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Genetic Diversity analysis by D² clustering of yield and yield attributing traits in French bean (*Phaseolus vulgaris* L.)

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Abstract

Genetic diversity analysis was conducted at College of Agriculture, UAHS, Shivamogga during summer 2014. In this study, 36 six genotypes were evaluated for 13 yield and yield attributing traits and grouped into six clusters through Mahalanobis' D² analysis. Cluster I was the biggest with 19 genotypes followed by cluster VI and Cluster II & III. Among the traits studied, green pod yield contributed the maximum to the diversity (40.17%) followed by plant height (18.89 percent). The genotype IIHR-103 recorded highest green pod yield of 165 g per plant, while it recorded an average number of pods (23.85). Cluster II with four genotypes secured 1st rank with an overall score of 40 across 13 characters and the cluster V obtained 5th rank with an overall score of 55. It is desirable to select genotypes from clusters showing high inter-cluster distance (cluster V and VI) for further crop improvement programme.

Keywords: French bean, Mahalanobis D² analysis, Cluster, Diversity

Introduction

French bean (*Phaseolus vulgaris* L.) is an annual, a self-pollinated, diploid with chromosome number 2n=22 belongs to the family Fabaceae. It is also known as kidney bean, snap bean, garden bean, string bean, hari root bean, parota parsha bean, wax bean, navy bean, dwarf bean, carrot and seed type varieties are called as rajma in India. It is used as a vegetable and also consumed as dried beans or in the fresh state as green beans. French bean originated from Central America and Peruvian Andes in South America (Vavilov, 1950) [19]. It is introduced to India during the 17th century From Europe. The genus *Phaseolus* contains approximately 50 species with 4 (Delgado-Salinas, 1985) [2] or 5 cultivated ones: *P. vulgaris*, *P. acutifolius*, *P. lunatus* and *P. polyanthus* (= *P. coocinus* sub sp Darwinians). According to an estimate for 2016-17, in India, beans were cultivated in 12,000 ha with a total production of 8000 MT (NHB, 2017) [11].

It is a rich source of grain proteins (21.1%), carbohydrate (69.9%), phosphorus (42.5 mg) and iron (12.4 mg) in 100gm of edible parts (Ali and Kushwaha, 1987) [1]. It also serves as a functional food as it contains a lot of bioactive compounds viz enzyme inhibitors, lectins, phytates, oligosaccharides, and various phenolic substances (Diaz-Batalla *et al.*, 2006) [3]. The best way to understand the potential of the available germplasm is by analysing its genetic diversity. For an outstanding breeding programme in the crop improvement, diversity analysis greatly helps the breeder in the identification and proper choice of parents for specific breeding objectives. The present study was to assess the genetic diversity among germplasm lines.

Materials and Methods

The present investigation is conducted in College of Agriculture, the University of Agriculture and Horticultural Sciences, Navile, Shimoga during *summer* 2014. The experimental material for the present study comprised of 36 genotypes collected from Indian Institute of Horticulture, Bengaluru (IIHR). The experiment was laid out in a simple lattice design with two replications. Every genotype in each replication is grown in a plot of 2m×2m with a spacing of 45cm x15cm. The seeds were hand-dibbled at a given spacing in the respective blocks and crop was grown as per the package of practices recommendation (Anon, 2015). Five plants were selected randomly for observation from each replication for 13 quantitative traits; the average from these ten plants was worked out for the statistical computation. Multivariate analysis was done utilising Mahalanobis D² statistic (Mahalanobis, 1936) [9] and genotypes were grouped into different clusters following Tocher's method.

Results and Discussions

The genetic diversity among 36 genotypes was measured by employing D^2 statistics and grouped into six clusters using Tocher's method given as by Rao (1952) [15]. Distribution of genotypes in each cluster is presented in Table 1 and Figure 1. Similar genetic diversity works were carried out by many workers on this crop viz., Kalia *et al.* (2001) [8], Govanakoppa *et al.* (2002) [4], Ramaprasad *et al.* (2006) [14], Sharma *et al.* (2009) [16] etc. Genetic diversity also evaluated in different crops by Haritha and Reddy (2003) [6], Gupta *et al.* (2004) [5], Parthasarathy *et al.* (2005) [13] etc. Cluster I was found largest with 19 genotypes followed by cluster VI comprising five genotypes, cluster II and III comprising four genotypes and cluster IV and V comprising of 2 genotypes.

The inter-cluster and intra-cluster D^2 values were estimated and had been presented in Table 2 and Figure 2. The inter-cluster D^2 value was maximum (2533.14) between cluster V and VI followed by between cluster II and VI with a high D^2 value of 1577.81. The minimum distance observed was 373.07 between cluster I and III, which indicate the close relationship between the genotypes involved. Cluster VI was the most diverse as many clusters showed maximum inter-cluster distances with it followed by cluster V. The intracluster distance was observed in all clusters from cluster I to VI. Intra cluster distance was highest in cluster VI (409.20) followed by cluster I (230.99), cluster III (167.66), cluster II (138.8), cluster V (59.79) and cluster IV (50.82). The nearest and farthest clusters from each cluster based on D^2 values are represented in Table 3. It is desirable to select genotypes from clusters showing high inter-cluster distance (cluster V and VI).

Cluster mean of 13 yield and yield contributing characters were assessed and is presented in Table 4 and depicted in Figure 3. The mean comparison of the different characters indicated considerable differences among the clusters for all the characters. Maximum mean for days to first flowering (38.30) was observed in cluster IV followed by cluster II (36.97), while minimum cluster mean of 36.22 observed in cluster V. The maximum mean for days to 50 percent flowering (40.30) was observed in cluster IV followed by cluster I (40.21) and minimum mean (38.60) was observed in cluster V.

The highest mean for the flower pod set ratio was recorded in cluster II (2.21) followed by cluster IV (2.20) while, the lowest mean of 1.90 was shown by cluster VI. The highest mean for plant height was recorded in cluster IV (93.17 cm) followed by cluster V (71.61 cm) while the lowest mean of 45.02 cm was shown by cluster II. Days to maturity recorded a maximum mean in cluster V of 48.65 followed by IV of 47.90 while the minimum mean of 45.65 was observed in cluster III. A number of primary branches recorded a maximum mean in cluster III of 5.54 followed by I of 4.12 while, the minimum mean of 3.72 was observed in cluster IV and V. The number of secondary branches had the highest mean of 12.00 in cluster III followed by 8.10 in cluster V and the lowest mean of 6.60 in cluster II. The cluster mean observed in some pods per plant was highest for cluster IV (26.95) followed by cluster VI (20.93) and it was lowest for genotypes under cluster V (11.75). A number of seeds per pod recorded highest mean of 7.50 in cluster II followed by cluster VI (6.06) and the lowest mean of 5.35 in cluster IV and V.

Cluster II had a maximum mean of 16.66 cm for pod length followed by cluster VI (12.64 cm) and cluster IV recorded minimum mean of 11.10 cm. Pod width recorded maximum mean in cluster III (1.25 cm) followed by cluster II (1.20 cm), while minimum mean of 1.09 was observed in cluster IV and V. A test weight, maximum mean was recorded by genotypes in the cluster V (50.17g) followed by cluster IV (40.85), while cluster VI depicted minimum mean of 20.91g. Cluster VI recorded a maximum mean of 142.78g of green pod yield per plant followed by 142.37g observed in cluster II. Whereas minimum mean of 134.37g was observed in genotypes under cluster V. Similarly divergence studies were carried out by Govanakoppa *et al.* (2002) [4], Smaranika *et al.* (2010) [18], Waliing *et al.* (2014) [20], Molosiva *et al.* (2014) [10], Panchbhaiya *et al.* (2017) [12]

All 36 genotypes were spread over 6 clusters and means were scored across the clusters for all the 13 characters, and this is given in Table 4. The highest cluster mean was given the first rank and next cluster is possessing next best means were given 2nd, 3rd and so on up to 6th rank for all the traits. Finally, the clusters are ranked based on the overall score obtained from 13 characters. The lowest scoring cluster was given the first rank, and next cluster is possessing the score above the previous ones were given 2nd, 3rd and so on up to 6th rank. Accordingly, cluster II with an overall score of 40 across the 13 characters elected the first rank followed by cluster IV, I, VI, III and V. Indicating presence of most promising genotypes in them and further breeding programme to generate new material. Cluster V with an overall score of 55.

The contribution of various characters towards diversity is given in Table 5 and Figure 3. Out of 13 characters studied, green pod yield contributed the maximum to the diversity (40.17 per cent) followed by plant height (18.89 per cent), pod length (18.10 per cent), number of vegetative branches (5.87 per cent), number of secondary branches (5.40 per cent). Whereas the number of seeds per pod (4.29 per cent), test weight (3.00 per cent), days to maturity (2.06 per cent), number of pods per plant (1.11 per cent), days to 50 per cent flowering (0.95 per cent), flower to pod set ratio (0.16 per cent). Days to first flowering and pod width contribution to divergence is negligible. These results were in line with Huque *et al.* (2012) [7] and Sharma and Mishra (1997) [17].

The genotype IIHR-103 recorded highest green pod yield of 165 g per plant, while it recorded an average number of pods (23.85). The genotype IIHR-23 recorded 162.25g green pod yield per plant followed by IIHR-81A (161.00g), IIHR-90 (160.00g), IIHR-99 (157.00g), Arka Komal (156.50g), IIHR-47 (156.00g), IIHR-88 (153.00g), IIHR-91 (152.00g) and IIHR-83 (151.50g).

Even though genotype IIHR-103 recorded highest green pod yield of 165g per plant, further improvement for green pod yield can be achieved through increasing number of primary branches because it was recorded lowest primary branches (3.95). By increasing primary branches it can accommodate some green pods per plant.

The genotypes which are superior and productive but genetically diverse are IIHR-103, Arka Komal, IIHR-81A, IIHR 23, IIHR-83 and IIHR-47. The genotypes like IIHR-83, IIHR-91, IIHR-88, IIHR-47, Arka Komal, IIHR-99, IIHR-90, IIHR-81A, IIHR-23 and IIHR-103 were identified as high yielding genotypes.

Table 1: Clustering pattern of 36 germplasm lines of French bean on D² analysis.

Sl. No.	Clusters	No. of genotypes	Name of genotype
1	I	19	IIHR-87, IIHR-99, IIHR-88, IIHR-70, IIHR-58, IIHR-42, IIHR-40, IIHR-103, IIHR-81, IIHR-31, IIHR-90, IIHR-89, IIHR-100, IIHR-85, IIHR-15, IIHR-91, IIHR-94, IIHR-96, IIHR-98
2	II	4	Arka Suvidha, Arka Bold, Arka Komal, Arka Sharath
3	III	4	IIHR-79, IIHR-83, IIHR-81A, IIHR-82
4	IV	2	IIHR-47, IIHR-49
5	V	2	IIHR-48, IIHR-95
6	VI	5	IIHR-2, IIHR-65, IIHR-66, IIHR-23, Arka Anoop

Note: IIHR: Indian Institute of Horticultural Research, Bengaluru

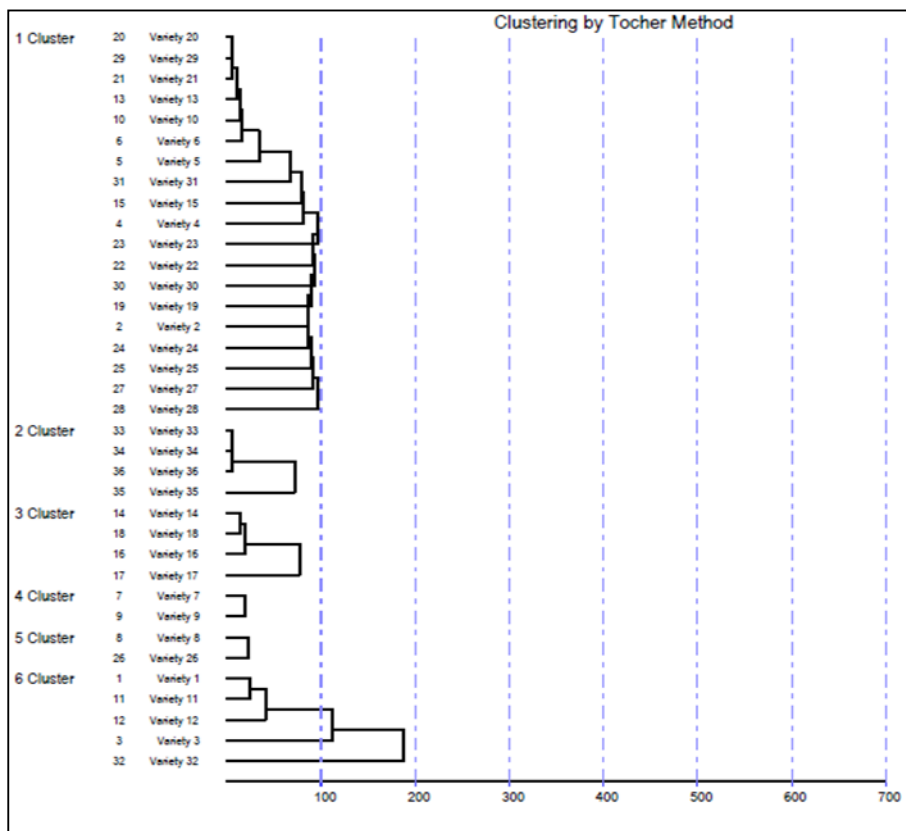


Fig 1: Clustering pattern of 36 French bean genotypes drawn according to Tocher method

Table 2: Average intra and inter cluster D² values of clusters in French bean

	I	II	III	IV	V	VI
I	230.99	535.82	373.07	407.24	590.98	1034.88
II		138.80	1031.79	804.31	644.25	1577.81
III			167.66	714.57	833.64	1212.47
IV				50.82	764.91	1036.63
V					59.71	2533.14
VI						409.20

Table 3: The nearest and farthest clusters from each cluster based on D² values in French bean.

Sl. No.	Clusters	Nearest cluster	Farthest cluster
1	I	III (373.07)	VI (1034.88)
2	II	I (535.82)	II (1577.81)
3	III	I (373.07)	VI (1212.47)
4	IV	III (714.57)	VI (1036.63)
5	V	I (1034.88)	VI (2533.14)
6	VI	II (590.98)	V (2533.14)

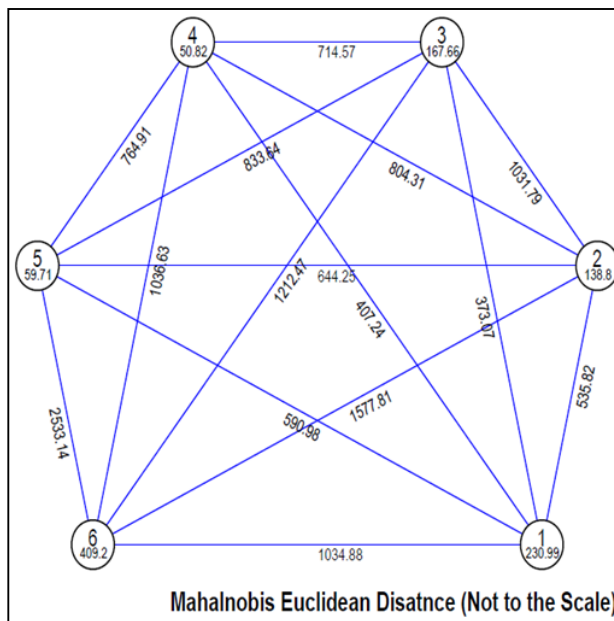


Fig 2: Intra and inter-cluster distances among six clusters of French bean genotypes

Table 4: Cluster mean analysis

Sl No	Clusters	No. of genotypes	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	Cluster score	Cluster rank
1	I	19	36.695 (3)	40.218 (2)	1.943 (4)	50.867 (3)	47.155 (4)	4.125 (2)	7.125 (4)	14.291 (3)	5.511 (3)	11.897 (3)	1.164 (3)	36.671 (5)	138.845 (4)	43	111
2	II	4	36.975 (2)	39.913 (3)	2.215 (1)	45.025 (6)	46.863 (5)	3.800 (4)	6.600 (6)	13.713 (4)	7.500 (1)	16.663 (1)	1.209 (2)	38.850 (3)	142.375 (2)	40	I
3	III	4	36.963 (4)	39.300 (5)	1.915 (5)	45.395 (5)	45.650 (6)	5.548 (1)	12.008 (1)	12.000 (5)	5.475 (4)	11.525 (4)	1.253 (1)	38.063 (4)	139.225 (3)	48	IV
4	IV	2	38.300 (1)	40.300 (1)	2.200 (2)	93.170 (1)	47.900 (2)	3.725 (5)	6.750 (5)	26.950 (1)	5.350 (5)	11.100 (6)	1.093 (5)	40.850 (2)	135.700 (5)	41	II
5	V	2	36.225 (6)	38.600 (6)	2.010 (3)	46.250 (4)	48.650 (1)	3.725 (5)	8.100 (2)	11.750 (6)	5.350 (5)	11.300 (5)	1.093 (5)	50.175 (1)	134.375 (6)	55	V
6	VI	5	36.950 (5)	39.710 (4)	1.909 (6)	71.612 (2)	47.710 (3)	3.880 (3)	7.358 (3)	20.930 (2)	6.060 (2)	12.640 (2)	1.136 (4)	20.912 (6)	142.785 (1)	43	III

Where,

X₁=Days to first floweringX₂ = Days to 50 per cent floweringX₃ = Flower: pod setting ratioX₄ =Plant height (cm)X₅ = Days to maturityX₆ = Number of vegetative branchesX₇ = Number of flowering branchesX₈ = Number of pods per plantX₉ = Number of seeds per podX₁₀ = Pod length (cm)X₁₁ = Pod width (cm)X₁₂ = Test weight (g)X₁₃ = Green pod yield (g)

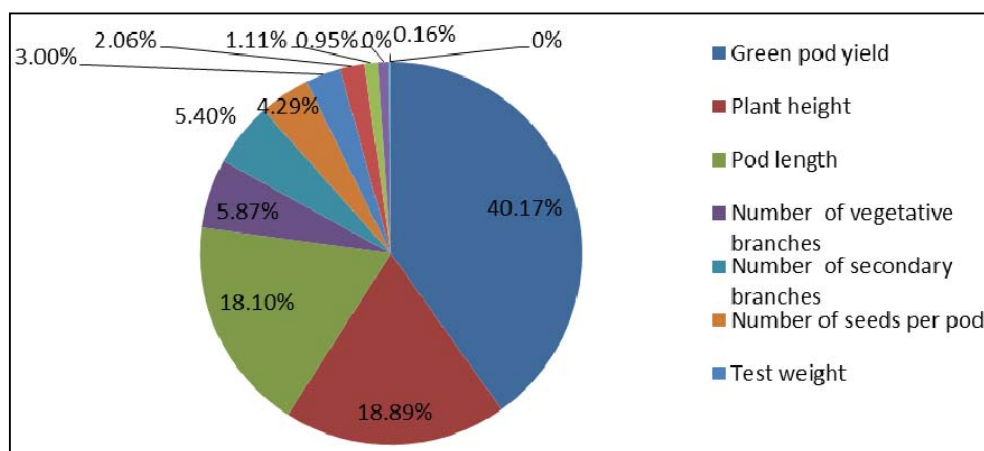


Fig 3: Per cent contribution of 13 characters towards diversity in French bean

Table 5: Percent contribution of 13 characters towards diversity in French bean

Sl. No.	Character	Contribution (in per cent)
1	Green pod yield	40.17
2	Plant height	18.89
3	Pod length	18.10
4	Number of vegetative branches	5.87
5	Number of secondary branches	5.40
6	Number of seeds per pod	4.29
7	Test weight	3.00
8	Days to maturity	2.06
9	Number of pods per plant	1.11
10	Days to 50 per cent flowering	0.95
11	Flower :pod setting ratio	0.16
12	Pod width	0.00
13	Days to first flowering	0.00

Conclusion

Mahalanobis (1936) D^2 analysis offers a reliable technique to estimate the divergence present in the population. This technique measures the forces of differentiation at intracluster, inter-cluster level and further helps in selection of genetically divergent parents for exploitation in hybridisation programme based on their superior mean performance.

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