



Research Article

STUDY OF PHENOTYPIC VARIATION FOR YIELD AND YIELD CONTRIBUTING TRAITS IN COMMON BEAN (*Phaseolus vulgaris* L) FROM NORTH-WESTERN HIMALAYAS

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Abstract- Ninety six genotypes (42 exotic and 54 indigenous) of Common bean (*Phaseolus vulgaris* L.) were investigated at two locations during Rabi 2016 (SKUAST-Jammu) and Kharif 2017 (SKUAST-Bhaderwah) to evaluate yield contributing traits for phenotypic variation and identify the selection indices important for common bean improvement. Seeds per pod have least variation among coefficients at phenotypic and genotypic level and yield per plant have highest PCV and GCV across both locations. High estimate of heritability (broad sense) was observed for 100 seed weight and signifying high potential for improvement of common bean through selection which is governed by additive gene action. Correlation coefficients at phenotypic level of both locations envisaged that yield per plant was having significant and positive correlation with pods per plant, seeds per pod and 100 seed weight. These are the important characters contributing towards crop yield and can be strategically used to improve the common bean yield.

Key words- Common bean, PCV, GCV, Heritability

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Introduction

Common bean (*Phaseolus vulgaris* L.) is one of the most important grain legume due to its high nutritional and commercial value [1-3]. It is also known as Rajmash, French bean, haricot bean, kidney bean, snap bean and navy bean. It is an annual, self-pollinated diploid ($2n = 2x = 22$) with cleistogamous flowers and a genome size of 473Mb. In sub-Saharan Africa, more than 200 million people depend on this crop as a primary staple food. Beans are also called “poor man’s meat” as it contains high protein, starch, dietary fibre and are excellent source of micronutrients like iron, zinc, potassium, selenium, molybdenum, thiamine, vitamin B6 and folate [4,5]. Beans are consumed either as dry bean (pulse) or snap bean (fresh vegetable) [6]. Globally, about 18 million metric tons of common beans are produced annually. The world leader in production of dry bean is India, followed by Brazil and Myanmar. Annually India produces around 4.8 million metric tonnes followed by Brazil with 3.2 million metric tonnes of dry bean [7]. In India, it is grown in hilly areas of Himachal Pradesh, Jammu and Kashmir, Uttarakhand, North-Eastern states during winter season and in parts of Uttar Pradesh, Maharashtra, Karnataka and Andhra Pradesh during autumn season. In Jammu & Kashmir, Common bean crop is cultivated over an area of about 2000 hectares with production of about 1600 tones and yield of about 0.8 t/ha. Present study is conducted to study 96 Common bean genotypes from Jammu & Kashmir including 42 exotic genotypes for yield contributing traits and select candidate germplasm lines for high yield which can be used for future breeding programs to improve yield of local genotypes of Jammu and Kashmir.

Materials and Methods

The present study was carried out at two locations viz., SKUAST-Jammu and Bhaderwah Jammu.

First trial was conducted at research farm of Division of Plant Breeding and Genetics SKUAST-Jammu during Rabi 2016 and second trial was conducted at Regional Horticultural Research Sub-station, Bhaderwah of SKUAST-Jammu in Kharif 2017. The trial at SKUAST-Jammu and Bhaderwah was conducted for trait phenotyping of the four yield contributing traits viz., pods per plant, seeds per pod, yield per plant and test weight. The experiment involved 96 common bean genotypes and each genotype was grown in two rows of 3 m length spaced 60cm apart. Standard agronomic practices were followed for normal crop growth at both locations. Five plants in each plot were selected for recording the data. The data of mean plot was subjected to analysis of variance following the standard statistical method [8]. The PCV and GCV were obtained by the method suggested by Burton and Devane, [9]. Heritability in broad sense and GA were estimated as per the formulae described by Johnson, *et al* [10]. The coefficients of correlation were calculated as described by Singh and Choudhary, [11].

Results and Discussion

Analysis of Variance (ANOVA)

The analysis of variance of the field trial experiment of 96 genotypes at two locations i.e., SKUAST-Jammu and Bhaderwah during Rabi 2016 and Kharif 2017 was conducted for quantitative traits namely pods per plant, seeds per pod, 100 seed weight and yield per plant and the results of mean sum of squares were calculated separately for both locations. For SKUAST-Jammu the replication showed non-significant difference among all four morphological traits, but among the genotypes all four traits pods per plant, seeds per pod, 100 seed weight and yield per plant exhibited significant differences at 1% level of significance in genotypes.

Table-1 Analysis of variance for morphological traits of 96 common bean lines at SKUAST-Jammu and Bhaderwah location

Source of variation	d.f.	Mean squares							
		Pods per plant		Seeds per pod		100 seed weight (g)		Yield per plant (g)	
		SKUAST-Jammu	Bhaderwah	SKUAST-Jammu	Bhaderwah	SKUAST-Jammu	Bhaderwah	SKUAST-Jammu	Bhaderwah
Replications	2	0.46	3.32	0.44	0.19	0.29	0.74	1.11	7.02
Genotypes	95	36.93**	45.07**	2.09**	2.51**	448.3**	483.57**	253.00**	276.12**
Error	190	2.05	2.02	0.18	0.25	0.18	0.36	9.88	8.90
Total	287	15.99	148.63	-0.08	-0.52	129.00	356.84	279.83	1937.36

* & ** significant at 5% and 1% level, respectively

Table-2 Genetic parameters of morphological traits of 96 common bean lines at SKUAST-Jammu and Bhaderwah location

Source of variation	Pods per plant		Seeds per pod		100 seed weight (g)		Yield per plant (g)	
	SKUAST-Jammu	Bhaderwah	SKUAST-Jammu	Bhaderwah	SKUAST-Jammu	Bhaderwah	SKUAST-Jammu	Bhaderwah
Var. phenotypic	13.68	16.37	0.82	1.00	149.56	161.43	90.92	97.97
Var. genotypic	11.63	14.35	0.64	0.75	149.38	161.07	81.04	89.07
PCV (%)	39.10	41.47	17.45	20.16	38.80	39.00	62.28	63.28
GCV (%)	36.05	38.82	15.38	17.50	38.78	38.95	58.80	60.33
Heritability (h^2) in (%)	85.01	87.64	75.68	77.37	99.78	99.88	89.13	90.91

Table-3 Phenotypic correlation coefficient of morphological traits of 96 common bean lines at SKUAST-Jammu

Character	Pods per plant	Seeds per pod	100 seed weight (g)	Yield per plant (g)
Pods per plant	-	0.1618**	-0.1735**	0.5645**
Seeds per pod		-	0.0705	0.4917**
100 seed weight (g)			-	0.5359**
Yield per plant (g)				-

* & ** significant at 5% and 1% level, respectively

Table-4 Phenotypic correlation coefficient of morphological traits of 96 common bean lines at Bhaderwah

Character	Pods per plant	Seeds per pod	100 seed weight (g)	Yield per plant (g)
Pods per plant	-	0.3003**	-0.1884**	0.6435**
Seeds per pod		-	-0.0873	0.5081**
100 seed weight (g)			-	0.4439**
Yield per plant (g)				-

* & ** significant at 5% and 1% level, respectively

Bhaderwah replication showed non-significant difference among all four yield traits [Table-1]. Among genotypes all four traits pods per plant, seeds per pod, 100 seed weight and yield per plant showed significant differences at 1% level of significance.

Trait Mean and Range

The mean performance and range of four morphological traits at SKUAST-Jammu and Bhaderwah has been estimated. The mean number of pods per plant at SKUAST-Jammu was 9.46 and at Bhaderwah location it was 9.76. The range of pods per plant at Bhaderwah was more than the range of pods per plant recorded at SKUAST-Jammu location [Fig-1]. The number of seeds per pod at SKUAST-Jammu location recorded mean of 5.19 and Bhaderwah location recorded mean of 4.95. The range of seeds per pod at Bhaderwah was higher than SKUAST-Jammu [Fig-2]. The test weight or 100 seed weight at SKUAST-Jammu location recorded mean of 31.39 gm and Bhaderwah location recorded mean of 32.58 gm. The range of 100 seed weight was higher at SKUAST-Jammu as compared to Bhaderwah [Fig-3]. The yield per plant at SKUAST-Jammu location recorded mean of 15.31 gm and Bhaderwah location recorded mean of 15.64 gm. The range of yield per plant was higher at SKUAST-Jammu as compared to Bhaderwah [Fig-4].

Genetic Parameters

The genetic parameters of 96 genotypes analysed across both locations *i.e.* SKUAST-Jammu and Bhaderwah include phenotypic variance, genotypic variance, phenotypic coefficient of variance, genotypic coefficient of variance and heritability. The results of these genetic parameters have been briefly presented in [Table-2].

Phenotypic variance

Phenotypic variance of all four morphological traits pods per plant, seeds per plant, 100 seed weight and yield per plant is high at Bhaderwah location as

compared to SKUAST-Jammu location.

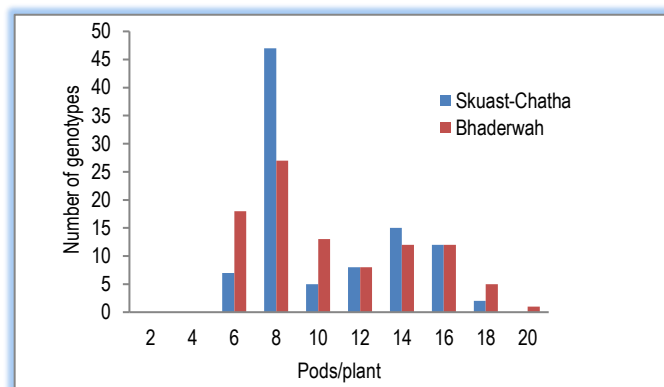


Fig-1 Distribution of pods per plant in 96 common bean lines at both locations

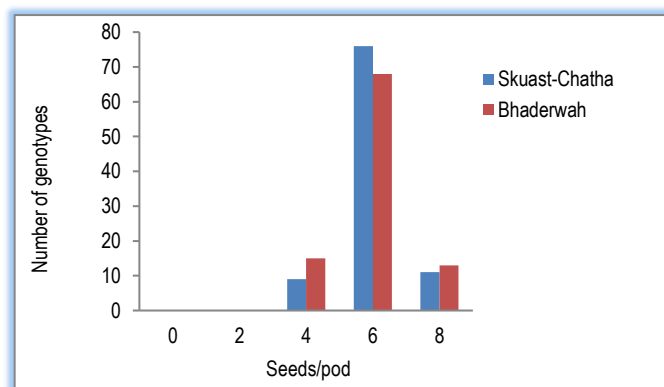


Fig-2 Distribution of seeds per pod in 96 common bean lines at both locations

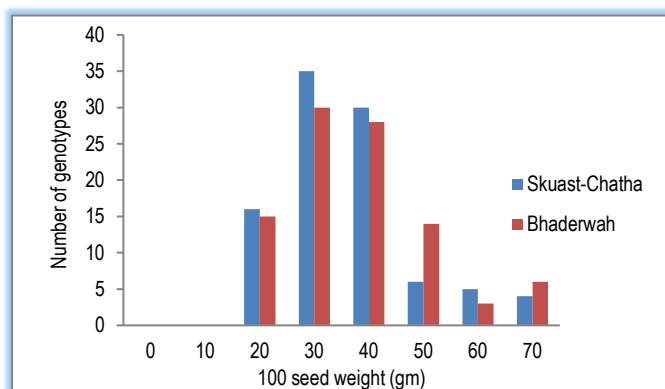


Fig-3 Distribution of 100 seed weight in 96 common bean lines at both locations

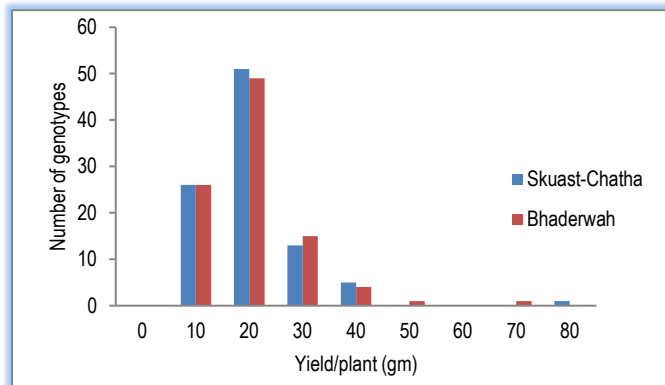


Fig-4 Distribution of yield per plant in 96 common bean lines at both locations

Genotypic variance

Genotypic variance of all four morphological traits pods per plant, seeds per plant, 100 seed weight and yield per plant is high at Bhaderwah location as compared to SKUAST-Jammu location.

Phenotypic coefficient of variation (PCV)

PCV content of all four morphological traits pods per plant, seeds per plant, 100 seed weight and yield per plant is high at Bhaderwah location as compared to SKUAST-Jammu location.

Genotypic coefficient of variation (GCV)

GCV content of all four morphological traits pods per plant, seeds per plant, 100 seed weight and yield per plant is high at Bhaderwah location as compared to SKUAST-Jammu location.

Heritability

The heritability in broad sense for all four morphological traits pods per plant, seeds per plant, 100 seed weight and yield per plant studied at both locations, SKUAST-Jammu and Bhaderwah were calculated separately. The heritability of all traits at Bhaderwah was higher than SKUAST-Jammu.

Correlation

In order to access the pattern of phenotypic association among four morphological traits at SKUAST-Jammu and Bhaderwah, the correlation coefficients were worked out and estimates are given in the [Table-3] & [Table-4]. Seeds per pod showed positive and significant correlation with pods per plant at 1% level of significance at both locations. Yield per plant showed positive and highly significant correlations with three other yield component traits viz. pods per plant, seeds per pod and 100 seed weight at 1% level of significance at both locations. Then 100 seed weight has negative and significant correlation with pods per plant at 1% significance level at both locations. The four morphological traits studied in the present study are quantitative in nature. The mean values of pods per plant,

100 seed weight and yield per plant of Bhaderwah location were higher than SKUAST-J location owing to favourable weather conditions for growth and development of common bean at temperate zone as compared to sub-tropical zone. The only trait seeds per pod have high mean value at Chatha than Bhaderwah location conferring that this trait is not variable due to environmental effect. Individual analysis of variance was carried out for four traits across both environments. Significant differences among genotypes were present for all the quantitative traits that agree with previous studies by [12,13]. No significant environmental effects were detected for two locations. The result variations of quantitative traits of this work assess about the need to evaluate the new or improved snap bean varieties in different locations and years before making reliable recommendations to growers. The study of variance component estimates show that environmental factors *i.e.*, different locations influenced most of the evaluated traits of common bean accessions of present study. The average and range for the bean genotypes indicate considerable genotypic variation for yield components including number of seeds per plant, number of pods per plant and yield per plant. High genotype variation for yield components as compared to phenotypic variation was also observed by [14-16] in earlier studies of common bean. The extent of genetic variation can be studied by the estimation of GCV in relation to PCV. The small variation between the two components indicate that observed variation and expression of traits is mainly due to genetic factors but larger difference between the two components show role of environment [3]. In our study small variation was observed for GCV in relation to PCV for all four traits conferring that variation is due to genetic factors only. The correlation coefficient is an important genetic parameter because it measures the degree of association *i.e.* genetic and non-genetic between two or more traits [17]. The phenotypic and genotypic correlations of the present study show that yield per plant had significant and positive correlation with pods per plant, seeds per pod and 100 seed weight. Also seeds per pod have significant positive correlation with pods per plant and 100 seed weight had significant negative correlation with pods per plant. Various other studies on common bean have concluded that number of pods per plant, number of seeds per pod, seed yield per plant and 100 seed weight had a positive correlation with seed yield [18-23]. The yield per plant is a quantitative trait in common bean and is mainly controlled by three yield components *i.e.* number of pods per plant, number of seeds per pod, and seed weight [24]. All three yield components are also quantitative in nature and are based on the interaction of physiological and morphological features of the plant [25]. The variability and interrelationship of characters between productivity and its components in common bean have been reported earlier also [26-28]. So, these traits are useful and can be used for high yield in future common bean breeding programs.

Conclusion

Morphological data of four yield components *i.e.*, number of pods per plant, number of seeds per pod, 100 seed weight and yield per plant was recorded on 96 lines at SKUAST-Jammu and Bhaderwah. Correlation coefficient and genetic parameters for these traits were analysed to study variation across both locations. Morphological data of both locations confers that common bean grows well in temperate region (Bhaderwah in present study) providing optimum temperature and cool conditions. All traits have overall higher values for all parameters at Bhaderwah location as compared to SKUAST-Jammu concluding that common bean can be grown in sub-tropical regions for seed multiplication and it shall be grown in temperate regions for maximum yield and good palatability of this legume crop.

Application of research: Correlation coefficient and genetic parameters are useful for study the genes interaction between different lines of common bean.

Research Category: Plant Breeding, Biometrics

Abbreviations: PCV = phenotypic coefficients of variation, GCV = genotypic coefficients of variation, GA = genetic advance,

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References

- [1] Rodino A.P., Santalla M., Gonzalez A.M., de Ron A.M. and Singh S.P. (2006) *Crop Sci.*, 46, 2540-2546.
- [2] Singh N., Kaur S., Rana J.C., Nakaura Y. and Inouchi N. (2012) *Food Res. Int.*, 47, 174-181.
- [3] Rana J.C., Sharma T.R., Tyagi R.K., Chahota R.K., Gautam N.K., Singh M., Sharma P.N. and Ojha S.N. (2015) *Euphytica*, 205, 441-457.
- [4] Beebe S., Gonzalez A.V. and Rengifo J. (2000) *Food Nutr. Bull.*, 21, 387-91.
- [5] Broughton W.J., Hernandez G., Blair M.W. and Beebe S. (2003) *Plant Soil*, 252, 55-128.
- [6] Santalla M., Fueyo M.A., Rodino A.P., Montero I. and de Ron A.M. (1999) *Biotechnol. Agron. Soc.*, 3, 225-229.
- [7] FAO (2017) *Food and agricultural commodities production*.
- [8] Gomez K.A. and Gomez A.A. (1983) *Statistical Procedure for Agricultural Research*, 2nd edition, pp 357-427. John Wiley Sons, New York.
- [9] Burton C.W. and De Vane E.H. (1953) *Agron. J.*, 45, 1476-81.
- [10] Johnson H.W., Robinson H.F. and Comstock R.E. (1955) *Agron. J.*, 47, 314-18.
- [11] Singh R.K. and Choudhary B.D. (1977) *Biometrical Methods in Quantitative Genetic Analysis*, pp 39-68. Kalyani Publishers, New Delhi
- [12] Joshi B.D. and Mehra K.L. (1984) *Progressive Horticulture*, 16, 78-84.
- [13] Gil J. and De Ron A.M. (1992) *Plant Breed.*, 109, 313-319.
- [14] Casquero P.A., Lema M., Santalla M. and De Ron A.M. (2006) *Genet. Resour. Crop Evol.*, 53, 1021-1032.
- [15] Bralewski T.W., Fiebig M. and Kotlinska T. (2007) *Zeszyty Problemowe Postepow Nauk Rolniczych*, 517, 179-186.
- [16] Stoilova T., Pereira G. and Tavares-De-Sousa M. (2013) *J. Central European Agri.*, 14, 854-864.
- [17] Dewey D.R. and Lu K.H. (1959) *Agron. J.*, 51, 515-518.
- [18] Blair M.W., Giraldo M.C., Buendia H.F., Tovar E., Duque M.C. and Beebe S.E. (2006) *Theor. Appl. Genet.*, 113, 100-109.
- [19] Bhushan K.B., Jadli S., Verma O. and Goswami A.K. (2009) *Int. J. Agri. Sci.*, 4, 667-669.
- [20] Apostolova E., Dimova D. and Svetleva E. (2009) *Acta Hort.*, 830, 191-197.
- [21] Karasu A. and Oz M. (2011) *Bulgarian J. Agri. Sci.*, 16, 203-211.
- [22] Ahmed S. and Kamaluddin (2013) *African J. Agri. Res.*, 8, 2027-2032.
- [23] Sofi P.A., Rana J.C. and Bhat N.A. (2014) *J. Food Legumes*, 27, 197-201.
- [24] Adams M.W. (1967) *Crop Sci.*, 7, 505-510.
- [25] Wallace D.H., Baudoin J.P., Beaver J.S., Coyne D.P., Halseth D.E., Masaya P.N., Munger H.M., Myers J.R., Silbernagel M., Yourstone K.S. and Zobel R.W. (1993) *Theor. Appl. Genet.*, 86, 27-40.
- [26] Sadeghi A., Cheghamirza K. and Dorri H.R. (2011) *Biharean Biologist*, 5, 102-108.
- [27] Golparvar A.R. (2012) *Genetica*, 44, 279-284.
- [28] Cokkizgin A., Colkesen M., Idikut L., Ozsisli B. and Girgel U. (2013) *Greener J. Agri. Sci.*, 3, 085-089.