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Research Article

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Genotypic, Phenotypic Coefficient Variation, Heritability and Regression of *Phaseolus* Genotypes Under Nineveh governorate, Iraq

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Abstract

Common bean is the most important legume as the source of protein, therefore, understanding the genetic variability, heritability and association between grain yield and other agronomic traits is necessary for effective plant breeding program. In this context, a field experiment was carried out during spring season 2019 at the field vegetable experiments of department of horticulture and landscape design, college of agriculture and forestry, Mosul University to study the genotypic, phenotypic coefficient variation, heritability and regression of (12) *Phaseolus* genotypes under Nineveh governorate, Iraq. The data were recorded Vais: plant height (cm), number of branches per plant, number of pods per plant, length and diameter of pod (cm) number of seeds per pod, length and diameter of seed (cm), 1000 seeds weight (gm), seeds weight per plats (gm), seeds yield per plant (gm) and total seeds yield per hectares.(ton). The result showed that the genotype Strick was best for the number of pods per plant and pod weight. While the genotype Bar-245 was superior for number of seeds per pod. The genotype Line 8K. MPh31 was different significantly for seed diameter (0.88 cm) and 1000 seeds weight (355.67g). While the genotype Line 8K. MPh. 31 and Line 4K. MPh. 45 gave the heights yield ton per hectare than all genotypes. The result showed that the GCV and PCV was higher for some traits, and the heritability in broad sense was higher than 40% for some traits.

Keywords: Coefficient Variation; Evaluation; Genotypes; Heritability; Phaseolus

Introduction

The common bean (*Phaseolus vulgaris* L.) revels to Fabaceae family, the *Phaseolus* is the most important food legume in the world [1]. Common bean is an important income source, its straw serves as food for livestock, and also improves soil fertility by its virtue of nitrogen fixation in the cropping system [2]. The local dry seeds and vegetative pod yield production in Iraq was more little when compared with some countries round the world. Common bean is a traditional crop of the neotropics, where it was domesticated several thousand years ago [3]. Vavilov (1951) reported the primary center of origin of *Phaseolus* is South Mexico and Central America, secondary center of origin in Peruvian Ecuadorian. Common bean is the most important seed legume for human consumption, Dried seed of *Phaseolus* contain 60.6% carbohydrate, 22.9% protein and 1.3% fat [4]. In addition, 100g of dry seeds of *Phaseolus* contains minerals viz calcium 260 mg, phosphorus 410 mg, and iron 5.8 mg [5]. Common bean is produced in many countries, whose planting range low external input, even the use of modern production technologies [6]. Dry seed yield is affected by genotype and environmental factors because it is a quantitative traits. Therefore, generally, seed yield has a low heritability. Using as selection criteria of traits relationship with seed yield increase the success selection in plant breeding [7]. Bean are also a crop of considerable global importance as a seed legume plant with the largest cultivation area in the world. In Iraq country the *Phaseolus* was cultivated for the green pod yield, and for the dry seed, it was planting at spring and winter season growing. The potential of a crop respond favorably to breeding program depends on the nature and magnitude of variability, seed yield is a complex trait and is the

produce of many yield. The large spectrum genetic variability in segregation populations depends on the level of genetic diversity between genotypes offer scope for selection. Several researches have indicated the presence of the genetic variation, reported the possibility of selecting lines with higher content for the dry seed yield and yield components in *Phaseolus* 8,9[]. Santalla., *et al.* [10] indicated that Andean gene pool in Argentina has a large genetic base on the basis of morphological and adaptive variability and biochemical analysis. The existence of introgressed populations with sympatric wild forms was evidenced. Yoseph., *et al.* [11] indicated in there research of analysis of variance showed that both of the phonological parameters studies were significantly affected by variation, there were significant variations observed between the common bean varieties for all the yield and yield components except number of seed per pod, and the effect of varieties on grain yield was significant and the best performing varieties of common bean namely Dinkinesh and SNNPR-1-20. Lobato., *et al.* [12] indicated in there studied the genetic analyses were performed to estimate the means and variances for each of the generations. Estimates of genetic variance components enabled the calculation of heritability estimates in a broad, the results show that additive genetic effects were involved in the majority of the total genetic variances, indicating a significant contribution for all traits evaluated. The values for heritability in a broad (H2) was high, indicating reliability in the transmission of traits to offspring. Thus, the additive effects played a greater role in the total genetic variance in relation to the genetic control of drought tolerance, Selection contributed to gains of 2.93 for grain production, 3.29 for the average weight of 100 seeds, 2.37 for the number of pods per plant and 0.73 for the number of seeds per pod. After selection in the F2 generation, the predicted genetic gains in these same traits for the F3 population were 9.79, 24.58, 9.39 and 5.34, respectively. Heritability estimates and selection gain of intermediate and high magnitude were obtained for cycle, insertion of the first pod, grain yield [13]. A successful breeding programme in common bean would need information on the nature and degree of genetic divergence in the available stock for choosing the right parents for further improvement and the selection of agronomically suitable diverse parents for hybridization is important for getting desired recombinants segregating generations [14]. Bacheri., *et al.* [15] there results showed that differences between genotypes in all parameters, except for internode diameter, number of seeds per pod, seed diameter, internode length and 100 seed weight were significant also The estimates of GCV were high for weight of pods per plant (54.13), grain yield per plant (50.33). Low broad sense heritability assign that if compared with number of nodes on the main stem, biological yield, weight of pods per plant. Bacheri., *et al.* [15] there results showed that differences between genotypes in all parameters, except for internode diameter, number of seeds per pod, seed diameter, internode length and 100 seed weight were significant also The estimates of GCV were high for weight of pods per plant (54.13), grain yield per plant (50.33). Low broad sense heritability's assign that if compared with number of nodes on the main stem, biological yield, weight of pods per plant.

Objective of the Study

Thus, this study was initiated with the objectives of estimating the genetic variability of Iraqi common bean commercial cultivars and promising genotypes as well as to evaluate their performance for economically important quantitative and qualitative traits.

Materials and Methods

This experiment was carried out during spring season 2019 at the field vegetable experiments of department of horticulture and landscape design, college of agriculture and forestry, Mosul University to study the Correlation and Path coefficient analysis in Common Bean (*Phaseolus vulgaris* L.). The experiments materials consisted of 12 genotypes of common bean (Table 1). The seeds of the genotypes were sowing at 15/3/2019 in rows of 1.5 m length and 30 cm with an approximate plant to plant distance of 15 cm (20 plant per plot). Using randomized complete block design (R.C.B.D.) with three replicate for each genotype possesses 12 plots. All other necessary cultural such as fertilizing, weeding and cultivation were applied to all plots uniformly.

S. No.	Genotypes	Source
1	Iranian	From local marker (Sulaimania), Kurdistan Iraq, 2018
2	Iranian (2)	From local marker (Sulaimania), Kurdistan Iraq, 2018
3	Brinco	From local marker Mosul, Iraq, (Turkish), 2018
4	Strick	From local marker Mosul, Iraq, (Netherlands), 2018
5	line 3 K.M. Ph -22	Esho 2019, College of Agri. & Fors. Mosul University
6	Bar-245	From local marker Erbil Kurdistan Iraq. (French), 2018
7	American	From local marker (Erbil), Kurdistan Iraq, 2018
8	Brs- Pitango	From local marker (Erbil), Kurdistan Iraq (Iranian)
9	Line 5 K.M. Ph. 28	Esho 2019, College of Agri. & Fors. Mosul University
10	Line 6 K.M Ph. 33	Esho 2019, College of Agri. & Fors. Mosul University
11	Line 8 K.M Ph. 31	Esho 2019, College of Agri. & Fors. Mosul University
12	Line 4 K.M Ph. 35	Esho 2019, College of Agri. & Fors. Mosul University

Table 1: List of Phaseolus genotypes used in the experiment.

The data were recorded for the traits. Vais: plant height (cm), number of branches per plant, number of pods per plant, length and diameter of pod (cm) number of seeds per pod, length and diameter of seed (cm), 1000 seeds weight (gm), seeds weight per plats (gm), seeds yield per plant (gm) and total seeds yield per hectares.(ton). All the agronomic data were recorded and being subjected to analysis using the SAS statistical software [16]. Estimated of GCV, PCV according

GCV% = ($\sqrt{O^2}$ g/$\hat{Y}$) x 100, PCV% = = ($\sqrt{O^2}$ P/$\hat{Y}$) x 100

$\hat{Y}$ = The average for the trait.

The Heritability was estimated according to: H^2b.s.= (O^2 g/O^2 P) x 100

Results and Discussion

Table 2 indicated that plant height of common bean was significantly ($P < 0.05$) affected by varieties, the highest plant height of 119.00 cm was recorded for the genotype Iranian and the least plant height of (70.933) was noted for the American genotype. The number of branches per plant advantages of 6.40 for the Iranian genotype which was different significantly for all genotypes, the lowest value for this character is for the Iranian2 genotype which was 4.57 branches per plant. The genotype Strick was superior in the number of pods per plant and for pod weight than all genotypes under this studied which gave 22.03 pods per plant and 1.25g for pod weight while the genotype American gave the least mean value 16.53 pods per plant and Bar -245 genotype for pod weight 0.99g. Bar-245 genotype was gave the height value for number of seeds per pod 7.10 which was significantly different among all genotype, the least value in this trait is for Strick genotype 4.17. The line 8K.MPh.31 gave the heights value for seed diameter (0.88 cm), 1000 seeds weight (344.67g) which was different significantly with all genotypes. In the other hands, the genotype Line 8 K.MPh.31 and Line 4 K.MPh. 35 gave a significant different effects for the trait total dry seeds 3.22 and 3.20 ton per hectare respectively than all genotypes. The same results was obtained from Beebe [17], Iqbal., *et al.* [18], Gurmu [19] and Yoseph., *et al* [11].

The genotypes	Plant height (cm)	No. of branches/ plant	No. of pods/ plant	Pod weight (g)	No. of seeds/ pod	Seed length (cm)	Seed diameter (cm)	1000 seeds weight (g)	Seeds yield/plot (g)	Seeds yield/ plant (g)	Total dry seeds (ton/ hectare)
Iranian	119.00a	6.40a	19.23cd	1.10de	4.23g	1.28bc	0.81b	240.33c	351.33e	19.99b	1.50d
Iranian (2)	115.27ab	4.57f	21.93ab	1.12d	4.63e-g	1.35ab	0.79b	302.67b	488.00cd	20.73b	1.65bc
Brinco	85.30de	5.03c-f	19.40b-d	1.05gh	6.13b	1.39a	0.69c	192.00d	393.33e	19.36b	1.83c
Strick	117.33a	5.57b-d	22.03a	1.25a	4.17g	1.32a-c	0.79b	334.67ab	389.33e	19.70b	2.84a
line 3 K.M. Ph -22	98.40c	4.93d-f	18.07de	1.06f-h	4.70e-g	1.29bc	0.79b	302.67b	550.00ab	16.01c	2.76ab
Bar-245	78.60e	5.67bc	23.13a	0.99i	7.10a	1.30bc	0.56d	203.00cd	370.00e	11.01d	1.54b
American	70.93f	6.00ab	16.53e	1.08eg	5.77bc	1.30bc	0.52d	220.33cd	526.67bc	12.57d	2.76 ab
Brs- Pitango	95.27c	4.67ef	15.97ef	1.20b	5.53b-d	1.32a-c	0.73c	225.33cd	379.33e	12.63d	2.61ab
Line 5 K.M. Ph. 28	108.57a	5.17c-f	21.27a-c	1.23ab	5.17c-e	1.32a-c	0.81b	313.67b	473.33d	19.30b	2.95a
Line 6 K,M Ph. 33	96.33c	5.67bc	20.33b-d	1.09d-f	4.40fg	1.27c	0.82b	341.00ab	390.33e	24.67a	2.75a
Line 8 K.MPh. 31	86.33d	4.87ef	18.27ed	1.04h	4.97d-f	1.39a	0.88a	355.67a	400.00e	18.74b	3.22a
Line 4 K.M Ph. 35	99.90c	5.27c-e	13.97f	1.15c	5.40cd	1.32a-c	0.79b	323.00ab	590.00a	15.75c	3.20a

Table 2: The mean value of the traits of Phaseolus genotypes during growing spring season 2019*.

Means with the same letters no significant differences according to Duncan's multiple range test at probability 0.05.

Table 3 showed the mean value and the range, coefficient variation and R-square, indicated that the range for the trait plant height was between 70.933 - 119.00 cm, while the range for the number of the branches per plant was between 4.567 - 6.400, the value of the trait number of pods per plant was between 13.967 - 23.133. Also in same table showed the range for pod weight was 0.997 - 1.250g, while the mean value for character number of seeds per pod was 4.17 - 7.100. This resulted gave the aim to the breeding for selected the best genotype for the superior of the trait value, which was needed for the farmer and for who produce the economic yield for marker shop and for human use. The same results were recorded by some researchers that there was different variation between the traits for growth and seed component for the *Phaseolus* genotypes [7-10,12]. The genetic analysis were performed to estimate the means and variances for each the genotype of common bean. Also table 3 indicated that the GCV and PCV were higher for total dry seeds yield per unit area ton per hectare which was (6.677, 10. 318) and the seeds yield trait per plot which was (7.455 and 7.922), for the 1000 seed weight the GCV and PCV were (6.871, 7.338), flowed for the seeds yield per plant (5.922, 6.299), for the number of seeds per pod it was 5.377, 5.905. the heritability broad sense (H^2b.s.) was more than 40% for most trait excepted the traits of seed length and total dry seeds per unit area which was 38.483% and 41.885%) respectively. The higher values of heritability was for seed diameter 93.938 flowed by plant height 93.663, pod weight 93.179 and seeds yield per plot 88.568. The R. square was high for most traits which was more than 0.900 for plant height, pod weight, seed diameter, 1000 seeds weight, seeds yield per plant, pod per unit of area. While it was 0.779 for number of branches per plant, 0.855 for number of pods per plant and

Traits	Range	Mean ± S.E.	GCV	PCV	H^2b.s	R-Square
Plant height(cm)	70.933 - 119.000	97.603 ± 3.987	5.235	5.409	93.663	0.956
No. of branches per plant	4.567 - 6.400	5.317 ± 0.363	3.221	3.945	66.656	0.779
No. of pods/plant	13.967 - 23.133	19.178 ± 1.410	4.580	5.194	77.752	0.855
Pod weight (g)	0.997 - 1.250	1.113 ± 0.021	2.363	2.448	93.179	0.955
No. of seeds/pod	4.167 - 7.100	5.183 ± 0.379	5.377	5.905	82.928	0.887
Seed length (cm)	1.270 - 1.393	1.321 ± 0.040	0.798	1.287	38.483	0.599
Seed diameter (cm)	0.523 - 0.883	0.750 ± 0.027	4.748	4.899	93.938	0.919
1000 seeds weight (g)	192.00 - 355.670	279.528 ± 21.581	6.871	7.338	87.700	0.929
Seeds yield/plant (g)	11.007 - 24.667	17.539 ± 1.409	5.922	6.299	88.379	0.925
Seeds yield/plot (gm)	351.330 - 590.00	441.806 ± 28.463	7.455	7.922	88.568	0.944
Total dry seeds (ton /hectare)	1.50 - 3.22	2.654 ± 0.165	6.677	10.318	41.885	0.953

Table 3: The range value, mean, genotypic, phenotypic coefficient variation, heritability and R-square for traits in Phaseolus genotypes during growing spring season 2019.

0.566 for seed length. Many researched recorded that the heritability was high in some traits vegetative growth and the components of the seeds yield for common bean [14,15,20].

Conclusion

From the result the present study revealed significant variation among genotypes for traits considered, The high yielding genotypes could be directly used as seed sources for production of common bean and genotype with high heritability can possibility used in common bean improvement program in breeding. Also due to higher values of heritability and genetic advance for pod yield seed weight and seed yield, direct selection could be useful for these reproductive attributes.

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