability in broad sense and genetic advance as a percentage ranged between 24.63 - 98.22% and 2.0 – 47.13% respectively .El-Shal and El-Sayed (2019) found that there is a positive significant direct effect of the 100 seeds weight followed by the direct effect of the trait number of seeds per plant with total seeds yield and there is an indirect effect of the number of seeds per plant and number of pods per plant that gave the highest values following the indirect effect between number of lateral branches per plant and weight 100 seeds . Al-falahy and Kanoush (2020) indicated that the heritability in broad sense was high for all traits in

five genotypes of faba bean, ranged between 0.94 – 0.99 % for the traits under the studied for vegetative growth and yield components.

The goal of the study is to estimate some of genetic parameters , heritability , and genetic advance for the yield and its components for the purpose of selecting the best traits in subsequent early generation and more effectively to continue with the best in education programs as well as assessing the phenotypic and genotypic correlation between pairs traits and conducting path coefficient analysis between the traits under the study to determine the component with a high direct effect on the seed yield to see which of them is important in improving the yield for 25 genotypes of faba bean entering to the country , under the conditions of Nineveh governorate , Iraq , to benefit from in breeding programs and improving the trait quantity for this crop..

MATERIALS AND METHODS

The study was carried out in vegetable research field , Department of Horticulture and landscape design , College of Agriculture and Forestry , Mosul university during growing season 2018/2019 to study the genetic parameters for the some genotypic of faba introduced to the country , Iraq , from ICARDA center table (1) .

The seeds of the genotypes were sowing in field on tow line for each genotype , with length of 4 m per line and at 20 cm distance between the plant within line , plot area was (2 lines) , the distance 50 between line and other under condition of the rudimentary area . The genotypes were planting in a randomized complete block design (RCBD) with three replicate. All agriculture service operations were performed equally on all treatments as recommended by (Matlob et al., 1989). All experimental unite of genotypes were provided with 30 kg, P60 kg and 60 kg of K per hectare (Othman and Assaf , 2009) .The process of controlling the aphids and whitefly was carried out using the pesticides 5% and vantex 6% mixed at an average of 3-5 gm /liter of water for each spraying the vegetative system and periodically every 2 week as a preventive spray to protected diseases and insect (Pro. Ali Karim, college of agriculture and forestry, department of plant productive, personal contact).

Data were recorded on random sample for five plants for each genotype in replicate and included the traits ; data of flower appearance (day) , number of days to maturity (day) , plant height (cm) , number of lateral branches per plant , number of pods per plant , pod length (cm) , number of seeds per pod , 100 seeds weight (gm) , total seeds yield kg/hectare , biological yield ton/hectare and harvest index . Data was analyzed for each trait according to the design used using the SAS program (2007) .genetic parameters were calculated genotypic ((O'^2g) phenotypic (O'^2p) variation from the table Anova according to the following:

$(O'^2g) = (Ms\ g - Ms\ e) / r$, $(O'^2p) = O'^2g + O'^2e$

The genetic coefficient variation (GCV) and phenotype coefficient variation (PCV) were estimated by using the following equation:

Genotypic coefficient variation (G.C.V.) = $\sqrt{G^2}\ g / \hat{Y} \times 100$

Phenotypic coefficient variation (P.C.V.) = $\sqrt{G^2}\ p / \hat{Y} \times 100$ Where ý = the mean of the trait.

The heritability is also calculated in the broad sense ($H^2_{b.s.}$) according the following:

$H^2_{b.s.} = (O'^2g) / (O'^2p)$

The limits of heritability values which the mentioned on Ali (1999) as follows:

$H^2_{b.s.}$ < 40% low , $H^2_{b.s.}$ 40-60 % medium and $H^2_{b.s.}$ > 60 are high , as calculated by the expected the genetic advance (GA) and the percentage of expected genetic advance from the mean (GAM) according to (Johnson et al., 1955) , the expected genetic advance ratio reported by Robinson (1966) as follows : les than 10 % low , 10-30 % medium and more than 30 % high .

$G.A. = K \times O'^2p \times H^2_{b.s}$

G.A. (as % of the mean) = $(G.A. / \hat{Y}) \times 100$

Where K = selection intensity at 5% was 2.06, O'^2p= phenotypic variation,

$H^2_{b.s}$ = heritability, $\hat{Y}$= general mean for trait. The genotypic and phenotypic coefficient correlation between pairs of different traits was estimated according the method presented by Walter (1975),

$$rP = \frac{Msp_{(cov.)}}{\sqrt{Msp_{(1)} \times Msp_{(2)}}} \qquad rG = \frac{\sigma_{G \times Y}}{\sqrt{Msg_{(1)} \times Msg_{(2)}}}$$

The method according Dofing and Knight (1992) and Rodriguez *et al*., (2001) was used to find the direct effect of the traits under the study for seeds yield (kg/hectare) by using Exel according to the following equation:

$$[P] = [R]^{-1}[r]$$

Table 1: The entry name and origin of the faba genotypes

No.	Entry name	Pedigree	Origin
1	FLP08- 051FB	DT/87/7244/04/05-HBP/DSO	ICARDA
2	FLP08-052FB	DT/B7/7318/04/05- HBP/DSO	ICARDA
3	FLP08- 053FB	DT/B7/7408/04/05- HBP/DSO	ICARDA
4	FLP08-054FB	DT/B7/7434/05/06- HBP/DSO	ICARDA
5	FLP08- 055FB	DT/B7/7516-1/05/06- HBP/DSO	ICARDA
6	FLP08-056FB	DT/B7/7516-2/05/06- HBP/DSO	ICARDA
7	FLP08- 057FB	DT/B7/7536-1/04/05- HBP/DS0	ICARDA
8	FLP08-058FB	DT/B7/7544/04/05- HBP/DS0	ICARDA
9	FLP08- 059FB	DT/B7/7547/04/05- HBP/DS0	ICARDA
10	FLP08-060FB	DT/B7/7626/04/05- HBP/DS0	ICARDA
11	FLP08- 061FB	DT/B7/7651/04/05- HBP/DS0	ICARDA
12	FLP08-015FB	DT/B7/7428-2/04/05- HBP/DS0	ICARDA
13	FLP08- 062FB	DT/B7/7822/04/05- HBP/DS0	ICARDA
14	FLP08-063FB	Selection 9055/0506 From ILBI8141	ICARDA
15	FB/7723/06	FB/7723/06	ICARDA
16	FL.P08-065FB	Selection 9074/0506 From ILB1814	ICARDA
17	DT/A11/9010/05-8	DT/A11/9010/05-06	ICARDA
18	FLP12-003FB	DT/B7/8135/0405- HBP/S0D	ICARDA
19	DT/11/9077/06	DT/11/9077/06	ICARDA
20	FLP10-070FB	FB/7001/06- HBP/DS0	ICARDA
21	FB/77224/06	FB/7724/06	ICARDA
22	FLP10-072FB	FB/7003/06/HBP/DS0	ICARDA
23	R.Blanca		Spain
24	ASCCT		Spain
25	Local - Check		-

Table 2: showed the rainfall during growing season 2018/2019 *

No.	Month , year	Rainfall (mlm)
1	October / 2018	28.5
2	November / 2018	183
3	December / 2018	146.5
4	January /2019	93
5	February /2019	52.5
6	March / 2019	205
7	April / 2019	118.5
8	May / 2019	17
Total		843

***** Ministry of Agriculture, Directress of Agriculture, Nineveh, Center of agriculture branch

Where [P] = vector of direct effects, [R] $^{-1}$= inverse matrix of correlation coefficients between all possible pairs of independent variable, [r] = vector of genetic correlation between seeds yield and traits under study. Using Minitab to find the inverse of the correlation matrix and multiply the inverse of the matrix by the product. The indirect effect were estimated by using the following, and using the Excel program

Indirect effect = PY (R)

The limits of direct and indirect effects path coefficient analysis according to Link and Mishra, 1973) are (0.0- 0.09) cancel, (0.1- 0.19) low, (0.20 – 0.29) medium (0.3-0.99) high and more than 1 very high.

RESULTSAND DISCUSSION

Table 3: indicated the results of analysis of variance of the studied traits, that there are significant differences between the genotypes under study for most the traits. this results was consistent with many researchers (Alghamdi , 2007 ; Abdel El-Zahar , 2007 ; Alan and Geren , 2007 ; Alabade and Al-kummer , 2010 ; Al-Shamaa , 2014

; Singh et al., 2015 ; Tadel *et al*., 2019 , El-Shall and El-sayed , 2019 and Kumar and Kaushik, 2020) , for the traits of number of seeds per pod , plant height , date of flowering and maturity , number of branches per plant , 100 seeds weight and total seeds yield . the presence of variation is important to study the genetic behavior of these traits in order to improved them in breeding program in future.

Table 4 : shows the mean values of the traits and genetic parameters of 25 genotypes of faba bean used in the study , as it appears from table , traits have shown a wide range of genotypic (O'^2g) , phenotypic (O'^2p) and environment (O'^2e) variation of the biological yield ,total seed yield per hectare , 100 seeds weight and in the plant height .These results may be discussed by these traits are a complex amount characterized by their wide affected on the environmental condition sourrounding the plant , while the variance was low for the traits of number of seeds per pod and length of pod . This result was consistent with (Alen and Geren , 2007 ; Alghamdi , 2007 ; Abdel El-Zaher , 2007 ; Solieman and Raghed , 2014 ; Singh *et al*., 2015 and El-Shal and El-Sayed 2019) . It is also showed from table 4 , the heritability in broad sense ($H^2_{b.s.}$) was higher for all traits according to the range proposed by Ali (1999) , this is due to the high values of genetic variation (O'^2g) (Walsh , 1981) , this result due to the importance of additive and non additive effects of gene that control inheritably this traits (Mather and Jinks , 1982) . An increase in heritability ($H^2_{b.s.}$) which indicates the possibility of direct improvements for these traits in the coming years through breeding programs for this aim, the heritability was range from 59.860 to 91.091. (Allard, 1960) .This result has been consistent with many researchers (Abdel Sattar and El-Mohamady , 2012 , Solieman and Ragheb , 2014 ; Sheelamary and Shivani 2015, and Al-Shamaa 2014) . The expected genetic advance (GA) was high for most the traits , the genetic advance as a percentage of mean (GAM) according to range Robinson (1966) was high for total seed yield, number of pods per plant and biological yield which was (35.824 ; 32.244 and 30.236) respectively . While in the other side it was low for harvest index (9.557) and number of days to maturity .

(5.540). The higher of heritability with the high values of the expected genetic advance gives an indication of the prediction that we will obtain in the selection process, and overall selection method achieves the desired success (Welsh , 1981) .

This results agreed with (kalia et al., 2003 ; Al-Fahadi , 2009 ; Alabade and Al-kummer , 2010 ; Tadele et al., 2019 , El-Shal and El-Sayed 2020 and Al-falahy and Kanoush , 2020) for the genetic advance for the number of pods per plant and number of seeds per pod .

Table (5) showed the phenotypic and genotypic correlation between pairs of traits studied, there is a positive significant coefficient correlation among the harvest index and number of days of flowering, number of maturity days of pods , number of pods per plant , number of seeds per pod and with total seeds yield per hectare . The biological yield had a positive significantly correlation with all traits and it take the same trend for the harvest index .In other side , the total seeds yield per hectare had positive significantly correlation with the number of days for flowering ; number of maturity days ; number of pods per plant and with number of seeds per pod . Also the table 5 , indicated that 100 seeds weight has a positive significantly correlation with number of days for flowering ; number of days for maturity and plant height , while the trait number of seeds per pod was positive significantly correlation with number of days for flowering ; number of days for maturity ; number of pods per plant and with pod length . the pod length had positive significantly correlation with number of days for flowering and pod maturity . Number of pods per plant had positive significantly correlation with number of days for flowering and pod maturity and with the number of branches per plant. We conclude from table (5) the total seeds yield per hectare showed an apparently positive significantly phenotypic and genotypic correlation with number of days for flowering and pod maturity ; number of pods per plant , number of seeds per pod and 100 seeds weight . This results agreed with many of researchers who indicated the positive significantly genotypic and phenotypic coefficient correlation among total seeds yield per unit area with the yield components (Alabade and Al-kummer , 2010 ; Abdel Sttar and El-Mouhamady, 2012 ; Solieman and Ragheb , 2014 ; Singh et al., 2015 , El-Shal and El-Sayed 2019 ; Kumar and Kaushik , 2020 , and Al-falahy and Kanoush , 2020) .

Table 3: ANOVA of data

S.O.V	d.f	Mean Square										
		DF	DM	PH	No.. B/P	No. P/P	PL	No.S/P	100 SW	SY	BY	HI
Replicate	2	6.6533	10.4933	25.1200	0.6917	25.7876	0.6425	0.9566	2.1207	6199670.90	3564079.1	1.7379
Genotypes	24	52.8088**	56.0555**	124.2811**	0.3891*	12.655**	5.3180**	0.9636*	231.46**	1317283.83**	5305378.9**	24.2624**
Error	48	1.6672	2.4655	14.1477	0.07108	1.7002	0.4086	0.07677	6.7607	111832.36	564702.9	4.1776
Total	74	61.1293	69.0143	163.5488	1.15188	40.1428	6.3691	1.99727	240.3414	7628787.09	9434160.9	30.1779

DF= Days for Flowers . ,DM= Days for Maturity , PH= Plant Height (cm) , No. B/P= number of Branches/Plant , No. P/P= number of Pods /Plant ,, PL= Pod Length (cm) , No.S/P= Number of Seed /Pod, 100SW = 100 Seeds Weight (gm), SY=Seeds Yield (t/ha.), BY=Biological Yield (t/ha.),HI= Harvest Index

Table 4: The genetic parameters for the traits in genotypes faba bean growing season 2018/2019 .

	DF	DM	PH	No. B/P	No. P/P	PL	No.S/P	100SW	SY	BY	HI
Means	78.507	147.333	79.840	3.572	10.084	9.515	3.524	93.636	3223.952	7351.216	43.765
Range	73.33—86.67	141.67—154.67	71.00—89.33	3.04—4.20	7.33—12.00	7.00—11.67	2.20—4.57	73.97—114.80	2045.33—4307.67	4869.33 --9244.33	37.63 – 48.67
$Б^2p$	18.714	20.329	50.859	0.177	5.352	2.045	0.372	81.663	513649.513	2144928.244	10.873
$Б^2g$	17.047	17.863	36.711	0.106	3.652	1.636	0.296	74.902	401817.158	1580225.325	6.695
$Б^2e$	1.667	2.466	14.148	0.071	1.700	0.409	0.077	6.761	111832.355	564702.919	4.178
$H^2_{b.s}$	91.091	87.872	72.182	59.860	68.231	80.019	79.384	91.721	78.228	73.673	61.575
GCV	5.259	2.869	7.589	9.115	18.949	13.445	15.431	9.243	19.662	17.100	5.912
GA	811.769	816.155	1060.428	51.894	325.166	235.732	99.794	1707.458	115494.754	222269.490	418.253
GA%	10.340	5.540	13.282	14.528	32.244	24.776	28.322	18.235	35.824	30.236	9.557

DF= Days for Flowers .DM= Days for Maturity ,PH= Plant Height (cm) ,No. B/P= number of Branches/Plant ,no. P/P= number of Pods /Plant ,, PL= Pod Length (cm) , No.S/P= Number of Seed /Pod, 100SW = 100 Seeds Weight (gm), SY=Seeds Yield (t/ha.), BY=Biological Yield (t/ha.),HI= Harvest Index

Table 5: The genotypic, phenotypic, environment correlation for the traits in genotypes faba bean growing season 2018/2019

		HI	BY	SY	100SW	No. S/P	PL	P/P	No. B/P	PH	DM	DF
DF	rp	0.448**	0.558**	0.648**	0.385**	0.503**	0.290*	0.598**	0.202	0.237	0.900	1
	rg	0.609**	0.674**	0.761**	0.423**	0.575**	0.374**	0.706**	0.274	0.298	0.983	1
DM	rp	0.436**	0.486**	0.571**	0.311*	0.495**	0.247	0.586**	0.261	0.362*	1	
	rg	0.561**	0.538**	0.624**	0.367**	0.530**	0.258	0.671**	0.352*	0.351	1	
PH	rp	0.068	0.052	0.065	0.307*	0.046	0.227	0.126	0.259	1		
	rg	0.191	-0.040	0.022	0.381*	0.072	0.237	0.103	0.302*	1		
No. B/P	rp	0.198	0.028	0.082	-0.094	0.172	0.211	0.290*	1			
	rg	0.334*	0.189	0.246	-0.128	0.277	0.204	0.370**	1			
P/P	rp	0.321*	0.669**	0.700**	0.030	0.673**	0.241	1				
	rg	0.484**	0.835**	0.859**	0.104	0.881**	0.250	1				
PL	rp	0.226	0.236	0.296*	0.271	0.345*	1					
	rg	0.312*	0.231	0.307*	0.307*	0.326*	1					
No.S/P	rp	0.386**	0.698**	0.743**	-0.104	1						
	rg	0.494**	0.836**	0.857**	-0.113	1						
100SW	rp	0.313*	0.131	0.222	1							
	rg	0.405**	0.191	0.284	1							
SY	rp	0.491**	0.945**	1								
	rg	0.588**	0.967**	1								
BY	rp	0.188	1									
	rg	0.365*	1									
HI	rp	1										
	rg	1										

DF= Days for Flowers .DM= Days for Maturity ,PH= Plant Height (cm) ,No. B/P= number of Branches/Plant ,No. P/P= number of Pods /Plant ,, PL= Pod Length (cm) , No.S/P= Number of Seed /Pod, 100SW = 100 Seeds Weight (gm), SY=Seeds Yield (t/ha.), BY=Biological Yield (t/ha.),HI= Harvest Index

Table 6 : the path coefficient analysis for the traits in genotypes faba bean growing season 2018/2019

	HI	BY	100SW	No.S/P	PL	P/P	No. B/P	PH	DF	DM
DF	0.039	0.043	0.027	0.037	0.024	0.045	0.018	0.019	0.013	0.064
DM	0.036	0.035	0.024	0.034	0.017	0.044	0.023	0.023	0.065	0.013
PH	0.005	-0.001	0.010	0.002	0.006	0.003	0.008	0.026	0.009	0.008
No. B/P	-0.022	-0.013	0.008	-0.018	-0.014	-0.025	-0.066	-0.020	-0.023	-0.018
P/P	0.014	0.024	0.003	0.025	0.007	0.029	0.011	0.003	0.019	0.020
PL	0.018	0.013	0.017	0.018	0.057	0.014	0.012	0.013	0.015	0.021
No.S/P	-0.093	-0.158	0.021	-0.189	-0.061	-0.166	-0.052	-0.014	-0.100	-0.108
100SW	-0.052	-0.024	-0.128	0.014	-0.039	-0.013	0.016	-0.049	-0.047	-0.054
BY	0.342	0.938	0.179	0.784	0.216	0.783	0.177	-0.037	0.504	0.632
HI	0.301	0.110	0.122	0.149	0.094	0.146	0.101	0.058	0.169	0.183
SY	0.587	0.967	0.284	0.857	0.307	0.859	0.246	0.022	0.624	0.761

DF= Days for Flowers .DM= Days for Maturity ,PH= Plant Height (cm) ,No. B/P= number of Branches/Plant ,no. P/P= number of Pods /Plant ,, PL= Pod Length (cm) , No.S/P= Number of Seed /Pod, 100SW = 100 Seeds Weight (gm), SY=Seeds Yield (t/ha.), BY=Biological Yield (t/ha.),HI= Harvest Index

Table (6) indicated the path coefficient analysis by dividing the genotypic correlation coefficient for direct and indirect effects , the higher direct effect on the total seeds yield (kg/hectare) was positive with biological yield and harvest index (0.938 and 0.301) respectively . It can be discussed for the high values for genotypic correlation between total yield and these traits . While the indirect effect for the biological yield on the seed yield throughout the number of seeds per pod (0.784) , number of pods per plant (0.783) , number of days for flowering (0.632) , number of days for maturity (0.504) and harvest index (0.342) . Where over , for the rest direct and indirect effect was not the same importance , Based on the foregoing , it is possible to recommend the trait that are electoral evidence in the breeding program to selected the seed yield as it a complex trait that inherits a large number of genetic factors and it is affected by environment is very large , therefore direct selection is difficult process from these traits comes biological yield , harvest index and 100 seeds weight . The results of the study were somewhat in line with Abdelmula and Abdalla , 1994 ; Sheelamary and Shivani 2015 ; Sharifi, , 2017 ; Fatih, 2017 ; Kumer et al., 2017 and El-Shal and El-Sayed 2019 .

CONCLUSION

From this study we concluded that all 25 genotypes of faba bean were significant for all traits, the genotype, phenotype were significant positive correlation coefficient with the total seed yield per unite area with the number of pods/plant and 100 seeds weight, the path coefficient analysis was positive direct effect observed for biological yield, harvest index and weight of 1000 seeds, with total seeds yield.

CONFLICT OF INTEREST

The authors declared that present study was performed in absence of any conflict of interest.

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AUTHOR CONTRIBUTIONS

The research K.B. Esho sowing the genotypes seeds according to the design used, took random data for the traits on the genotypes and classified them in the calculator and wrote the research. M.M.Salih researcher, he performed the statistical analysis of the data and organized them in tables using the Excel program and interpreted the results.

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