

## GENETIC DIVERGENCE STUDIES OF RICE BEAN GENOTYPES

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### SUMMARY

Genetic divergence of 65 genotypes of rice bean was carried out using Mahalanobis  $D^2$  statistics. The genotypes were grouped into eight clusters. Cluster I with 14 genotypes was the largest. The inter-cluster distance was maximum between clusters VIII and V. The intra-cluster distance was maximum for cluster VI. The genotypes LRB-313 and LRB-314 were found to be early maturing. LRB-412, LRB-453, HRB-12 and RBL-160 showed higher number of branches/plant and clusters/plant. HRB-412, RBL-160 and LRB-453 showed higher number of pods/plant and seed yield/plant. Thus, the above genotypes from diverse clusters can be used in hybridization programme of crop improvement to obtain heterotic response and transgressive segregants of desirable type for these characters.

**Key words :** Genetic divergence, rice bean,  $D^2$  analysis

Rice bean [*Vigna umbellata* (Thumb) Ohwi and Ohashi] is such a legume, grown in western, northern and eastern India and Nepal. It is widely grown as an intercrop, particularly with maize. It has rapid establishment, is pest resistant and has the potential to produce large amount of high quality seed, nutritious animal fodder and can be grown as green manure crop. Rice bean has a good amino acid composition and is rich in several compared to other grain pulses. Increase in intake of rice bean was shown to have less severe nutrient deficiencies of calcium, potassium, iron, lysine and some B vitamins (Anderson, 2007; Anderson and Chandyo, 2010). The knowledge of genetic divergence in a crop is very important for initiating a breeding strategy because genetically diverse parents are likely to produce high heterotic effect and more variability in segregating generations, which can be exploited for desired crop improvement programme. Therefore, present study was undertaken to assess genetic divergence among 65 genotypes of rice bean to identify genetically divergent parents to be used in hybridization programme aimed at improvement of rice bean.

### MATERIALS AND METHODS

The experimental material consisted of 65 genotypes of rice bean. These genotypes were collected from CCSHAU, Hisar; PAU, Ludhiana; OUAT,

Bhubneshwar; MPKVP, Rahuri and NDUAT, Faizabad. The material was evaluated in randomized block design with three replications at the experimental area of Department of Genetics and Plant Breeding, CCSHAU, Hisar during **kharif** 2011. Each genotype was grown in single row of 3 m length spaced 40 cm apart. The plant to plant distance was 10 cm. Observations were recorded on five random plants from each plot for 10 characters. The characters were days to 50 per cent flowering, days to maturity, plant height (cm), number of branches/plant, number of clusters/plant, number of pods/plant, pod length (cm), number of seeds/pod, 100-seed weight (g) and seed yield/plant (g). In order to quantify the genetic distance between two genotypes Mahalanobis (1936)  $D^2$  statistic as described by Rao (1952) was employed and constellation of genotypes into clusters was done following Tocher's method (Rao, 1952) and intra- and inter-cluster distances were computed. The cluster-wise means of all the characters were also computed for comparison.

### RESULTS AND DISCUSSION

Wide range of variation and significant difference among the genotypes for all the characters under study were observed. Sixty-five genotypes were grouped into eight clusters based on  $D^2$  analysis. Grouping of genotypes into eight clusters has been shown in Table

TABLE 1  
Distribution pattern of 65 genotypes into eight clusters

Clusters	No. of genotypes	Genotypes	D <sup>2</sup> (D)
I	14	HRB-1, HRB-6, BR-4, BRB-102, NDRB-4, RRB-12, RRB-13, LRB-385, LRB-433, LRB-437, LRB-440, LRB-443, LRB-492, LRB-494	2.651 (1.628)
II	12	BRBM-107, BRBM-109, BRBM-111, BRBM-112, LRB-126, LRB-235, LRB-378, LRB-423, LRB-429, LRB-452, LRB-457, LRB-493	3.015 (1.736)
III	10	HRB-3, HRB-10, HRB-14, HRB-15, HRB-18, HRB-19, LRB-216, LRB-306, LRB-314, RBL-184	3.283 (1.811)
IV	9	LRB-179,LRB-218,LRB-298,LRB-309, LRB-313 ,LRB-326,LRB-347,LRB-353, RBL-99	2.710 (1.646)
V	9	RL-3, LRB-305, LRB-333, LRB-365, LRB-403, LRB-450, LRB-464, RBL-1, RBL-6	3.181 (1.781)
VI	6	BRB-101, LRB-412, LRB-427, LRB-453, RBL-35, RBL-50	3.742 (1.934)
VII	3	HRB-99, LRB-339, LRB-367	2.866 (1.692)
VIII	2	HRB-12, RBL-160	3.516 (1.875)

1. Cluster I was the largest comprising 14 genotypes followed by cluster II with 12 genotypes. A close examination of dendrogram (Fig. 1.) revealed that all genotypes were divided into two major groups. One group which includes clusters II, VIII, IV, I and V containing all genotypes from Haryana were further grouped into clusters, indicating that genotypes developed from same geographical location were quite dissimilar in multivariate traits and formed different clusters. There was no parallelism between genetic and

geographical diversities in rice bean as revealed in clustering pattern. So, geographical diversity cannot always be used as an index of genetic diversity as also suggested by Singh *et al.* (1998) in rice bean.

The intra-cluster D<sup>2</sup> varied from 2.651 to 3.742 (Table 2). Cluster VI showed maximum (3.742) followed by cluster V (3.516), cluster III (3.283), cluster V (3.181), cluster II (3.015), cluster VII (2.866), cluster IV (2.710) and cluster I (2.651). The genotypes of clusters VIII and V (7.622) exhibited maximum inter-

TABLE 2  
Inter-and intra-(diagonal) cluster average of D<sup>2</sup> and D values among different clusters in rice bean

Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
2.651 (1.628)	3.096 (1.976)	4.391 (2.095)	4.335 (2.082)	3.516 (1.875)	4.494 (2.120)	4.012 (2.003)	6.560 (2.561)
	3.015 (1.736)	4.352 (2.086)	5.358 (2.315)	4.537 (2.130)	4.257 (2.063)	4.913 (2.216)	5.824 (2.413)
		3.283 (1.811)	3.896 (1.973)	4.318 (2.077)	5.707 (2.389)	4.604 (2.145)	6.296 (2.509)
			2.710 (1.646)	4.072 (2.018)	6.361 (2.522)	4.102 (2.003)	7.446 (2.729)
				3.181 (1.784)	5.514 (2.384)	4.630 (2.152)	7.622 (2.760)
					3.742 (1.934)	4.833 (2.198)	5.518 (2.349)
						2.866 (1.693)	5.629 (2.373)
							3.516 (1.875)

cluster distance followed in descending order by the genotypes of VIII and IV (7.446), VIII and I (6.560), whereas it was minimum between clusters I and II (3.096) followed by clusters I and V (3.516). The higher inter-cluster distance indicated the presence of more genetic diversity among the genotypes included among these clusters. Thus, more heterosis and greater number of useful transgressive segregants can be obtained by hybridization between genotypes from distant clusters. A comparison of average contribution of characters to genetic divergence revealed that seed yield/plant contributed maximum (36.73%) followed by days to 50 per cent flowering (27.64%) and plant height (12.21%), rest of the characters contributed in a range of 0.14 to 7.26 per cent.

Cluster mean for different characters was able to bring out differences in characters among the genetic clusters (Table 3). The genotypes in cluster IV took minimum number of days to flowering and genotypes in cluster VIII took minimum number of days to maturity, whereas the genotypes in cluster I took maximum days to flowering and maturity. The mean plant height of genotypes was minimum in cluster I and maximum in cluster II. Number of branches/plant was maximum for genotypes of cluster VI and minimum genotypes of cluster III. The genotypes of cluster VIII showed maximum, while genotypes of cluster V showed minimum number of clusters/plant and pods/plant. The mean pod length and number of seeds/plant were maximum for the genotypes of cluster II and minimum for the genotypes of cluster VII. The cluster VIII genotypes showed maximum, while cluster IV genotypes showed minimum 100-seed weight and mean seed yield/

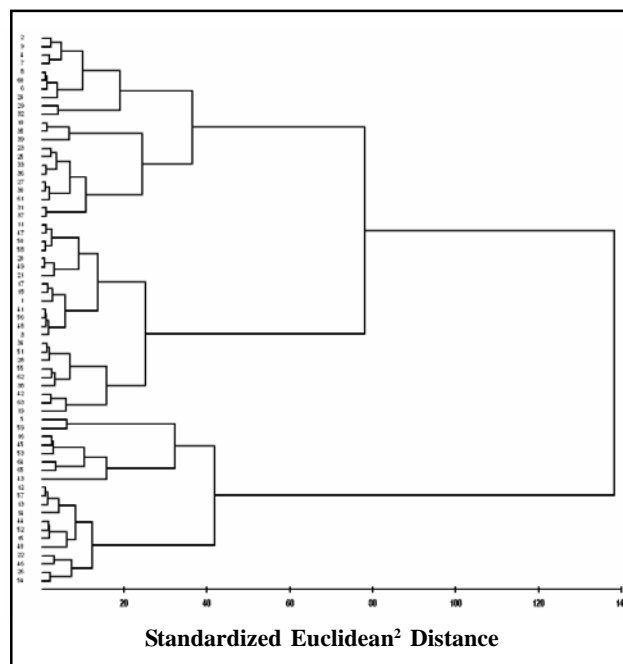


Fig. 1. Ward's minimum variance dendrogram.

plant. In the present study, the hybridization between genotypes in clusters VIII, VI, IV, II and III will be effective in combining early flowering and maturity, number of branches/plant, number of clusters/plant, number of pods/plant and seed yield/plant.

The genotypes LRB-313 and LRB-314 in clusters IV and III were found to be early maturing type. LRB-412 and LRB-453 of cluster VI, HRB-12 and RBL-160 of cluster VIII showed higher number of branches/plant and clusters/plant. HRB-412, RBL-160 and LRB-453 showed higher number of pods/plant and seed yield/plant. Thus, hybridization between these genotypes could

TABLE 3  
Cluster mean for 10 characters in 65 genotypes

Character	Clusters								Mean	Contribution (%)
	I	II	III	IV	V	VI	VII	VIII		
Days to 50% flowering	66.43	61.58	43.03	41.89	59.33	65.39	45.57	43.67	55.79	27.64
Days to maturity	166.26	162.00	142.30	142.41	163.81	166.22	147.78	141.83	156.54	5.24
Plant height (cm)	104.03	128.22	104.19	105.64	117.07	121.23	119.80	111.92	113.12	12.21
No. of branches/plant	5.07	5.17	4.60	4.71	4.74	7.22	5.78	5.67	5.17	0.19
No. of clusters/plant	10.59	10.86	9.10	7.85	7.70	14.17	13.56	17.83	10.32	1.88
No. of pods/plant	38.55	40.31	32.13	28.56	26.26	42.89	45.00	59.67	36.15	5.58
Pod length (cm)	8.40	9.21	8.93	8.08	8.40	8.76	7.84	8.92	8.61	7.26
No. of seeds/pod	8.17	9.28	8.80	7.85	7.93	8.72	7.67	8.67	8.44	0.14
100-seed weight (g)	6.47	6.49	6.61	6.18	6.67	6.61	6.50	6.72	6.51	3.13
Seed yield/plant (g)	12.28	18.40	14.64	9.41	10.27	21.83	12.41	38.10	14.78	36.73

be effective in future breeding programme in developing early maturing and high yielding varieties of rice bean with more number of branches, clusters and pods per plant.

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