



## GENETIC DIVERGENCE STUDIES IN INDIGENOUS FRENCH BEAN (*PHASEOLUS VULGARIS* L.) GERMPLASM

P. Arun Kumar<sup>1\*</sup>, R. V. S. K. Reddy, S. R. Pandravada, Ch. V. Durga Rani and V. Chaitanya

Vegetable Research Station, A.R.I., Dr. Y.S.R.H.U., Rajendranagar, Hyderabad - 500 030 (Andhra Pradesh), India.

<sup>1</sup>College of Horticulture, Dr. Y. S. R. H. U., Rajendranagar, Hyderabad - 500 030 (Andhra Pradesh), India.

### Abstract

Mahalanobis  $D^2$  statistic was used to study genetic divergence for eighteen traits in a collection of forty four French bean genotypes, which were grouped into seven clusters. Hundred seed weight contributed 33.83% towards total divergence followed by pod weight and protein content. Maximum numbers of genotypes were found in cluster II and VI. Highest intracluster distance was observed for cluster V and lowest in cluster I, while maximum intercluster distance was observed between cluster III and cluster VI and minimum between cluster I and VI. Mean performance of individual clusters revealed that cluster VI genotypes performed better compared to genotypes of other cluster, which may be used for further improvement.

**Key words :** French bean, genetic divergence, cluster analysis.

### Introduction

French bean is a popular vegetable of the country grown for green tender pods, dry seeds and for processing known by several names *viz.*, common bean, runner bean, garden bean, faras bean, black bean, rajmash bean, kidney bean, haricot bean, dwarf bean, pole bean, navy bean, pinto bean, string bean and snap bean. It is one of the most ancient among the cultivated vegetables and presently grown throughout the world in subtropical and temperate climates. Southern Mexico, Brazil and Central America are considered to be the primary centre of origin, while the secondary centre lies in Peru-Bolivia-Ecuador region of American continent (Vavilov, 1950 and Smartt, 1970). A wild species *Phaseolus aborigineus* Burk. is considered to be the progenitor of French bean (Yarnell, 1965). It is a multipurpose crop grown for vegetable, dry seed, fodder and also as a canned vegetable (Biswas *et al.*, 2010 and Singh, 2000). It is rich in protein (19-31%) and is closely compared with meat (Joshi and Rana, 1995). A successful breeding programme is associated with genetic diversity of parents used in hybridization. The exploitation of variability is of great importance and is a prerequisite for the effective screening of superior genotypes. Therefore, a study of genetic divergence has become the prime prerequisite for improvement of this crop.

### Materials and Methods

Forty four genotypes of French bean were evaluated during 2012 with three replications at Vegetable Research Station, A.R.I., Rajendranagar, Hyderabad (A.P.), India. All the genotypes are collected from National Bureau of Plant Genetic Resources (NBPGR) Regional Station, Rajendranagar, Hyderabad (A.P.), India. Each genotype was sown in a two row plot of 6 m length with intra and inter row spacing of 60 × 90 cm. Observations were recorded on ten randomly tagged plants for eighteen characters *viz.*, plant height (cm), number of primary branches, days to first flowering, days to 50% flowering, length of inflorescence (cm), number of inflorescence per plant, number of flowers per inflorescence, number of pods per inflorescence, days to first pod harvest, days to last pod harvest, pod length (cm), pod width (cm), pod weight (g), number of pods per plant, number of seeds per pod, 100 seed weight (g), protein content (%) and marketable pod yield per plant (g). The mean values were used to know the genetic divergence (Mahalanobis, 1936) and genotypes were grouped into various clusters by Tochers method as described by Rao (1952).

### Results and Discussion

Present results revealed that 100 seed weight contributed maximum (33.83%) towards total divergence followed by pod weight (17.02%) and protein content (11.52%) (table 1) suggesting that these are potent factors

\*Author for correspondence: E-mail-arunhort02@yahoo.com

**Table 1 :** Percent contribution of different traits towards diversity in French bean germplasm.

Character	No. of times ranked 1 <sup>st</sup>	Percent contribution
Plant height (cm)	20	2.11
Number of primary branches/plant	0	0.00
Days to first flowering	86	9.09
Days to 50 percent flowering	0	0.00
Length of inflorescence (cm)	45	4.76
Number of inflorescences/plant	45	4.76
Number of flowers/inflorescence	6	0.63
Number of pods per inflorescence	4	0.42
Days to first pod harvest	10	1.06
Days to last pod harvest	41	4.33
Pod length (cm)	7	0.74
Pod width (cm)	28	2.96
Pod weight (g)	161	17.02
Number of pods per plant	44	4.65
Number of seeds per pod	2	0.21
100 seed weight (g)	320	33.83
Protein content (%)	109	11.52
Marketable pod yield per plant (g)	18	1.90

in differentiating the germplasm of French bean. Patil *et al.* (2008) and Sureja and Sharma (2001) reported that protein content and pod length contributed maximum towards divergence in French bean.

Clustering pattern grouped forty four genotypes into seven clusters (table 2). Maximum number of genotypes (9) felled under cluster II and VI. Cluster V had 7 genotypes while cluster I, III and VII with 5 genotypes each and cluster IV with 4 genotypes. From the clustering behaviour, it is obvious that the selection of different diverse genotypes have played a greater role in total divergence between the clusters than the geographical diversity *i.e.* the genotypes have grouped into different clusters irrespective of their geographical origins, which means that the genetic constitution of the varieties was more dominant than their geographical origin while forming a cluster. These results are in consonance with the findings of Rai *et al.* (2010).

The mean intra and Intercluster D<sup>2</sup> are presented in table 3. Maximum genetic distance was observed between cluster II and VI (697.52) followed by cluster I and III (643.25). While, cluster I and VI displayed the lowest degree of divergence suggesting close genetic makeup

**Table 2 :** Clustering pattern in forty four genotypes of French bean (Tocher's method)

Cluster	Number of genotypes	Genotypes
I	5	SRS-13451, SRS-13454, SRS-13459, RSMP-842, AYOKA.
II	9	SRS-13430, SRS-13470, SRS-13483, SRS-13499, SRS-13500, SRS-13527, SRS-13530, SRS-13536, SRS-13546.
III	5	SRS-13461, SRS-13471, SRS-13491, SRS-13498, AUV-315.
IV	4	SRS-13429, SRS-13480, SRS-13481, PLB-10-01.
V	7	SRS-13462, SRS-13497, SRS-13504, SRS-13522, SRS-13525, SRS-13526, PMA-01-237.
VI	9	SRS-13443, SRS-13444, SRS-13449, SRS-13460, SRS-13463, SRS-13496, SRS-13505, SRS-13547, AUV-317.
VII	5	SRS-13456, SRS-13482, SRS-13494, SRS-13552, KENTUCKY WONDER.

**Table 3 :** Average intra (bold) and intercluster D<sup>2</sup> values for eighteen traits in forty four genotypes of French bean. (Tocher's method).

Clusters	I	II	III	IV	V	VI	VII
I	<b>62.42</b>	268.31	643.25	274.07	271.23	106.42	172.15
II		<b>105.12</b>	221.09	146.37	214.83	360.51	259.31
III			<b>102.03</b>	240.71	371.35	697.52	606.05
IV				<b>0.00</b>	180.60	352.24	416.89
V					<b>207.61</b>	310.05	346.41
VI						<b>0.00</b>	191.94
VII							<b>0.00</b>

\*Bold diagonal values indicate intracluster distance, rest of the values show the intercluster distances.

of the genotypes included in these groups. Cluster I showed minimum intracluster distance (64.42), while maximum intracluster distance was exhibited by cluster V (207.61) followed by cluster II (105.12) and cluster III (102.03) indicating good scope for selection within the cluster. Intra cluster distances being much smaller than inter cluster distances, indicating homogenous and heterogenous nature of the genotypes within and between the clusters, respectively.

The mean values of cluster for various characters are presented in table 4. Almost all the clusters were highly distinct to each other with respect to all the

**Table 4 :** Mean values of clusters for eighteen traits in forty four genotypes of French bean (Tocher's method).

Cluster number	Plant height (cm)	Number of primary branches per plant	Days to first flower-ring	Days to 50 percent flower-ring	Length of inflorescence (cm)	Number of inflorescences per plant	Number of flowers per inflorescence	Number of inflorescence	Days to first pod harvest	Days to last pod harvest	Pod length (cm)	Pod width (cm)	Pod weight (g)	Number of pods per plant	Number of seeds per pod	100 seed weight (g)	Protein content (%)	Marketable pod yield per plant (g)
I	152.16	2.44	37.55	42.88	3.17	21.63	3.84	2.21	52.33	105.11	12.42	1.18	5.60	21.98	4.51	39.55	22.02	125.52
II	152.67	3.68	37.20	41.03	6.55	33.63	5.65	2.48	51.87	95.33	10.58	1.03	3.83	42.71	4.75	22.47	26.66	164.70
III	163.03	3.26	41.33	43.86	8.36	53.77	5.35	3.19	54.66	97.93	10.44	0.81	3.27	78.55	6.30	13.16	27.26	264.65
IV	139.10	3.44	41.33	44.66	6.23	40.33	6.77	3.22	56.66	109.00	11.75	1.13	6.25	31.69	5.44	18.50	34.47	194.36
V	145.89	3.29	44.88	47.86	6.39	29.99	5.21	2.55	59.64	96.24	11.93	1.17	5.43	35.93	4.47	20.94	23.10	206.17
VI	121.74	3.66	37.33	38.33	5.43	35.21	5.66	1.88	54.33	95.00	12.17	1.18	5.92	55.77	4.55	47.40	17.60	294.87
VII	123.05	3.55	32.00	34.33	10.56	26.33	3.44	2.11	45.33	80.66	7.76	1.25	3.59	34.84	2.99	41.33	20.49	127.87

characters studied. Cluster IV exhibited more or less average values for most of the traits. Among seven clusters, the genotypes in the cluster VI showed higher marketable pod yield per plant (294.87 g) followed by cluster III (264.65 g) and cluster V (206.17 g) while lowest marketable pod yield per plant was exhibited by Cluster I (125.52 g) followed by cluster VII (127.87 g) and cluster II (164.70 g). Genotypes belonging to cluster VII taken least number of days for first flowering (32.00), days to 50% flowering (34.33), days to first pod harvest (45.33) with maximum length of inflorescence (10.56 cm), highest pod width (1.25 cm) and hundred seed weight (41.33 g). Maximum pod length (12.42 cm) was recorded in cluster I while highest pod weight (6.25 g) was recorded in cluster IV with highest protein content (34.47). Maximum number of pods per plant (78.55) was recorded in cluster III with highest number of seeds per pod (6.30). Hence, these genotypes can be utilized in crop improvement as progressive donors.

The present results can be concluded that more emphasis should be given to 100 seed weight and protein content for making selection of high yielding genotypes of Indian bean. The maximum D<sup>2</sup> values exist between cluster III and cluster VI followed cluster I and III indicated that the genotypes included in these clusters may give useful transgressive segregants in further generations.

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