Genetic Diversity of French Bean (Bush Type) Genotypes in North-West Himalayas

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A lot of variability is available in French bean in South American continent. To breed new and better cultivars, the breeder requires a comprehensive knowledge on variability existing at the germplasm hot spots. Fifty-one French bean (bush type) genotypes of different eco-geographical origin from India and abroad were grown in replicated plots under complete randomized block design to measure the extent of diversity for further use in breeding programmes. The data recorded on 14 characters were subjected to analysis of variance. By multivariate analysis (D^2 analysis), the genetic divergence among the genotypes was quantitatively measured. The total 51 genotypes were grouped into 8 clusters by this technique. There was no relationship between clustering pattern and geographical origin. Further, the effect of genetic divergence among different genotypes, which possessed differential expression in respect of specific agronomic traits, was also worked out. Introgression of these useful gene sources from diverse clusters may prove to be useful in gene pool maintenance and will be beneficial in designing appropriate breeding strategy in future French bean improvement.

Key Words: Cluster analysis, D^2 Statistics, Diversity, French bean, Performance

Introduction

French bean is important vegetable and pulse crop belonging to family Fabaceae. It is popular among the growers and consumers because of better nutritional qualities. This vegetable not only plays an important role in human nutrition but also improve soil fertility and fits well in crop rotations because of short growing period. In the hilly regions of the country, the crop is produced during summer and rainy seasons as vegetable and fetches off-season prices to the growers in the markets in nearby plains, where the normal season of availability if spring or autumn. Therefore, to breed new and suitable planting material is always in demand. In self pollinating crops like French bean, germplasm is available in the form of a multitude of homozygous lines which can be released as genetically improved cultivars in specific ecological regions. However, for a long term crop improvement programme, a large and diverse germplasm collection is an invaluable source of parental strains for hybridization and subsequent development of improved varieties. The limiting factors resulting from normal pollination concerning biparental heredity, makes a critical choice of parents in breeding programme necessary, especially when polygenic traits are involved. Since studies on diversity are meager in this crop, the present investigation was carried out to estimate genetic divergence in French bean (bush type) genotypes including both indigenous and exotic collections. D^2 statistics proposed by Mahalanobis (1936) offers a reliable technique to estimate the genetic divergence present in the population. These techniques measures the force of differentiation at intra cluster and inter cluster level and further helps in selecting genetically divergent parents for exploitation in hybridization programmes based on the superior mean performance. The precise information on the degree of genetic diversity and their agronomic evaluation could help in embarking upon an appropriate breeding strategy to tailor ideal genotypes, besides introgression of desirable genes from the diverse gene pool.

Materials and Methods

The experimental materials for the present study comprised of 51 genotypes obtained from different sources (Table 1). These genotypes were grown in three replications in a Randomized Block Design and spacing was maintained at 50 cm between the rows and 20 cm between the plants. The whole experiment was conducted during *Kharif* season of 2006 at the Vegetable Research Farm, Department of Vegetable Crops, Dr YS Parmar University of Horticulture and Forestry, Solan, located under the North-western Himalayan region of India. Observations were recorded on 10 randomly taken plants per replication on 14 quantitative traits such as, days to first flowering (X_1), node at which first flower appears (X_2), number

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Table 1. List of genotypes with their source

Genotype	Source	Genotype	Source
Payal	FIL India Ltd.	UHFB-19	CIAT, Colombia
IIHR-909	IIHR, Bangalore	UHFB-22	CIAT, Colombia
HAFB-3	HARP, Ranchi	UHFB-25	CIAT, Colombia
HAFB-4	HARP, Ranchi	UHFB-24	CIAT, Colombia
Arka Anoop	IIHR, Bangalore	UHFB-17	CIAT, Colombia
DWDFB-2003	UAS, Dharwad	UHFB-20	CIAT, Colombia
VLFB-2003	Almora	UHFB-12	CIAT, Colombia
VLFB-103	Almora	UHFB-11	CIAT, Colombia
EC405209	NBPGR, New Delhi	UHFB-18	CIAT, Colombia
EC405251	NBPGR, New Delhi	UHFB-10	CIAT, Colombia
PLB-44	Ludhiana	UHFB-32	CIAT, Colombia
EC8392	NBPGR, New Delhi	UHFB-33	CIAT, Colombia
Local yellow	Kinnour	UHFB-34	CIAT, Colombia
FB yellow	Ludhiana	UHFB-35	CIAT, Colombia
PLB-14	Ludhiana	UHFB-39	CIAT, Colombia
EC-8396	NBPGR, New Delhi	UHFB-40	CIAT, Colombia
CHFB-I	CHES, Ranchi	UHFB-15	CIAT, Colombia
PDR-21	IIVR, Varanasi	UHFB-03	CIAT, Colombia
EC99539	NBPGR, New Delhi	UHFB-16	CIAT, Colombia
ET-8392	NBPGR, New Delhi	UHFB-09	CIAT, Colombia
CH-812	CHES, Ranchi	UHFB-07	CIAT, Colombia
EC8391	NBPGR, New Delhi	UHFB-08	CIAT, Colombia
EC500257	NBPGR, Phagli	UHFB-28	CIAT, Colombia
EC500222	NBPGR, Phagli	Faguni	Semnis India(Pvt.) Ltd.
UHFB-23	CIAT, Colombia	Contender (Check)	Katrain, HP
UHFB-26	CIAT, Colombia		

of flowers/cluster (X_3), number of pods/cluster (X_4), number of pods/plant (X_5), pod length (X_6), pod breadth (X_7), pod weight (X_8), green pod yield/plant (X_9), number of seeds/pod (X_{10}), 100 seed weight (X_{11}), seed yield/plant (X_{12}), days to first marketable maturity (X_{13}) and plant height (X_{14}). An analysis of variance and co-variance were done on the mean values of each plot. From the estimate of variance and covariance 'V' statistics, which in turn utilizes Wilk's criterion (Λ), a simultaneous test of differences between mean values of a number of correlated variables was done. Further, the analysis of genetic divergence using D^2 statistics (Mahalanobis, 1936). On the basis of the magnitude of generalized statistical distance D ($D=\sqrt{D^2}$) values, the varieties were grouped into a number of clusters as suggested by Tocher (Rao, 1952). The relative contribution of each character to the total D^2 value between each pair of genotypes was determined following the procedures outlined by Bhatt (1970).

Results and Discussion

The analysis of variance for the 14 characters evaluated revealed significant differences among the genotypes. Using 'V' statistics, the analysis of dispersion for the test of significance of differences in the mean performance based on Wilk's criterion revealed highly significant differences between the genotypes for aggregate of 14 characters (Table 2). By using D^2 values, the 51 genotypes were clustered into 8 groups. The clustering pattern and the geographical distribution of the genotypes are presented in Table 3. A very large majority of genotypes from India and CIAT Columbia were found in cluster VII and VIII, followed by cluster V (Columbia) and cluster IV (India). The assumption of this technique is that the best parental materials may be those showing the maximum genetic divergence (Bhatt, 1970). However, the clustering pattern of bush bean genotypes did not indicate any relationship between genetic divergence and eco-geographical distribution. Cluster VII and VIII contained the geographically diverse genotypes from India and Columbia. Duddley and Davies (1960), Bhatt (1970), Dasgupta and Das (1984), Dahiya *et al.* (2002) and Gupta and Singh (2005) working with cultivars of alfalfa, Okra, Black gram and French bean respectively, also noted that genotypes are clustered in different groups irrespective of their countries of origin. Inter-cluster divergence values (D^2) between the eight clusters and their statistical distances are presented in Table 4.

The highest genetic divergence occurred between clusters IV and V (D^2 = 86.56), followed closely by that between clusters V and VI (D^2 = 84.56). However, the lowest divergence was between clusters VII and VIII (D^2 = 22.75). It is expected, therefore, that any cross between genotypes, namely, EC405251, PLB-44, ET-8392, EC99539 and EC8392 in cluster IV, and any

Table 2. Analysis of variance for 14 characters in French bean (Bush type)

Source	df	Mean sum of square													
		X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}	X_{13}	X_{14}
Replications	2	2.35	0.20	0.03	0.35	90.70	0.05	0.02	0.22	5055.33	0.12	10.22	150.93	0.19	1.50
Genotypes	50	257.55*	3.25*	8.31*	1.33*	189.41*	12.29*	0.41*	0.87*	6756.52*	5.12*	163.51*	1639.96*	284.17*	208.04*
Error	100	5.62	0.15	0.15	0.13	21.64	0.82	0.03	0.05	1134.24	0.26	1.92	167.70	0.77	7.20

* Significant at 5% level

• $X_1, X_2 \ldots X_{14}$ (Subscripts)

Table3. Clustering pattern of 51 genotypes of French bean on the basis of genetic divergence

Cluster	No of genotypes	Genotypes	Source
I	3	Contender, EC8396, EC500222	India
II	2	EC8391, UHFB-03	India, Columbia
III	2	Local Yellow, CH-812	India
IV	5	EC405251, PLB-44, ET8392, EC99539, EC8392	India
V	7	UHFB-26, UHFB-19, UHFB-22, UHFB-25, UHFB-24, UHFB-07, UHFB-08	Columbia
VI	2	CHFB-1, EC500257	India
VII	15	IIHR-909, HAFB-3, HAFB-4, DWDFB-2003, VLFB-2003, VLFB-103, PDR-21, UHFB-12, UHFB-18, UHFB-10, UHFB-32, UHFB-33, UHFB-35, UHFB-40, UHFB-16	India, Columbia
VIII	15	Faguni, Payal, Arka Anoop, EC405209, FB Yellow, PLB-14, UHFB-23, UHFB-17, UHFB-20, UHFB-11, UHFB-34, UHFB-39, UHFB-15, UHFB-09, UHFB-28	India, Columbia

Table 4. Average intra and inter cluster distance

Cluster	I	II	III	IV	V	VI	VII	VIII
I	16.67	51.21	43.17	39.05	59.42	50.57	35.75	36.88
II		13.55*	67.48	68.61	26.43	66.24	30.27	29.64
III			19.36**	33.31	79.83	41.89	54.33	44.63
IV				19.05	86.56**	37.40	60.85	56.36
V					15.91	84.56	31.87	36.55
VI						15.98	68.41	53.12
VII							15.53	22.75*
VIII								13.68

* Minimum Value; ** Maximum value

genotype from either V or VI will produce transgressive genetic variation within a segregating population. Further, in selecting parental materials, the important characteristics such as disease resistance, quality of produce and stability of performance should be considered. Furthermore, cluster IV had maximum cluster mean performance to days to first flowering, Number of pods per cluster, number of seeds per pod and 100 seed weight (Table 5). The genotypes included in the cluster had desirable performance for seed yield component traits. Similarly, cluster VI had genotypes with desirable number of pods/ plant and days to marketable maturity. Therefore, the introgression between the genotypes belonging to these groups will lead to the synthesis of new gene pool which combine higher seed yield and other component traits and can act as repository for superior genetic recombinants.

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Table 5. Cluster means for different characters among 51 genotypes

Characters	Cluster							
	I	II	III	IV	V	VI	VII	VIII
Days to 1st flowering	41.73	45.03	35.75	52.94	31.33	60.13	31.79	34.92
Node at which 1st flower appears	3.75	4.40	3.47	4.81	3.84	6.35	3.99	4.46
No. of flowers per cluster	3.97	5.40	2.97	3.51	3.31	2.64	3.76	3.42
No. of pods per cluster	3.01	2.75	2.42	3.13	1.92	2.43	2.58	2.24
No. of pods per plant	17.69	8.57	20.16	19.28	7.58	20.35	12.42	12.96
Pod length (cm)	15.31	11.15	14.07	13.83	11.95	13.24	14.15	13.69
Pod breadth (cm)	1.38	1.54	1.39	1.24	1.50	1.41	1.09	1.32
Pod weight (g)	5.49	6.76	5.97	6.27	5.99	5.55	6.07	6.13
Pod yield per plant (g)	90.41	57.79	121.28	118.64	43.18	111.97	70.29	77.80
No. of seeds per pod	5.51	3.71	3.98	5.91	4.58	5.06	5.64	5.45
100 seed weight (g)	39.40	24.67	24.57	30.46	27.14	24.32	24.68	23.23
Seed yield per plant (g)	33.82	8.03	19.13	31.49	10.85	24.51	16.40	16.36
Days to 1st marketable maturity	55.87	58.76	48.40	67.32	45.29	75.01	44.67	47.74
Plant height (cm)	64.44	43.89	50.90	45.04	53.45	55.32	54.80	53.17