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ABSTRACT

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Variability was studied among 21 French bean (*Phaseolus vulgaris* L.) germplasm collected from different research stations and traditional farming villages of the Bangladesh. The collected genotypes were evaluated in the field at the Plant Genetic Resources Centre, Bangladesh Agricultural Research Institute (BARI), Gazipur during 2013-2014. Qualitative variations were found in plant characters, leaf characters, pod characters and seed characters. Medium and dark intensity of green color in leaf was also noticed among the accessions. However ovate shape pod in cross section and presence of second color in pod were found in only one accession. Among the 21 French bean accessions, 1accession showed short, 12 accessions showed medium and 8 accessions showed long pod beaklengths. Purple color seeds were found in eight accessions whereas, only one accession exhibited cream color seed. All of the accessions exhibited dwarf type plant, pink color of standard, white color of wing, green pod ground and concave shape pod. Quantitative variations were observed among the accessions. Number of pods per plant and hundred seed weight ranged from 5.66 to 29.67 (no.) and 19.16 to 47.28 (g), respectively, where pod width was from 1.05 to 1.40 cm. The highest coefficient of variation was found in pods per plant (44.15%) followed by peduncle length (27.41%), pod beak length (26.39%) and 100 seed weight (21.83%). Principal component analysis was showed thatthe first five principal components accounted for 83.73% of the total variation. The genotypes were grouped into four clusters. The highest inter-clusterdistance was observed between clusters I and IV whereas the maximum intra-clusterdistance was found in cluster I. Therefore, the genotypes belonging these clusters could be selected for future hybridization program.

Key wards: Phaseolus vulgaris L.*, variability, qualitative and quantitative characters, germplasm*

INTRODUCTION

Beans, the "meat of the poor", contribute essential protein to the under-nourished people. Bean is an unavoidable food component in diets of people elsewhere in the world. It is main source of protein and energy and is gaining importance in human diet. Among major food legumes the French bean (*Phaseolus vulgaris* L.) is the third most important worldwide, superseded only by soybean [*Glycine max* (L.) Merr.] and peanut (*Arachis hypogea* L.) (Stoilova and Berova, 2009). Furthermore, the adequate nutritive composition and variable uses of beans in different culinary forms (canned or frozen grain and pod, dry seeds) make it an interesting crop both for consumers and processors (Escribano *et al.* 1997). Beans are grown for their green pods as a fresh vegetable and the dried seeds are used as pulse and for seed purposes, while the foliage is consumed as fodder and is used to restore soil fertility. Farmers regard beans as a cash-generating crop in the hills and grow a number of landraces with varying morphologies (Neupane and Vaidya, 2002). French bean (*P. vulgaris* L.), a native of central and South America (Swaider *et al.* 1992) has one of the longest histories of cultivated plants and according to Hidalgo (1991), the genus *Phaseolus* mainly grows in the tropical, subtropical and temperatezones. Much of the genetic variability of this species in the world has been maintained and conserved ex situ, outside the centers of origin, in genebanks (Borda 2011). Material from the world collection of *Phaseolus*, stored in International Center for Tropical Agriculture(CIAT), has been characterized in detail and its genetic diversity has been calculated (Frankel 1987). There have been observed special characters that allow identifying a given accession introduced. Various data confirming variability can be collected at phenotypic level of the plant, as well as at various protein and nucleotide levels (Singh 1991; Fotana *et al.* 2001; Tomlekova *et al.* 2009). The assessment includes identification of characters that are important for the potential of species, i.e. those that can be introduced into breeding programs. Based on recentstudies, the transfer of a gene from *P. vulgaris* to *Pisumsativum* and *Vigna vulgaris*, which has a key role in determining resistance to the bruchid beetle *Callosobruchus maculates* (Tomlekova 1998). Negri and Tosti, (2002); Galvan *et al.* (2006) stated that some genotypes exhibited good quality fresh bean seed and are preferred by the consumers who would be willing to pay high prices for these specific characteristics. In order to develop such cultivars, a preliminary characterization and evaluation of the genetic variability among and within local bean landraces for quality traits could be useful for exploitation of this genetic material for *ex situ* conservation and breeding programs.

In Bangladesh, French bean is not an important crop, cultivated areas being located in Hill, Sylhet and sporadically some region of the country. In cropping areas farmers have maintained some French bean landraces. In most cases these traditional cultivars have been progressively replaced with different elite crop cultivars and as intercrop with potato and maize that ensure higher yield and income meeting the farmer's demand. *P. vulgaris* L. collection includes local old varieties and populations, landraces. Recently we pay attention to local material (landraces) which still grown in gardens to collect and conserve them. They are well adapted to agro-climatic conditions and grains are with high quality and very tasty. However, these landraces

are going to extinction due to lack of proper conservation. Therefore, an attempt was taken to collect, characterize and conserve them. The present research could help in collection, evaluation and characterization of available indigenous germplasm, so that they can be utilized for varietal improvement and commercial cultivation.

MATERIALS AND METHOD

French bean germplasm were collected from government farms, markets and farm households from long period of time. A total of 21 landraces were collected from different parts of Bangladesh. Special attention was given regarding variability among the accessions during collection so that we collect the different types of genotypes and covered total gene pool. The genotypes were evaluated from December, 2013 to March 2014 at the Plant Genetic Resources Centre, BARI Gazipur. The field trials were in a randomized complete block design with three replications. Each accession was grown in three rows plot. Seeds are sowing in a row maintaining distance 15 cm. BARI-recommended cultural practices were followed (Islam *et al.* 2004). In each plot, 10 plants per replication were randomly chosen for biometric measurements. Plant data were measured by visual observation as a combination of active growth and plants appearing to be healthy and strong. All qualitative characters/traits were measured by a team following IBPGR (International Board for Plant Genetic Resources) descriptors for *Phaseolus vulgaris* (IBPGR 1982). Quantitative data measurements were averaged from 10 randomly selected plants. Scoring of agro-morphological characters was done according to the procedures given in the descriptor. The data were analyzed using Genstat software (version 12.1.).

RESULTS AND DISCUSSION

Qualitative descriptor

Qualitative variation of different descriptors in French bean accessions were evaluated (Table 1). Dwarf type growth pattern was found in all 21 accessions. Majority number of accessions (17 accessions) did not express plant pigmentation and 4 accessions showed very slight pigmentation. Intensity of green color in leaf was dark in maximum accessions (19 accessions) whereas, only 2 accessions showed medium intensity. Variation was found in leaf rugosity, where very strong, strong and medium rugosity was found in 15, 4 and 2 accessions, respectively. However variation was not found in terminal leaflet shape, and variation was found in leaflet tip length but only 3 accessions possessed medium tip whereas, long tip was found most accessions (18 accessions). On the other hand, variation was not found in flower traits. For instance, predominant foliage inflorescence position was found among all accessions used in this study. Similar results were found in case of color of standard (pink) and wing (white). Variation was found in all pod characteristics except pod ground color, stringiness of ventral suture and shape of pod curvature, whereas elliptic shape pod with absence of second color was found in 20 accessions and only one accession possessed ovate shape pod with presence of second color. Among the pod characteristics, degree of pod curvature and pod shape of distal part (excluding beak) possessed more variation, whereas, degree of pod curvature was weak in most of the accessions (13 accessions) and only 1 accession showed very strong degree of pod curvature. Similarly, acute to truncate shape distal part of pod was found in the most of the accessions (19 accessions). Medium length of beak with very weak beak curvature was found in most accessions in 12 and 7 accessions, respectively but short beak length in one accession and strong beak curvature were in two accessions (Table 1). In case of seed, Kidney (17 accessions), rectangular (2 accessions) and ovate (2 accessions) shape were found among the accessions. Different seed colors such as creamy (1 accessions), brick red (2 accessions), purple (9 accessions), deep purple (4 accessions), violet (2 accessions) and black (3 accessions) were noticed among the 21 accessions. There was no variation observed in seed color distribution (Table 1).

Table 1. Qualitative variation of different characters in French bean

Name of descriptor	Descriptor state	No of acc.	% of acc.
Plant growth type	Dwarf	21	100
Plant pigmentation	None	17	80
	Very slight	4	20
Intensity of leaf color	Medium green	2	10
	Dark green	19	90
Leaf rugosity	Medium	2	10
	Strong	4	20
	Very strong	15	70
Terminal leaflet shape	Triangular	21	100
Terminal leaflet length	Medium	3	15
	Long	18	85
Inflorescence position	Predominantly in foliage	21	100
Color of standard	Pink	21	100
Color of wing	White	21	100
Pod shape in cross section	Elliptic	20	95
	Ovate	1	5
Pod ground color	Green	21	10
Presence of secondary color on pod	Absent	20	95
	Present	1	5
Stringiness of ventral suture of pod	Absent	21	100
Degree of pod curvature	Absent or very weak	3	15
	Weak	13	60
	Medium	1	5
	Strong	3	15
	Very strong	1	5
Shape of pod curvature	Concave	21	100
Pod shape of distal part (excluding beak)	Acute	1	5
	Acute to truncate	19	90
	Truncate	1	5
Length of pod beak	Short	1	5
	Medium	12	55
	Long	8	40
Beak curvature	Absent or very weak	9	40
	Weak	7	35
	Medium	3	15
	Strong	2	10
Seed shape	Kidney	17	80
	Ovate	2	10
Seed color	Creamy	1	5
	Brick red	2	10
	Purple	9	40
	Deep purple	4	20
	Violet	2	10
	Black	3	15
Seed color uniformity	Yes	21	100

Quantitative descriptor

Range, mean, standard deviation and coefficient of variations are shown in Table 2. On an average, plant height, leaflet length and leaf width were 9.70, 5.67 and 4.26 cm, respectively. In general, 14.96 and 1.96 number of pods was found in each plant and each peduncle, respectively. In addition, pod length and width ranged from 9.60 to 14.53 and 1.05 to 1.40 cm, correspondingly. Average beak length was observed 1.72 cm among the accessions. Remarkable difference was observed among accessions with number of pod per plant and weight of pods, weight of seeds per. The accessions exhibited 19.16 to 47.28 g of hundred seed weight. The highest CV was found in pods per plant (44.15%) followed by peduncle length (27.41%), beak length (26.39%) and 100 seed weight (21.83%). The most constant characters with small differences among them are, pod width, pod

length and plant height. The lowest CV (6.29%) was found in pod width. On the basis of yield and yield contributing characters the accessions L-1, L-4, L-7, L-9 and L-10 may be selected for further study.

Table 2. Quantitative variation of different descriptors in French bean

Name of descriptor	Range	Mean	SD	CV (%)
Plant height (cm)	20.74-34.72	28.82	3.60	12.48
Leaflet length (cm)	5.90-13.40	9.70	1.84	19.01
Leaflet width (cm)	3.60-8.20	5.67	1.32	23.25
Peduncle length (cm)	1.70-6.23	4.26	1.17	27.41
Number of pods per peduncle	1.33-2.66	1.93	0.36	18.60
Number of pods per plant	5.66-29.67	14.96	6.61	44.15
Pod length (cm)	9.60-14.53	12.36	1.29	10.47
Beak length (cm)	0.68-2.50	1.72	0.45	26.39
Pod width (cm)	1.05-1.40	1.21	0.08	6.29
Weight per pod (g)	5.46-10.21	7.20	1.26	17.55
Number of seeds per pod	3.00-5.50	4.50	0.59	13.12
100 seed weight (g)	19.16-47.28	35.04	7.65	21.83

Principal component analysis

Multivariate analysis of the accessions revealed that the first five Principal Components (PC1 to PC 5) gave eigen- values > 1 and cumulatively accounted for 83.73% of the total variation (Table 3). The first PC axes accounted for 29.29% of the total multivariate variation, while the second accounted for 20.7% and the third for 12.99%. The cumulative proportion of the variation reached 62.98% in the first three PC axes and 83.73% in the first five axes. The high degree of variation in first five PC axes indicates a high degree of variation of these characters. Though there are no guidelines to determine the significance or importance of a coefficient, that is eigen – vactor (Duzyaman 2005). However higher coefficients for a certain trait indicate the relatedness of the trait to respective PC axes (Sneath and Sokal, 1973). Characters with high coefficients in the PC1 to PC5 should be considered as more important since these axes explain more than half of the total variation (Table 3). The variation in PC1 was mainly associated with 100 seed weight, in PC2 with pods per plant, and in PC3 plant height (Table 3). The fourth PC axes separated leaflet length and leaflet width, respectively while PC5 was associated with peduncle length, pod length, pod weight and number of seed per pod. PCA analysis indicate that 100 seed weight, pods per plant, plant height, leaflet length, leaflet width, peduncle length, pod length, pod weight and number of seed per pod were among the most important descriptors which accounted for more than 50% of the phenotypic variation expressed in this germplasm collection. Theses descriptors were therefore found to be most useful for studying the variability of population. It is suggested that the use of these characters will save considerable amount of time for identification of French bean germplasm. A two dimensional scatter diagram was constructed based on two principal axes (Fig. 1). The scatter diagram revealed that there were four apparent clusters. The genotypes were distantly located from each other. According to scatter diagram all the genotypes were apparently distributed into four clusters. It is assumed that maximum amount of heterosis will be manifested in cross combination involving the genotypes belonging to most divergent clusters.

Table 3. Extraction of eigen vectors, eigen values, percent of variation and cumulative variations for five principal components of French bean germplasm accessions

|	PC 1	PC 2	PC 3	PC 4	PC 5
Eigen value	3.5147	2.4842	1.5586	1.4266	1.0628
Explained proportion of variation (%)	29.29	20.7	12.99	11.89	8.86
Cumulative proportion of variation (%)	29.29	49.99	62.98	74.87	83.73
Variables	**Eigen- vectors**				
Plant height (cm)	0.01222	0.17195	-0.96723	0.06777	0.12701
Leaflet length (cm)	-0.0864	-0.05622	-0.05606	-0.81567	-0.12082
Leaflet width(cm)	-0.07441	-0.04464	-0.07577	-0.53077	0.01493
Peduncle length (cm)	-0.07094	0.05838	0.03705	0.0406	-0.23629
Pods/peduncle (No.)	-0.00839	0.01243	0.01284	-0.04605	0.03884
Pods/plant (No.)	-0.42374	0.88297	0.15762	-0.0402	0.09668
Pod length (cm)	0.0159	0.08079	-0.13347	-0.02065	-0.62847
Beak length (cm)	0.01988	0.0225	0.01562	-0.0548	-0.12736
Pod width (cm)	-0.00169	0.00049	0.00068	0.0022	-0.03174
Pod weight (cm)	0.00022	0.0743	-0.02154	0.13645	-0.67637
No. of seed/pod	-0.00306	0.04409	-0.06415	0.04254	-0.1785
100 seed weight (g)	0.89528	0.40937	0.08097	-0.1383	0.02873
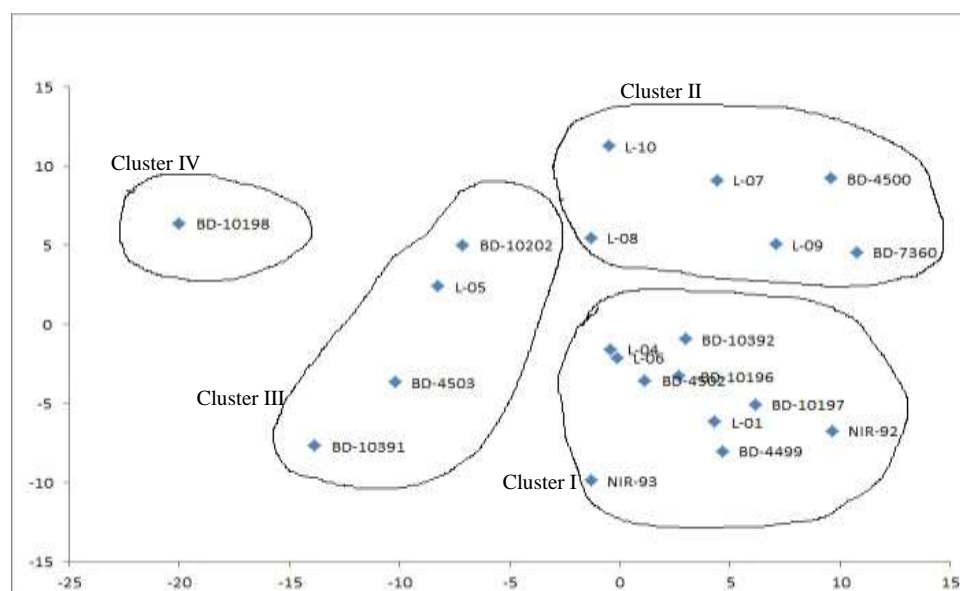
Fig. 1. Scatter diagram of the 21 French bean germplasm

Cluster analysis

Hierarchical clustering of the 21 French bean germplasm based on quantitative characters was carried out. A dendrogram using all clusters in vertical orientation was determined using between groups linkage measured in squared Euclidean distance (Fig. 2). The population was grouped in four major clusters (Table 4). Cluster I was the largest with ten (BD-4499, BD-4502, BD-10196, BD-10197, BD-10392, L-01, L-04, L-06, NIR-92, NIR-93) accessions followed by six (BD-4500, BD-7360, L-07, L-08, L-09, L-10) in cluster II. Cluster III consisted of four (BD-4503, BD-10202, BD-10391, L-05) accessions and remaining cluster (cluster IV) was found with only one accession (BD-10198). According to the cluster means, Cluster II showed better performance in case of pod length, beak length, pod width, weight per pod, number of seeds per pod and 100 seed weight (Table 5). Thus indicates that genotype of this cluster could be used for parent in future hybridization program for higher seed yield. The genotypes included in cluster III were leaflet length, leaflet width, peduncle length, pods per peduncle, pods per plant as well as batter pod yield because of higher number of pods per peduncle as well as pods number per plant.

Table 4. Number of cluster and genotypes under each cluster and within parenthesis, the value indicates the serial number of the accessions

Cluster number	Accessions
Cluster I	BD-4499(1), BD-4502(3), BD-10196(6), BD-10197(7), BD-10392(11), L-01(12), L-04(13), L-06(15), NIR-92(20), NIR-93(21)
Cluster II	BD-4500(2), BD-7360(5), L-07(16), L-08(17), L-09(18), L-10(19)
Cluster III	BD-4503(4), BD-10202(9), BD-10391(10), L-05(14)
Cluster IV	BD-10198(8)

Table 5. Cluster means for 12 quantitative characters in 21 French bean accessions

Characters	Cluster I	Cluster II	Cluster III	Cluster IV
Plant height (cm)	27.75	29.95	26.62*	30.33**
Leaflet length (cm)	10.08	8.4*	11.5**	10.24
Leaflet width (cm)	5.93	4.62*	6.82**	6.32
Peduncle length (cm)	3.83	4.35	6.23**	4.71
Number of Pods per peduncle	1.90*	1.94	2.0**	1.99
Number of Pods/plant	9.63*	19.38	29.67**	17.97
Pod length (Ex. Beak) (cm)	11.70*	13.38**	11.72	12.63
Beak length (cm)	1.73	1.93**	1.6	1.40*
Pod width (cm)	1.21	1.22**	1.2*	1.22
Weight per pod (g)	6.66*	8.12**	6.68	7.32
Number of seeds/pod	4.21*	4.97**	4.4	4.57
100 seed wt. (g)	35.87	42.47**	20.12*	25.55

Within rows, * and ** indicate minimum and maximum cluster mean value, respectively

Canonical Variate Analysis (CVA)

CVA was done to compute the inter-cluster distances. The intra and inter-cluster distance (D^2) values were shown in Table 6. The highest inter-cluster distance was observed between clusters I and IV (12.98), followed by the distance between clusters II and IV (10.91), I and III (6.74). In contrast, the lowest inter-cluster distance was observed between cluster I and II (5.96), followed by II and III (5.97). However, the maximum inter-cluster distance was observed between the clusters I and IV (12.98) indicating that genotypes from these two clusters, if involved in hybridization, may produce a wide spectrum of segregating population (Dhillon *et al.* 1999). On the other hand, the maximum intra-cluster distance was found in cluster I (0.69), which contained of ten genotypes, while the minimum distance was found in cluster IV, which was comprised of one genotypes. The magnitude of heterosis and potential for transgressive segregation largely depends on the degree of genetic diversity in the parental lines (Bhadra and Akhtar, 1991). This suggests that parents for hybridization should be selected from two clusters with wide inter-cluster distance to get more variability among the segregants.

Table 6. Mean intra- (bold) and intercluster distances in 21 French bean accessions

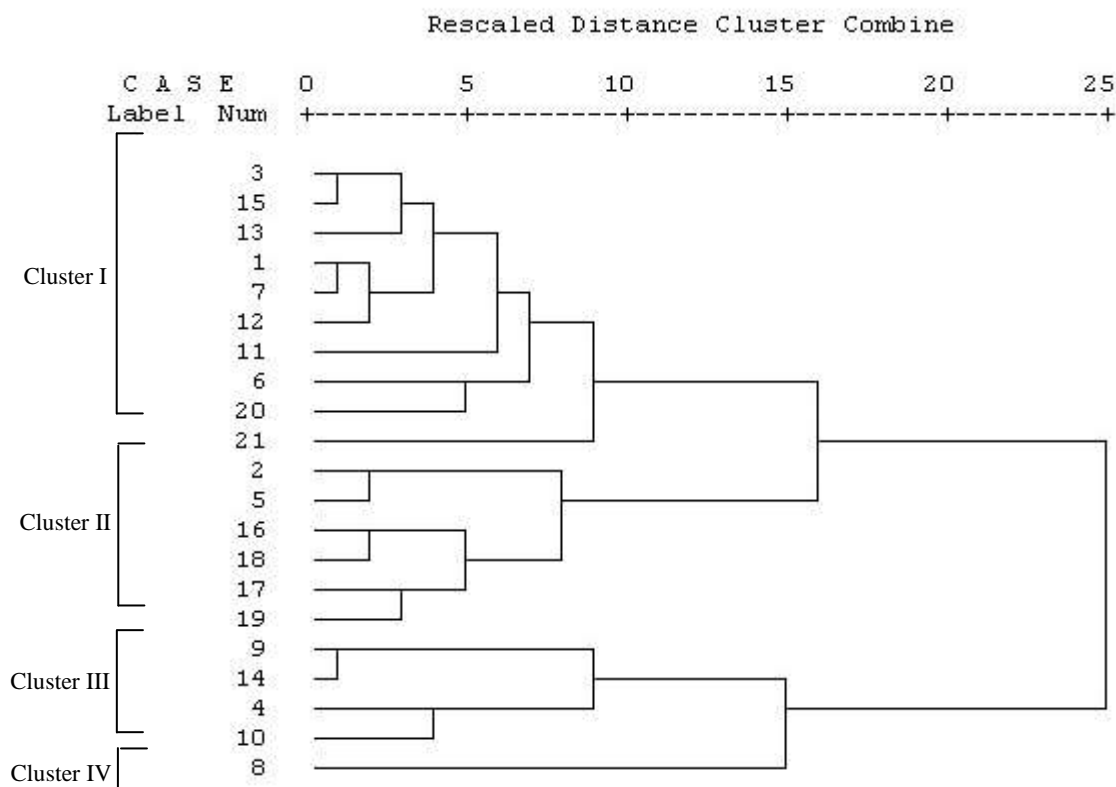| Cluster number	I	II	III	IV
I	**0.69**			
II	5.96	**0.37**		
III	6.74	5.97	**0.59**	
IV	12.98	10.91	6.25	**0**

Fig. 2. Dendogram showing of the 21 French bean germplasm

CONCLUSION

Wide range of variations were found among the 12 qualitative characters like plant pigmentation, intensity of leaf color, leaf rugosity, presence of secondary color in pod, pod shape in cross section, degree of pod curvature, pod shape of distal part, beak curvature, length of pod beak, seed shape and seed color. The accession formed two to six groups among the qualitative characters. On the basis of yield and yield contributing characters the accessions. L-1, L-4, L-7, L-9 and L-10 may be selected for further study. Remarkable variations were also found among the quantitative characters. The coefficient of variations ranged from 6.29% in pod width to 44.15% in number of pods per plant. The scientific information obtained from this study is useful for others gene banks, breeding programs and farmers.

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