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Effect of genetic diversity assessment of for crop improvement in french bean (*Phaseolus valgaris* L.) Germplasm

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Abstract
Forty genotypes of french bean were evaluated in Randomized Block Design with two checks during summer season of 2016 at the Vegetable Research Centre, Pant University of Agriculture and Technology, Pantnagar, Uttarakhand to assess the genetic diversity for further use in breeding programmes. Approximately 73.329 % of variation was recorded due to four principal components on various genotypes. The genotypes were further subjected to non- Hierarchical cluster analysis that resulted into seven non-overlapping clusters. The maximum number of genotypes was included in cluster III. Cluster IV had maximum cluster mean performance to number of pods per plant, number of seeds per pod, internodal length can be utilized for the development of high yielding varieties. An analysis of the percentage contribution of individual characters towards genetic diversity revealed that plant height, number of pods per plant, test weight and green pod yield per plant (gm) were the major characters contributing to genetic diversity in French bean.

Keywords: Principal component analysis, D^2 analysis, Tocher method, Cluster means, Divergence

Introduction
Beans, the "meat of the poor", contribute essential protein to the under nourished people. 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) [13]. French bean (*Phaseolus vulgaris* L.), a native of central and South America (Swaider *et al*. 1992) [19] has one of the longest histories of cultivated plants and is widely cultivated in the temperate and subtropical regions and in many parts of the tropics. It is the most important legume worldwide for human consumption (Singh 1999) [16]. Being such an important part of the diet around the world, french bean as a crop is subjected to various improvement programs (Hanai *et al*. 2010) [6]. 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 genotypes including both indigenous and exotic collections. For estimation of diversity within the germplasm, several workers have postulated principal component analysis and clustering of genotypes (Smith *et al*. 1995) [17]. These techniques identify plant traits that help in characterization of the distinctness among selected genotypes. They are often extended to the classification of a population into groups of distinct orders based on similarities in one or more characters and thus guide in the choice of parents for hybridization (Nair *et al*. 1998) [12]. Principal component analysis or simply PCA is a statistical procedure concerned with elucidating the covariance structure of a set of variables. In particular it allows us to identify the principal directions in which the data varies. For the principal component analysis each genotype was identified on the basis of correlation matrix as a single point in a standardized multidimensional space. The axes of this space were principal components obtained from the original data as orthogonal transformation of the original variety. In this way each principal component becomes a linear combination of the varietal scores corresponding to the original

variables D^2 statistics proposed by Mahalanobis (1936) [10] 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.

Hence the present study was undertaken with 40 germplasm of French bean to determine the genetic divergence and to examine relative importance of the characters.

Material and methods

The present investigation was conducted at Vegetable Research Centre, G.B. Pant University of Agriculture and Technology, Pantnagar, U.S. Nagar (Uttarakhand) during Jan-May, 2016. The experimental material comprised of 74 genotypes. The experiment was laid out in randomized block design with three replications. Each genotype was sown in three meter row length following plant spacing at 90x 60 cm apart. The seeds were sown at a depth of 4-5 cm. The crop was well managed for optimum growth and yield. The observations were recorded on randomly taken ten plants of each genotype for fifteen traits in each replication *viz.*, days to first initial flower, days to germinate, number of pods per cluster, number of pods per plant, pod length (cm), pod width (cm), seed length (cm), seed width, internodal length (cm), number of clusters per plant, test weight (gm), green pod yield per plant (gm), plant height (m), number of seeds per pod, green pod yield per plant (q). PCA and non-hierarchical Euclidean cluster analysis were calculated as per Hotelling (1933) [7] and Mahalanobis (1936) [10] respectively.

Results and Discussion

Genetic diversity and the diverse gene pool are the basis of plant breeding. Genetic diversity is essential if higher level of productivity is to be achieved because it providing genetic building blocks for further improvement. Hence, genetic diversity is necessary for progress to be made in plant breeding as well as during selection of parental genotypes for crossing programme.

Principal component analysis is a statistical procedure that uses an orthogonal transformation to convert a set of observations of possibly correlated variables into a set of values of linearly uncorrelated variables called principal components. The number of principal component is less than or equal to the number of original variables. The principal component analysis of 40 genotypes along with 2 checks based on correlation matrix of the morph-agronomical traits yielded 7 Eigen roots and Eigen vectors, is presented in Table 1. The Eigen root of first principal component was accounted approximately 36.961% of total variation followed by second to six components which accounted 19.033, 9.208, 8.127, 7.458, and 5.236 % of total variation presented among the genotypes, respectively. These elements may be interpreted as the relative weight given to the variables in each component. The important variables are those which have high positive or negative weights or values (Jeffers 1967) [8].

The first principal component had high positive weight or value to plant height (0.369) followed by number of clusters per plant (0.345) and high negative weight to pod length (-0.349) followed by seed length (-0.248), While the second principal component had high positive weight to days to first initial flower (0.202) followed by days to germinate (0.159), and high negative weight to pod width (-0.485) followed by test weight (-0.419). The third principal component had high positive weight or value to pod width (0.364) followed by days to first initial flower and internodal length (0.269) and high negative weight to number of pods per cluster (-0.525) followed by green pod yield per plant (q) (-0.400)**.** The fourth principal component had high positive weight or value to internodal length (0.507) followed by number of pods per cluster (0.444) and high negative weight to days to germinate (-0.442) followed by green pod yield per plant (gm) (-0.286). The fifth principal component had high positive weight or value to seed width (0.381) followed by days to first initial flower (0.252) and high negative weight to days to germinate (-0.587) followed by internodal length (-0.545). The sixth principal component had high positive weight or value to green pod yield per plant (q/ha) (0.347) followed by pod length (0.226) and high negative weight to number of pods per cluster (-0.484) followed by days to germinate (-0.424).

Principal component analysis (PCA) revealed that only the first five principal component axes in the PCA analysis had eigen-vector values whose loads were more than unity. The present findings are in accordance with the result of Abdi and Williams (2010) [1]. Value of Eigen root fell lower than one after the 5th principal component.

The first principal component largely accounted for the variation among the genotypes which alone contributed 36.961 % of the variations. Similar results have been supported by Madakbas *et al*. (2011) [9], Stoilova *et al*. (2012) [18] Panchbhaiya *et al*. (2017) [14]. Including these four principal components circa 73.329% has been estimated, which is not enough to completely comprehend divergence in French bean collection. Increment of circa more than 80% of total variance is sufficient that is why fifth and sixth principal component is considered for analyzing divergence.

PCA is a powerful technique for data reduction which removes interrelationships among components. Results reported by various researchers showed multivariate analysis as a valid system to deal with germplasm collection. Smith *et al*. (1995) conducted average linkage cluster and principal component analyses, and reported the utility of these results in preservation and utilization of germplasm.

Cluster analysis by Tocher method based on principal component analysis was found to be more useful measure for estimating divergence. The estimates of average intra- and inter-cluster distances for seven clusters (Table 2 and figure 1) revealed that the genotypes present within a cluster have little genetic divergence from each other with respect to aggregate effect of fifteen characters under study, while greater genetic diversity was observed between the genotypes belonging to different clusters. Similar findings were also supported by Pushpavalli *et al*. (2017) [15]. The intra cluster distance ranged from 0.00- 977.38. The maximum intra cluster distance was noted in cluster IV (977.38) followed by cluster VII (557.11), whereas minimum intra cluster distance recorded in cluster V and cluster VI (0.00). Maximum inter cluster distance was noticed between cluster IV and VII (3495.67) followed by cluster IV and V (2757.04). Whereas, minimum inter cluster distance was noticed between cluster I and III (575.98). Maximum fifteen genotypes were received by cluster III (Table 3). The second biggest cluster was cluster IV having seven genotype each. Minimum one genotype was received by cluster V and VI. The minimum inter-cluster D2 value observed between clusters I and III indicated that

genotypes of these two clusters were more or less genetically same.

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) [3]. This suggests that parents for hybridization should be selected from two clusters with wide inter-cluster distance to get more variability among the segregants. Therefore that any cross between genotypes, namely, PI-226868, PCPGR-2011-446, PGR-FB-208, EC-1(C), PCPGR-2895, PI-196936, H-905A(C) included in cluster IV and any genotype from either VII (PGR-FB-26-07, PCPGR-2916, EC-216, PCPGR-2874) (3495.67) and V (PGR-FB-46-07) will produce transgressive genetic variation within a segregating population. (Misra *et al*. 2010, Ahmed *et al*. 2015) [11, 2].

The cluster means for all the characters are given in Table 4. Cluster I had highest mean value for pod width, seed width, test weight whereas cluster II had highest mean value for number of clusters per plant, green pod yield per plant (gm) and plant height. Cluster III had highest mean value for green pod yield per plant (q/ha). Cluster IV had maximum cluster mean performance to number of pods per plant, number of seeds per pod, internodal length can be utilized for the development of high yielding varieties. The genotypes with high mean values of any cluster can be used either for direct adoption or for hybridization for further selection and improvement (Dalsaniya *et al*. 2009; Gangadhara *et al*. 2014) [4, 5].

The selection and choice of parents mainly depends upon contribution of characters towards divergence (Table 5and figure 2). Contribution of each character towards genetic divergence has been estimated from the number of times that each character appeared in the first rank. The present study showed that plant height (19.74), number of pods per plant (16.15), test weight (16.03) and green pod yield per plant (gm) (13.46%) were considered to be important traits contributing towards genetic divergence. These characters together recorded for more than 65% of the total divergence in the forty genotypes studied. Similarly divergence studies were carried out by Gangadhara *et al*. 2014, Panchbhaiya *et al*. 2017) [5, 14].

Table 1: Eigen vector, Eigen root and associated variation for principal component in French bean based on economic traits

S. No.	Characters	1	2	3	4	5	6
1.	Days to first initial flower	0.242	0.202	0.269	0.185	0.252	0.069
2	Days to germinate	0.018	0.159	0.239	-0.442	-0.587	-0.424
3.	Pods/cluster	0.078	-0.147	-0.525	0.444	-0.014	-0.484
4.	Pods/plant	0.313	-0.289	0.074	-0.128	0.008	-0.339
5.	Pod length (cm)	-0.349	-0.077	-0.173	-0.068	-0.210	0.226
6.	Pod width (cm)	-0.016	-0.485	0.364	-0.041	-0.053	0.009
7.	Seed length (cm)	-0.248	-0.366	-0.087	-0.194	0.059	-0.283
8.	Seed width (cm)	-0.245	-0.314	0.243	0.006	0.381	-0.115
9.	Internodal length (cm)	0.062	-0.202	0.269	0.507	-0.545	0.218
10.	Clusters/plant	0.345	-0.179	0.179	-0.002	0.046	0.222
11.	Test weight (gm)	-0.200	-0.419	-0.184	0.107	-0.162	0.201
12.	Green pod yield /plant (gm)	0.333	-0.237	-0.190	-0.286	-0.028	0.185
13.	Plant height (m)	0.369	-0.188	0.082	0.015	0.161	-0.129
14.	Seeds/pod	0.336	0.049	-0.138	0.203	-0.203	-0.116
15.	Green pod yield /plant (q)	0.262	-0.114	-0.400	0.347	-0.053	0.347
	Eigen value	5.544	2.854	1.381	1.219	1.119	0.785
	% variation	36.961	19.033	9.208	8.127	7.458	5.236
	Cumulative variation	36.961	55.994	65.202	73.329	80.787	86.023

Table 2: Average distance of inter and intra cluster centroids

	I	II	III	IV	V	VI	VII
I	234.79	845.74	575.98	984.18	1240.15	1187.40	1691.38
II		358.20	1096.06	1055.46	2711.97	2554.73	3382.43
III			478.88	1230.72	1322.68	1072.64	2183.77
IV				977.38	2757.04	2446.57	3495.67
V					0.00	670.44	683.02
VI						0.00	1677.222
VII							557.11

Table 3: Distributing pattern of germplasm along with check of French bean into 7 clusters

Cluster number	Number of germplasm	Germplasm included
I	6	PGR-GP-2011-379, PCPGR-2935, PI-169902, PGR-FB-31-207, PCPGR-2864,PI-196967
II	6	PGR-FB-38-2007, PCPGR-2488, PCPGR-2876, PCPGR-2483, PGR-FB-29-207,PCPGR-2906
III	15	EC-21, PCPGR-2865,PGR-AB-13-2007, PGR -FB-2807, PGR-FB-40-2007,PCPGR-2919, PCPGR-2909(C),PGR-FB-4907, PI-300658, PCPGR-2904, PCPGR-2905, PCPGR-2913, PCPGR-2901, PCPGR-2470, PCPGR-2486
IV	7	PI-226868, PCPGR-2011-446, PGR-FB-208, EC-1(C), PCPGR-2895, PI-196936, H-905A(C)
V	1	PGR-FB-46-07
VI	1	PCPGR-2910
VII	4	PGR-FB-26-07, PCPGR-2916, EC-216, PCPGR-2874

Table 4: Cluster mean for different economic traits in french bean genotypes

S. No.	Characters	Clusters						
		I	II	III	IV	V	VI	VII
1.	Days to first initial flower	69.50	69.17	71.00	69.00	60.00	77.00	61.75
2	Days to germinate	15.50	16.33	16.20	16.43	18.00	17.00	16.25
3.	Pods/cluster	3.83	3.83	3.47	3.57	2.00	4.00	3.25
4.	Pods/plant	43.33	56.83	38.13	63.57	18.00	11.00	19.75
5.	Pod length (cm)	14.53	13.17	12.25	12.41	14.00	9.80	14.73
6.	Pod width (cm)	1.35	1.33	1.19	1.30	1.20	1.00	1.35
7.	Seed length (cm)	1.82	1.67	1.44	1.57	1.50	1.20	1.85
8.	Seed width (cm)	1.02	0.87	0.83	0.99	.70	0.80	1.00
9.	Internodal length (cm)	15.10	15.20	14.05	15.37	13.20	10.40	14.33
10.	Clusters/plant	14.17	18.17	14.73	17.86	5.00	6.00	6.25
11.	Test weight (gm)	433.33	265.04	147.74	170.90	102.12	77.70	99.53
12.	Green pod yield /plant (gm)	0.19	0.34	0.19	0.23	0.14	0.11	0.13
13.	Plant height (m)	143.07	265.04	147.74	170.90	102.12	77.70	99.53
14.	Seeds/pod	2.98	2.92	2.35	3.00	0.80	2.10	0.63
15.	Green pod yield /plant (q)	5.83	4.83	5.93	5.71	5.00	5.00	4.75

Table 5: Relative contribution of different characters to the total divergence in French bean

S. No.	Characters	Contribution %
1.	Days to first initial flower	0.00
2	Days to germinate	0.00
3.	Pods/cluster	9.87
4.	Pods/plant	16.15
5.	Pod length (cm)	0.26
6.	Pod width (cm)	0.13
7.	Seed length (cm)	1.92
8.	Seed width (cm)	3.33
9.	Internodal length (cm)	2.82
10.	Clusters/plant	2.95
11.	Test weight (gm)	16.03
12.	Green pod yield /plant (gm)	13.46
13.	Plant height (m)	19.74
14.	Seeds/pod	5.51
15.	Green pod yield /plant (q)	7.82

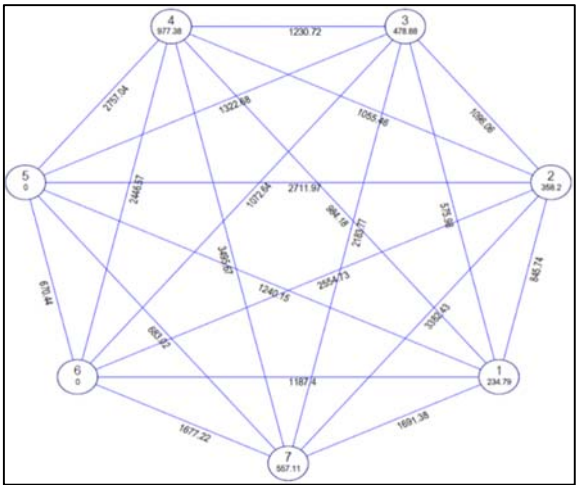

Fig 1: Average distance of intra and inter-cluster centroids based on various traits in 40 French bean genotypes

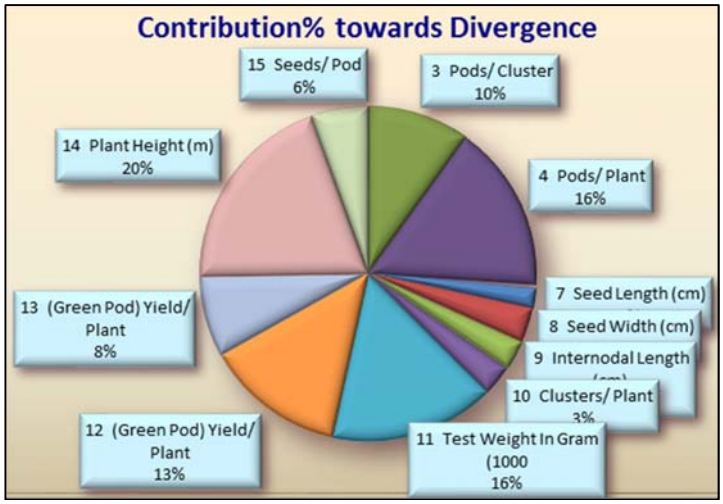

Fig 2: Contribution percent of different characters towards genetic divergence

Conclusion

A considerable range of genetic diversity was found in the genotypes. The cluster analysis grouped the genotypes into seven divergent clusters. The highest genotypes possessed in Cluster III. The Principal component analysis revealed that the first principal axis largely accounted for the variation among the genotypes which alone contributed 36.961% of the variations. The maximum number of pods per plant was found in cluster IV and the genotypes of this cluster could be used for developing high yielding variety. it is suggested that the best genotypes namely PI-226868, PCPGR-2011-446, PGR-FB-208, EC-1(C), PCPGR-2895, PI-196936, H-905A(C), PGR-FB-46-07, PGR-FB-26-07, PCPGR-2916, EC-216, PCPGR-2874 could be utilized for further improvement.

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