



Morphological variability and phylogenetic analysis in common bean (*Phaseolus vulgaris* L.)

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ABSTRACT

Thirteen common bean (*Phaseolus vulgaris*) accessions collected from different ecological regions of Jammu and Kashmir were evaluated at four diverse locations during *kharif* 2009. Significant variation was observed for most of the morphological traits. Estimates of heritability (h^2) were high (>60 %) for all the traits except pod length. The expected genetic gain (per cent of mean) was high (>30 %) for days to maturity, number of pods plant⁻¹, number of seeds pod⁻¹, 100-seed weight and seed yield plant⁻¹ while it was moderate (10.0-30.0%) for days to 50 per cent flowering, number of branches plant⁻¹, pod length and protein content. Seed yield plant⁻¹ was observed to have a highly positive and significant correlation both at phenotypic and genotypic levels with number of pods plant⁻¹, pod length, number of seeds pod⁻¹ and 100-seed weight. But negative and significant correlations with days to 50 per cent flowering and days to maturity were estimated from pooled analysis. Classification of accessions led to the formation of two clusters wherein the maximum number 7 accessions were grouped in cluster I and the remaining six were grouped in cluster II. Analysis of traits contributing maximum to the divergence revealed that traits *viz.*, 100-seed weight (37.10%), protein content (15.26%), number of seeds pod⁻¹ (11.28%) and days to maturity (10.14%) to contribute to the divergence in the present experimental material.

Key words: Characterization, Common bean, Correlation, Genetic Diversity, Variability.

INTRODUCTION

Legumes constitute the third largest family of higher plants, with 20,000 species and second in agricultural importance based on area and total production (Graham and Vance, 2003). Among pulses which are the second most important food crops after cereals, common bean (*Phaseolus vulgaris* L.) is the most widely distributed legume species of the genus *Phaseolus*, comprised of some 70 species (Freyt and Debouck, 2002) that has contributed to human welfare with five cultigens domesticated in pre-Columbian times *viz.*, the common bean (*P. vulgaris*), the year bean (*P. dumosus* Macfad.), the runner bean (*P. coccineus* L.), the temporary bean (*P. acutifolius* A. Gray), and the lima bean (*P. lunatus* L.). Among the five domesticated species, the common bean (*P. vulgaris*) accounts for more than 90 per cent of the cultivated crop worldwide and is by far the most widely consumed grain legume in the world (Singh, 2001). In India common bean is one of the most important summer season pulse crop and is regarded as grain of hope as it is an important component of subsistence agriculture. It feeds about 300 million people in tropics and 100 million people in Africa alone. However most of the genetic variability of this species in the world is maintained and conserved *ex-situ* outside the centers of origin in gene banks. Hence, for a practical use and exploitation of the germplasm conserved,

its characterization is essential (Faleiro and Junqueira 2010). Several characters can be used to characterize genetic resources particularly morphological, agronomic (Singh 2001), biochemical and molecular characters (Beebe *et al.*, 2000). In the preliminary characterization of the genotypes, morphological and agronomic traits of the plants are preferred, for being cheaper and easier to assess. Genetic diversity is an important phenomenon on which future progress in crop improvement relies. In crops like common bean where breeding for a particular set of growing conditions holds promise, it is highly imperative to conserve and use the local population since in them the relationship among yield components are balanced and in harmony with the effect of the specific climatic and edaphic factors (Vasic *et al.*, 2008). Therefore the present investigation was carried out with an objective to characterize the variability, inter-relationship and genetic diversity using morphological and agronomic traits.

MATERIALS AND METHODS

The present investigation was carried out during *kharif* 2009. The experimental material comprised 13 germplasm accessions collected from diverse ecological regions of Kashmir and temperate areas of Jammu division. The material was evaluated at four diverse locations in a randomized complete block design with three replications

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at each location. The random locations were i). Experimental farm of division of plant breeding and genetics, main campus Shalimar SKUAST-Kashmir, ii). Pulse research substation Naseembagh Habak, Srinagar, iii). Regional Research Station and Faculty of Agriculture, Wadura Sopore, Baramullah, iv). Krishi Vigyan Kandra, Pombay, Kulgam. The experimental plot consisted of three rows of 3 m length. The material was sown with 30 cm spacing between the rows and plant to plant spacing of 10 cm. The experimental fields were well prepared and standard recommended package of practices were followed to raise a good crop. Data were collected from five randomly selected competitive plants from each replication at each location on various morphological, maturity, yield and yield contributing traits as per the descriptors developed by NBPGR New Delhi, and (IBPGR 1982). The statistical analysis was done using WINDOSTAT version 8.5 Indostat.exe biometrics software.

RESULTS AND DISCUSSION

Significant variation was observed for most of the morphological traits measured (Table 1). All the accessions except (Canadian Red) collected from pulse research sub-

station and two traditional cultivars from Pulwama (PBG-29, PBG-30) had determinate (type-I) growth habit. On the other hand accessions collected from Doda, Kishtward and Poonch had indeterminate (type II and IV) growth habit. Kidney and rectangular seed shape were observed in 4 accessions each, while three had elongated and two oval shaped seeds. Testa colour of five accessions was dark red, 3 had white, light red and yellow was present in two accessions each and the remaining one (SKUA-R-34) had chocolate coloured testa. Most of the genotypes are plain while two genotypes (SKUA-R-19, PBG-30) had strips on testa and the remaining two (SKUA-R-28, SKUA-R-34) were variegated Table 1. Analysis of variance revealed significant differences among the genotypes for each character indicating existence of variability in the material under study Table 2. The coefficient of variation estimated from pooled analysis indicating that there were significant differences among the accessions for the characters under study. The phenotypic variance σ_p^2 was higher than the corresponding genotypic variance σ_g^2 for all the characters suggesting the presence of environmental influence to some extent in the

Table 1: Place of collection and description of common bean accessions evaluated for morphological traits.

Accession	Place of collection/ status*	Growth habit**	Seed shape	Tests colour	Testa color marking
SKUA-R-1	PRSH/BL	I	Elongated	Light Red	Plain
SKUA-R-11	PRSH/BL	I	Oval	Yellow	Plain
SKUA-R-19	PRSH/BL	I	Kidney	Yellow	Stripes
SKUA-R-21	PRSH/BL	I	Rectangular	Dark Red	Plain
SKUA-R-28	PRSH/BL	I	Oval	White	Variegated
SKUA-R-34	PRSH/BL	I	Elongated	Chocolate	Variegated
PBG-1	Doda/TC	II	Rectangular	Dark Red	Plain
PBG-3	Doda/TC	II	Kidney	Dark Red	Plain
PBG-9	Kishtward/TC	IV	Kidney	light Red	Plain
PBG-16	Poonch/TC	IV	Rectangular	Dark Red	Plain
PBG-29	Pulwama/TC	I	Elongated	Creamish	Plain
PBG-30	Pulwama/TC	I	Kidney	White	Stripes
C Red	PRSH/BL	II	Elongated	Dark Red	Plain

Abbreviations, *PRSH = Plus Research Substation Srinagar, BL = Breeding Line, TC = Traditional Cultivar

**Growth habit classified using the CIAT 1 to 4 scale were I = determinate, II = erect indeterminate with a short to medium guide and IV = indeterminate stems and branches prostrate with little or no climbing ability.

Table 2: Pooled estimates of variability parameters for different maturity, quality, yield and yield component traits in common bean

Traits	Mean	Range	Mean sum of squares	Variance	
				σ_g^2	σ_p^2
Days to 50% flowering	52.59	39.80-63.34	167.51**	55.21	57.06
Days to maturity	110.19	71.81-143.30	1276.23**	432.62	428.398
No. of branches plant ⁻¹	9.62	7.23-10.43	2.76*	0.83	1.09
No. of pods plant ⁻¹	10.13	5.36-13.73	19.43**	6.36	6.70
Pod length (cm)	10.19	6.84-13.57	12.47**	3.35	5.75
No. of seeds pod ⁻¹	5.12	3.53-6.34	2.34*	0.76	0.80
100 seed weight (g)	32.28	21.89-54.93	237.2**7	79.04	79.68
Seed yield plant ⁻¹ (g)	17.61	6.11-32.37	218.74**	72.25	74.24
Protein content (%)	21.45	18.89-24.27	8.67**	2.87	2.91

**,*Significant at p=0.01 and p=0.05 levels respectively.

expression of these characters. Rafi and Nath 2004 reported similar results in common bean. Medium to high variance was observed for days to maturity, followed by 100 seed weight, seed yield plant⁻¹ and days to 50 per cent flowering and 100-seed weight, while small variance was observed for the traits like number of seeds pod⁻¹ and number of branches plant⁻¹. Estimates from pooled analysis indicate that medium to high heritability was observed for all the traits (Table 3) which reveals that in the present set of material, the scope of improvement for these traits by simple selection would be effective. High heritability coupled with high genetic advance expected in the next generation for 100-seed weight, seed yield plant⁻¹, protein content, number of seeds pod⁻¹ and days to maturity suggesting that these characters are governed by additive genetic effects to a greater extent and improvement of these traits would be effective through selection. Singh (1989) observed high heritability for days to maturity and 100-seed weight, while Scully *et al.*, (1991) reported high values for days to maturity, seed yield, biological yield and harvest index. Similar results were also reported by Rafi and Nath 2004.

Correlation coefficients between all possible combinations at both phenotypic and genotypic levels were estimated (Table 4). Results indicated that most of the traits were highly significant correlated with seed yield plant⁻¹, except number of branches plant⁻¹ and protein content. The effects of number of pods plant⁻¹ (r=0.68**), pod length (r=0.51**), and 100-seed weight (r=0.37**) were positive while the effects of days to 50% flowering (r= -0.46**) and days to maturity (r= -0.47**) on seed yield plant⁻¹ were negative. The significant positive correlation of number of seeds plant⁻¹, number of pods plant⁻¹ and pod length with grain yield has also been reported by Salehi *et al.*, (2008). Number of pods plant⁻¹ revealed the highest correlation value (0.68) followed by pod length (0.51) with seed yield plant⁻¹ in comparison with other traits. These results indicated the importance of these traits as a criterion for common bean improvement and were in agreement with the results of

Table 3: Heritability in broad sense (h²b), genetic advance (GA), genetic advance as per cent of mean and coefficient of variation for various maturity, quality, yield and yield component traits in common bean (Pooled over environments)

Traits	h ² b	G.A.	G.A. as % of mean	CV (%)
Days to 50% flowering	0.968	28.63	15.05	2.58
Days to maturity	0.987	38.23	42.13	2.10
No. of branches plant ⁻¹	0.764	17.11	1.64	5.27
No. of pods plant ⁻¹	0.950	49.98	5.06	5.69
Pod length (cm)	0.583	28.25	2.88	15.19
No. of seeds pod ⁻¹	0.952	34.36	1.76	3.84
100 seed weight (g)	0.998	56.67	18.29	1.18
Seed yield plant ⁻¹ (g)	0.973	98.04	17.27	8.00
Protein content (%)	0.985	16.15	3.46	0.97

Table 4: Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients for maturity, yield, yield attributing and quality traits in common bean (*Phaseolus vulgaris* L.) (Pooled over environments)

Traits	Days to 50% flowering	Days to maturity	No. of branches plant ⁻¹	No. of pods plant ⁻¹	Pod length (cm)	Number of seeds pod ⁻¹	100 seed weight (g)	Seed yield plant ⁻¹ (g)	Protein content (%)
Days to 50% flowering	-	0.73**	0.30**	-0.38**	-0.31**	0.03	-0.39**	-0.46**	-0.03
Days to maturity	0.71**	-	0.029*	-0.39**	-0.34**	0.002	-0.38**	-0.47**	-0.002
No. of branches plant ⁻¹	0.29*	0.26*	-	0.31**	0.21	0.38**	-0.21	0.17	0.03
No. of pods plant ⁻¹	-0.34**	-0.37**	0.29*	-	0.48**	0.37**	0.04	0.68**	-0.25*
Pod length (cm)	-0.27*	-0.31**	0.20	0.46**	-	0.48**	0.07	0.51**	-0.12
No. of seeds pod ⁻¹	0.02	0.02	0.36**	0.35**	0.47**	-	-0.38**	0.36**	-0.14
100 seed weight (g)	-0.34**	-0.34**	-0.20	0.03	0.06	-0.36**	-	0.37**	0.02
Seed yield plant ⁻¹ (g)	-0.42**	-0.45**	0.15	0.64**	0.49**	0.34**	0.35**	-	-0.10
Protein content (%)	-0.03	-0.02	-0.03	-0.24*	-0.10	-0.12	0.02	-0.09	-

**,*Significant at p=0.01 and p=0.05 levels respectively.

Table 5: Grouping of Common bean accessions into different clusters on the basis of divergence (pooled over environments)

Cluster	Frequency	Accession name
I	7	PBG-1, PBG-3, SKUA-R-11, PBG-9, SKUAR-I, PBG-16 SKUAR-19
II	6	PBG-30, SKUAR-34, SKUAR-21, SKUAR-28, C Red, PBG-29

Table 6: Mean intra and inter-cluster distance (D^2) among common bean accessions (Pooled over environments)

Cluster No.	Cluster I	Cluster II
Cluster I	559.28	6321.44

Coiambara (1998), Chand (1990), Gonzales (2003), Dursun (2007) and Singh *et al.*, (2009). Days to 50% flowering had positive and significant correlation with days to maturity but were negatively correlated with all other traits except protein content. Days to maturity also showed similar results. Number of branches plant⁻¹ had positive and significant correlation with number of seeds pod⁻¹ and protein content. Number of Pods plant⁻¹ showed significant and positive correlation with pod length, number of seeds pod⁻¹ while it was negatively correlated with protein content which is in agreement with the findings of Leleji *et al.*, (1972). Pod length exhibited significant and positive correlation with number of seed pod⁻¹ and 100-seed weight. Rest of the associations observe among yield components were non-significant.

Analysis of genetic diversity is a platform for stratified sampling of breeding population and to identify the desirable genotypes for hybridization. In the present study 13 common bean accessions were evaluated in four random environments to estimate genetic divergence on the pooled analytical basis as per Mahalonobis D^2 statistics. Analysis of variance for divergence revealed that the values of V-statistic (measuring Wilk's criteria) were high and significant,

indicating presence of substantial genetic diversity in the material under study. Based on D^2 values accessions were grouped in two clusters Table 5. The maximum number of genotypes was found in cluster I (8) and the remaining five accessions got grouped in cluster II. The intra and inter cluster distances from pooled analysis among two groups are given in Table 6. The intra cluster distance ranged from (417.37) cluster II to (559.28) cluster I. The inter cluster distance was greater than intra cluster distance indicating considerable amount of genetic diversity among the genotypes studied. The classification of common bean genotypes into different clusters have been reported in different studies Jones *et al.*, (1997), Duarte *et al.*, (1999), Barelli *et al.*, (2005) and Sharma *et al.*, (2009). The pattern of group constellation in the present study, suggested that geographical diversity was not an essential factor to group the genotypes from particular source into one particular cluster. This means that, geographical diversity, though important, was not the only factor in determining the genetic divergence (Singh 1997 and Duran *et al.*, 2005). The comparison of pooled cluster means for different clusters (Table 7) indicated that the genotypes included in cluster II are a good source of yield per plant, 100- seed weight, pods/plant and pod length. The cluster I exhibited maximum protein content. The contribution of various characters from pooled analysis towards genetic divergence indicated that 100-seed weight (37.10%), protein content (15.26%), seeds per pod (11.28%) and days to maturity contributed maximum towards divergence in the present material (Table 7). They account nearly 75 per cent of total divergence. Therefore these four characters should be considered while selecting the parents for hybridization. Characters contributing to divergence are reported to vary from crop to crop. In general the traits contributing maximum to genetic divergence in common bean has been identified as 100-seed weight, number of pods plant⁻¹, days to flowering and grain oil content (Mirjana, 2005 and Coelin *et al.*, 2007).

Table 7: Cluster means and per cent contribution towards total divergence for different traits in common bean (Pooled over environments)

Traits	Clusters		No. of times appearing 1 st in the rank	Per cent contribution towards divergence
	I	II		
Days to 50% flowering	52.85	49.42	5	6.38
Days to maturity	110.52	106.28	8	10.14
No. of branches plant ⁻¹	9.56	10.30	5	6.30
No. of pods plant ⁻¹	10.04	11.24	4	5.08
Pod length (cm)	9.95	13.18	3	3.44
No. of seeds pod ⁻¹	5.12	5.18	9	11.28
100 seed weight (g)	30.40	54.93	29	37.10
Seed yield plant ⁻¹ (g)	16.39	32.37	4	5.08
Protein content (%)	21.58	19.98	12	15.26

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