STUDY THE GENETIC PARAMETERS IN PHASEOLUS

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Abstract- The experiment was conducted at vegetable research farm, horticulture and landscape design, college of agriculture and forestry, Mosul University, Iraq, during spring season 2018. The aim of this study was to determine of genetic parameters and correlation coefficients and heritability in 8 genotypes of common bean, genotypes were sown in a randomized complete block design with three replications. Result showed that significant difference between genotypic in all the 16 parameters. Genotype BRS Pitango is the best in most the traits, while genotype G11867 is best in the 100-seeds weight. The $Б^2$ phenotypic and genotypic were higher in plant height, leave area, seeds weight /plot. The heritability in broad sense and genetic advance were higher in plant height, seed weight /plot and total dry seeds (t/ha.). The results recorded higher positive significant genotypic and phenotypic correlation coefficients between total dry seeds yield (t/ha.) with the plant height, seeds weight /plot, seed diameter and 100- seeds weight.

Keywords- Common Bean, Genetic Parameters, Heritability, Correlation, Agronomical Traits.

I. INTRODUCTION

The common bean(Phaseolus vulgaris L.) is the world's most important grain legume for direct human consumption (Goncalves, et al., 2008), it use as fresh pods (sanap bean) or for dry seeds, it is very rich in carbohydrate, protein, Thiamine, raypovlavin Vitamin C and minerals, as Ca, P, Fe, it is grown in warm season , and during the cool. The bean sowing in Iraq at two season,the first at spring season at march gave their yield at the beginning in May for fresh pods, at the end of June for dry seed, and the second at fall season at the end of July or the beginning of August it gave the yield at September and October for fresh pods (Al-Rekaby and Meshaal,1981).The area increased in Iraq from 940 to 1039 to 1273 hectares from 2010,2011 and 2012. (Albo-hamad, 2017). Common bean is a diploid (2n=2x=22) and predominantly self-crossing species although 3% or more out crossing rate has also been observed (Ibarra –Perez et al., 1997).

Success in crop breeding is also depending on the isolation of genetically superior genotypes based on the amount of variability present in the material. There-fore, information on genetic variability existed in a group of populations of dry bean are essential (Raffi and Nath, 2004). Previous some studies were carried out by Raiet al. (2001), Peksen and Gulumser (2005). Santallaet al. (2004) recorded in their studies indicated that Andean gene pool in common bean Argentina has a large genetic base on the basis of morphological and adaptive variability and biochemical analysis. For effective selection information on traits association with yield and among themselves influence on the expression of these traits are necessary (Yagdi, 2009). Development of new genotypes with higher genetic potential for grain yield is the aim of breeding programs .According to Nogueiraet al. (2012) throughout selection process, goal to improve the main traits,maintaining for enhancing the expression of other simultaneously.Yield is the principal factors for determining improvement of a crop, like other crops, seed yield in common bean is a quantitative traits and influenced by a number of yield traits. Yosephet al.(2014) recorded in their study to evaluation of common bean varieties for yield and components that analysis of variance showed that both of the phonological parameters studies were significantly affected by varieties, there were significant variation observed among the bean varieties for all the yield and yield components except number of seed per pod.Vidyakaret al. (2017) recorded in their studies that all 24 genotypes of French bean showed significant genetic divergence, the traits like plant height, number of seeds per plant, seed yield per plant exhibited high GCV, PCV,heritability and genetic advance should be given top priority during selection,the grain yield exhibited positive and significant correlation with yield per plant and test weight both at genotypic and phenotypic level.

Correlation study indicated that positive and significant genotypic correlation was observed between fresh pod yield with number pod per plant single fresh pod weight, pod dry weight, pod length and leaf area per plant, (Alemuet al. 2017). Bagheriet al. (2017) recorded in their studies showed that difference between genotypes in all the parameters, except for internode diameter, in other sides number of seeds per pod, seed diameter and hundred seed weight were significant, the estimates of GCV were high for weight of pods per plant, grain yield per plant, grain yield per plant showed high significant positive genetic and phenotypic correlation with only weight of pods per plant.

The present study was undertaken to study the genetic parameters, correlation and of some varieties in common bean.

II. MATERIALS AND METHODS

The experiment was conducted at vegetable research farm, horticulture and landscape design, college of agriculture and forestry, Mosul University, Iraq, during spring season 2018.The experiments material consisted of 8 genotypes of common bean (Table 1).

Table (1).The names and the source of the genotype of common bean:

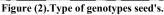| No.	Names	Seed color	Country	Source
1	Bar-245	White	French	Local market, Erbil
2	G11867	White	Iranian	
3	Strike	Brown dusky	Netherland	Local market, Mosul
4	Brinco	Brown dusky	Turkish	
5	Si Scresiatainp aleta	Brown	U.S.A.	Local market, Duhok
6	BRS Executivo	Brocaded (Mobarqesh)	Iranian	
7	Della regina	White	Argentina	Local market, Erbil
8	BRS Pitango	Red	Iranian	

Figure (1).The seed of the genotypes of common bean

The seeds of the genotypes were sown in randomized complete block design (R.C.B.D.) with three replicate, the experimental field was divided into three blocks of equal size and each block possesses 8 plots, each line was accommodated in two rows of 1.5 m length spaced at 30cm with an approximate plant to plant distance of 15 cm(Vidyakaret al., 2017). Under drip irrigation, fertilizer at a rate of 100 kg/ha DAP and 50 kg/ ha urea was applied, all other necessary cultural such as weeding and cultivation were applied to all plots uniformly. The data were recorded for traits includingplant height (cm), number of branches/plant, leave area (cm^2), dry pod length, diameter (cm), number of seeds /pod, seed weight /plot (gm), seed length, diameter (cm), 100-seeds weight (gm) and total dry seeds yield (t/ha.).

Figure (2).Type of genotypes seed's.

The data were subjected to statistical and biometrical analysis was carried out using the SAS package (SAS, Institute, 2000). Phenotypic and genotypic coefficients of variation were estimated by following the procedure given by Burton (1952), Heritability in broad sense (H^2) was estimated according to Falconer, (1989). The mean values were used for genetic analysis to determine Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV), according to Singh and Chaudhury (1985). Genetic advance (GA) was calculated with the method suggested by Allard (1960). Phenotypic and genotypic correlations were approximation using the standard procedure suggested by Miller et al., (1958). Path coefficient analysis which refers to direct and indirect effects of the yield attributing traits was calculated following the method given by Dewey and Lu (1959).

III. RESULTS AND DISCUSSION:

Table (2) showed the analysis of variance, which showed significant difference for all traits of the genotypic of common bean under the study, indicates the presence of variation for all traits among the population, significant at the 0.01 and 0.05 probability levels. High genetic variability for difference quantitative characters, in effort to determine the extent to which diversity in yield components are responsible for differences in yield among genotypes in common bean was also reported earlier by Santallaet al. (2004), for seeds/pod, pod weight, pod length, pod width, dry seeds weight , seed length and seed width. Iqbalet al., (2010) for primary branches per plant, number of pod s per plant , pod length, seeds per pod and 100-seeeds weight, Arungaet al. (2010), for number of pods/plant , pod weight /plant, pod length and pod diameter. Yosephet al., (2014) for pods per plant, seeds per pod and grain yield, Bagheriet al.,(2017) for plant height, number of seeds /pod and weight of pod /plant.

Table (3) showed the mean value of the 11 characters in genotypes of common bean.The genotype BRS Pitango gave the high in plant height (140.3 cm),leave area(158.31cm^2) dry pod diameter

(0.94cm), seeds weight per plot (917.33 gm) and total dry seeds yield (5.82t/ha.), which differ with all the genotypes of common bean under the study, while the genotype G11867 gave the highest value, and 100-seeds weight (31.77 gm) and total dry seeds yield t/ha. (5.36) in the other hands the genotype Si Scresiatainpaleta gave highest value of the traits vias dry pod length(12.2) and number of seeds per pod (7.00). While the genotypes strike and Brinco gave a least value at most the traits. These result are similar to the finding of (Santallaet al., 2004, Arungaet al., 2010, Iqbalet al., 2010, Iqbalet al., 2012, Onderet al., 2013, Yosephet al., 2014, Darkwaet al., 2016, Bagheriet al., 2017, and Vidyakaret al., 2017), whose indicated that the genotypes of common bean were differ in the vegetative growth and in yield components.

Genetic parameters which include the phenotypic variance ($Б^2p$), genotypic variance ($Б^2g$), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability ($H^2_{b.s}$) , expected genetic advance (GA) and the genetic advance as the mean value were estimated for all 11 traits are present in table (4).Analysis of variance showed significant variance among the genotype of common bean for most the traits the highest ($Б^2p$) and ($Б^2g$) were observed seeds weight per plot, plant height , leave area , and 100-seeds weight. Many of researcher indicated that there was differ in ($Б^2p$) and ($Б^2g$), Labatoet al., (2014) for grain production, average weight of 100 seeds, Iqbalet al., (2010) for weight 100 seeds and pod length, Bagheriet al., (2017) for plant height, number of seeds per pod, seed diameter, where ever,(GCV), (PCV) was recorded highest in most traits of common bean under the study. The high heritability (H^2) was recorded for traits plant height (97.65), seed diameter(92.809), seeds weight per plot (84.011), number of seeds per pod (84.13), and total dry seeds yield, as well as high genetic advance was highest for the plant height (81.29), seeds weight per plot (51.56) and total dry seeds yield (51.647), so effective selection may be made for these characters and suggested that these characters could be controlled additive genetic effect and can therefore be used for improvement through phenotypic selection.When heritability of the characters to high selection bases on additive level of performance allows a relatively rapid rate of improvement higher heritability is known to be important selection of superior genotype based phenotypic performance. Knowledge of the genetic control of traits and the role of non-allelic interaction is essential to the breeder when deciding on the selection method and breeding procedure (Esmail, 2007). Santallaet al., (2004) , Arungaet al., (2010), Iqbalet al., (2010), Lobatoet al., (2014), Darkwaet al., (2016), Bagheri et al., (2017) and Vidyakaret al., (2017) reported that the high GCV, PCV , H^2 , and GA, for seed per pod, dry seed weight, number of pod per plant, pod length,

100-seeds weight, number of seeds per pod, grain production, plant height, and seed diameter.

Estimates of phenotypic and genotypic coefficient of correlation represented in table (5) .plant height, exhibit significant and positive association with leave area, total dry seeds yield, 100-seeds weight, seed diameter, seeds weight per plot. number of branches per plant correlated significant and positive with seed length, the trait seeds weight per plot exhibit significant and positive association with the total dry seeds yield, 100-seeds weight and with seed diameter, in other side the trait seed diameter associated significant and positive with 100-seeds weight, the 100- seeds weight associated significant and positive with total dry seeds yield.Seeds yield is one of the main purposes in breeding programs, it is recommended to develop the useful plant genotypes and phenotypes which are adaptive to the region, in this respect, breeders who need to specify the basics of selection should determine the impact factors and the degree of relationships through yield components (Torun and Koycu, 1999). These results are substantial with those of Amorimet al., (2008), Karasu and Oz (2010), Onderet al., (2013), Goncalveset al., (2017), Ejara et al., (2017), Alemuet al., (2017) and Bagheriet al., (2017) who reported positive and highly significant genotypic and phenotypic correlation of dry seed yield with yield and its component traits in common bean, and observed that correlation provides measure of genetic and phenotypic association between characters which helps to identify important traits for selection program.

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Table (2).Anova table analysis for the traits of 8 genotypes of common bean.

s.ov	d.f.	Mean squar										
		Plant height (cm)	No. of branches /plant	Leave area (cm²)	Dry pod Length (cm)	Dry pod diameter cm	No. of seeds /pod	Seeds weight /plot (gm)	Seed length (cm)	Seed diameter (cm)	100 seeds weight (gm)	Total yield (Dry seeds, t/ha.
Replicate	2	0.4659	0.5067	0.674	0.5999	0.7612	0.0286	0.4314	0.415	0.1766	0.8942	0.4465
Genotype	7	3437.7 **	0.5342 **	875.879 **	2.19 99 *	0.00839 **	0.93552 **	10438 3.8 **	0.0192 **	0.0344 **	52.6138 **	4.2018 **
Error	14	27.315	0.1698	542.989	0.21 21	0.00149	0.05532	6226.708	0.0026	0.0008	2.4993	0.2515

*,** Significant at 1% &5% levels respectively.

Table (3) Mean value for traits of common bean .* significant at 5% level.

Genotypes	Plant height (cm)	No. of bran./plant	Leave area (cm²)	Dry pod Length (cm)	Dry pod diameter cm	No. of seeds /pod	Seeds weight /plot (gm)	Seed length (cm)	Seed diameter (cm)	100 seeds weight (gm)	Total yield (Dry seeds, t/ha.
Bar-245	51.5 e	4.97bc	118.55 ab	10.26 cd	0.84c d	5.60 ed	511.33 de	1.21 bc	0.58c	22.13 cd	3.22 de
G11867	112.9 b	5.37ac	110.31 b	10.83 bc	0.92a b	5.93 cd	848.0a	1.28 b	0.79a	31.77 a	5.36 ab
Strike	66.87 c	5.40ac	142.28 ab	11.37 ab	0.84c d	6.45 b	436.67 e	1.19 bc	0.71b	21.10 cd	2.77 e
Brinco	65.8 c	5.33ac	111.82 b	11.13 b	0.79d	6.15 cb	441.33 e	1.22 bc	0.56c	19.80 d	2.80 e
Si Scresiatainp aleta	55.53 de	5.60ab	142.47 ab	12.20 a	0.87ac	7.00 a	640.33 cd	1.24 bc	0.57c	22.83 c	4.06 cd
BRS Executivo	117.93 b	5.43ac	130.57 ab	9.72d	0.93a b	5.92 cd	702.33 bc	1.27 bc	0.80a	28.37 b	4.45 bc

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Della regina	64.63 cd	6.07a	140.71 ab	11.52 ab	0.86b c	5.2e	801.67	1.43 a	0.82a	25.93 b	5.08 ab
BRS Pitango	140.3 a	4.63c	158.31 a	9.91d	0.94a	5.61 de	917.33 a	1.18 c	0.72b	28.10 b	5.82 a

Different letters within the same column indicate significant differences at the probability level (P <0.05).

Table (4): The genetic parameters for the traits of genotypes of common bean

Genetic parameters	Plant height (cm)	No. of branches /plant	Leave area (cm²)	Dry pod length (cm)	Dry pod diameter (cm)	No. of seeds /pod	Seeds weight /plot (gm)	Seed length (cm)	Seed diameter (cm)	100 seeds weight (gm)	Total yield (Dry seeds, t/ha.
$Ƃ^2p$	1164.11	0.29131	653.952	0.874571	0.003798	0.348722	38945.76	0.00819	0.012044	19.20411	1.568285
$Ƃ^2g$	1136.79	0.121488	110.963	0.66239	0.002301	0.293401	32719.05	0.005536	0.011178	16.70482	1.316736
GCV	14.9747	2.443117	2.99536	2.808613	2.056602	3.395544	10.24065	2.225395	5.718351	6.129708	10.26072
PCV	15.1535	3.783161	7.27163	3.22725	2.642529	3.701847	11.17268	2.706818	5.935748	6.572278	11.19802
H^2	97.6535	41.70413	16.9681	75.73887	60.57044	84.13595	84.01184	67.59212	92.80913	86.98567	83.96022
GA	68.6361	0.463686	8.93870	1.459095	0.076898	1.023502	341.537	0.126009	0.209819	7.852573	2.165974
GA. EAN	81.2903	8.66702	6.77801	13.42726	8.792584	17.10945	51.56249	10.05058	30.26231	31.40506	51.64768

Table (5) : Correlation between the traits in genotypic common bean. *, Significant at 1% &5% levels respectively**

Correlation coefficients	11	10	9	8	7	6	5	4	3	2
RP (1)	0.173	0.663**	0.760**	0.548**	-0.113	0.661**	-0.258	0.700**	-0.628**	-0.327*
RG	0.372*	0.754**	0.805**	0.593**	-0.172	0.752**	-0.295	0.927**	-0.716**	-0.585**
RP (2)	-0.234	-0.035	-0.044	0.279	0.527**	-0.035	0.104	-0.325*	0.555**	
RG	0.178	-0.077	-0.071	0.333*	1.110**	-0.078	0.051	-0.198	0.750**	
RP (3)	0.013	-0.215	0.404*	-0.250	0.275	-0.217	0.468*	-0.501**		
RG	0.102	-0.325*	-0.459*	-0.316*	0.287	-0.325*	0.577**	-0.520**		
RP (4)	0.247	0.739**	0.711**	0.539**	-0.045	0.739**	-0.115			
RG	0.694**	0.914**	0.995**	0.693**	0.107	0.914**	-0.274			
RP (5)	-0.122	0.381*	-0.385*	-0.452*	-0.425*	-0.383*				
RG	0.221	-0.477*	-0.380*	-0.540*	-0.474*	-0.480*				
RP (6) RG	0.214	1.000**	0.766**	0.613**	0.268					

	0.592 **	1.000 **	0.949 **	0.678* *	0.434 *
RP (7) RG	0.083	0.269	0.292	0.437*	
	- 0.321	0.433 *	0.331	0.659* *	
RP (8) RG	0.038	0.614 **	0.269		
	0.444 *	0.679 **	0.433 *		
RP (9) RG	0.098	0.764 **			
	- 0.034	0.949 **			
RP (10) RG	0.217				
	0.596 **				

(1) Plant height (cm) , (2) No. of branches /plant , , (3) Dry pod length (cm), (4) Dry pod diameter (cm) ,(5) No. of seeds /pod , (6) Seeds weight /plot (gm) , (7) Seed length (cm), (8) Seed diameter (cm) , (9) 100 seeds weight (gm) , 10) Total yield (Dry seeds , t/ha. , (11) Leave area (cm^2)

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