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## Studies on genetic divergence in rice bean by using $D^2$ statistics

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**Abstract**

Forty seven rice bean genotypes were analyzed for genetic divergence which resulted in nine clusters having maximum inter-cluster distance between clusters III and IX and least between clusters V and VIII. Maximum intra-cluster distance was exhibited by cluster II followed by cluster I. Putative lines selected were from cluster II (JRB 08-6, JRB 08-6-1 and JRB 07-4) for days to flower initiation, dry matter yield per plant, dry matter yield per plant per day, crude protein yield per plant and crude protein yield per plant per day; cluster VI (JRO 15-6, KRB 86-1 and JRB 07-35-3) for green fodder yield per plant, number of leaves per plant, plant height, days to 50 per cent flowering, number of branches per plant, green fodder yield per plant per day and leaf : stem ratio, and cluster IV (JRO 15-1, JRO 15-4 and JRO 15-3) for leaf area, stem diameter, root length, fresh root weight and dry root weight. These lines can be used as patents in different hybridization programmes to obtain maximum variation for further selection.

**Keywords:** Genetic divergence,  $D^2$  analysis, cluster analysis, rice bean, fodder yield

**Introduction**

Rice bean [*Vigna umbellata* (Thunb.) Ohwi and Ohashi] is a potential, multipurpose and underutilized fodder legume. It has an important role in human, animal and soil health improvement. It seems to be good source of protein, essential amino acids, essential fatty acids and minerals. Rice bean is a lean period crop that provides subsistence to the farmers with fodder supply throughout growing season for animal population.

It is susceptible to frost, can tolerate high temperature is best grown where temperature averages 18-30 °C and rainfall as 1,000-1,500 mm per annum. It is best adapted to drought-prone sloping areas and flat rainfed conditions. It is grown preferably on marginal lands. The crop has been reported to be generally resistant to many diseases common to leguminous crops (Chandel *et al.*, 1988)<sup>[1]</sup>.

Accumulation of different desirable traits spread over the diverse genotypes into one genotype is important for the rapid advancement in yield improvement of any crop. To initiate hybridization, the genotypes are to be classified into clusters based on genetic divergence and the extent of genetic diversity between them, need to be estimated so that the parents could be chosen from the clusters with wide genetic divergence (Pandey, 2007)<sup>[10]</sup>. The present study was taken up with an objective to estimate the genetic diversity for seed yield and its components in rice bean using Mahalanobis  $D^2$  statistics during kharif 2017.

**Materials and Methods**

The experiment was carried out on 47 genotypes under All India Coordinated Research Project on forage crops, Department of Genetics & Plant Breeding at Seed Breeding Farm, College of Agriculture, JNKVV, Jabalpur (M.P). Geographically, Jabalpur is situated in the semi-arid sub-tropics at 23.91° North latitude and 79.5° East longitudes with an altitude of 411.78 meters above the mean sea level.

The experiment was conducted in Randomized Complete Block Design (RCBD) with three replications in *kharif* season 2017. Each entry was planted in 3.0 m X 0.9 m plot size and spacing between rows was kept 30 cm. Gap filling wherever necessary was done within a week after germination to maintain uniform plant population.

Observations were recorded on randomly selected five competitive plants in each plot, excluding the border plants for twenty characters *viz.*, days to flower initiation, days to harvest, plant height (cm), number of leaves per plant, number of branches, stem diameter (mm), root length (cm), root volume (ml), number of root nodules per plant, leaf area (cm<sup>2</sup>), fresh root weight (g), dry root weight (g), green fodder yield per plant (g), green fodder yield per plant per day (g), dry matter yield per plant (g), dry matter yield per plant per day (g), crude protein yield per plant (g), crude protein yield per plant per day (g), leaf stem ratio and chlorophyll

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content index. The  $D^2$  analysis was done by using the method suggested by Mahalanobis (1936) <sup>[2]</sup> and elaborated by Rao (1952) <sup>[3]</sup>.

**Table 1:** Distribution of Rice bean genotypes in different clusters

Cluster No.	Number of genotypes	Genotypes
I	23	KRB-86, KRB-69-3, KRB-69, JRB-6, JRB 07-43-4, KRB-99, JRB 06-8, JRB 15, BFRB-57, JRB 07-28-1, JRB 07-51-1, JOR 17-2, KRB-73, JRB 06-114, JRB 11, JRB 06-11, JRB 14-2, JRB 06-10, KRB-65, JOR 17-1, JRB 14, JRB 08-1, KRB-99-1
II	15	BFRB-3-1, JRB 07-48-1, JRB 07-2, JRB 07-2-2, JRB 06-3, JRB 06-8-1, KRB-86-1, JRB 06-8-2, Bidhan-1, JRB 07-49-1, JRB 16, JRB 07-50-2, JRB 07-43-3, JRB 14-1, JRB 04-1
III	1	JRB 10-1
IV	2	RBL-6, KRB-63
V	1	JOR 16-2
VI	1	JRB 06-9
VII	2	JRB 06-6, JRB 06-7
VIII	1	JOR 16-7
IX	1	JRB 07-1

## Results and Discussion

### Grouping of genotypes

On the basis of  $D^2$  values, the 47 genotypes were grouped into 9 clusters following Tocher's method. Cluster wise distribution of genotypes is summarized in Table 1. Clustering of genotypes was not associated with the geographical distribution and was mainly grouped due to their morphological differences. Cluster I was the largest among all clusters comprising 23 genotypes followed by Cluster II which had 15 genotypes. Cluster IV and VII had twin genotypes while, Cluster III, V, VI, VIII and IX had solitary genotype each.

The cluster analysis indicated presence of substantial amount of diversity in the material evaluated. Similar results have been observed by Nagalakshmi *et al.* (2010) <sup>[4]</sup> for cluster I being largest with 22 genotypes, Vavilapalli *et al.* (2014) <sup>[6]</sup> for cluster I with 11 genotypes and Nguyen (2017) <sup>[5]</sup> revealed that cluster I and II were the largest groups (8 genotypes). Presence investigation suggested that this material might serve as good source for selecting the diverse parents for hybridization programme aimed at isolating desirable combination for fodder yield as well as other characters.

### Inter and Intra-Cluster $D^2$ value

The average intra and inter-cluster  $D^2$  values are presented in Table 2. The inter-cluster  $D^2$  values were greater than the intra-cluster  $D^2$  values, further indicating the considerable amount of diversity among the genotypes studied. The highest intra cluster distance was recorded in Cluster II (42.32) followed by Cluster I (33.74), Cluster VII (20.58) and Cluster IV (13.39). Cluster III, V, VI, VIII and IX was mono-genotypic with no intra cluster divergence. The inter cluster distance was highest between the clusters III and IX (302.30) followed by cluster VII and IX (296.47), III and VIII (234.70), VII and VIII (216.70), III and V (211.93), V and VII (205.74) and I and IX (192.80). The lowest inter cluster distance was observed between clusters V and VIII (29.76). Therefore, the crossing between the genotypes of most divergence clusters *i.e.* III and IX could be able to produce high fodder yielding transgressive segregants. The findings reported by Bhandari and Verma (2007) <sup>[7]</sup>, Nagalakshmi *et al.* (2010) <sup>[4]</sup>, Chandrakar *et al.* (2016) <sup>[8]</sup>, Nguyen (2017) <sup>[5]</sup>, Vishwanatha and Yogeesh (2017) are contradictory to present study.

**Table 2:** Average intra and inter cluster  $D^2$  values of Rice bean genotypes

Cluster No.	I	II	III	IV	V	VI	VII	VIII	IX
I	33.74	80.22	53.99	63.74	124.02	99.51	63.21	132.96	192.80
II		42.32	161.32	81.71	65.77	64.27	139.32	87.18	98.12
III			0.00	66.70	211.93	163.31	74.41	234.70	302.30
IV				13.39	84.09	92.36	114.17	126.50	167.81
V					0.00	134.41	205.74	29.76	153.48
VI						0.00	159.56	160.07	61.14
VII							20.58	216.70	296.47
VIII								0.00	146.23
IX									0.00

### Cluster mean and contribution of individual characters towards genetic divergence

The cluster means for the 20 quantitative characters studied in 47 rice bean genotypes revealed that considerable difference among all the clusters exists (Table 2). From the data, the highest cluster mean values were recorded for characters days to flower initiation (137.67) and days to harvest (148.67) in cluster VI, plant height (203.07 cm) and stem diameter (5.58 mm) in cluster II, green fodder yield per plant (369.06 g), number of root nodules per plant (186.09), days to harvest

(148.67), number of leaves per plant (148.33), dry matter yield per plant (83.22 g), green fodder yield per plant per day (2.48 g) and crude protein yield per plant per day (0.09 g) in cluster IX, number of branches per plant (8.67) and dry matter yield per plant per day (0.65 g) in cluster V, leaf area (137.47 cm<sup>2</sup>), root length (77.93 cm), root volume (26.67 ml) and dry root weight (7.09 g) in cluster IV, chlorophyll content index (43.80) and fresh root weight (19.09 g) in cluster III, leaf stem ratio (1.17) in cluster VII, crude protein yield per plant per day (0.09 g) in cluster VIII.

**Table 3:** Percent contribution of characters towards divergence of 47 genotypes on *Vigna umbellata*

S.No.	Character	Times Ranked 1 <sup>st</sup>	Percentage (%) contribution of traits towards divergence
1	Green fodder yield/plant/day (g)	288	26.64
2	Crude protein yield/plant (g)	200	18.5
3	Fresh root weight (g)	162	14.99
4	Dry root weight (g)	94	8.7
5	Dry matter yield/plant/day (g)	80	7.4
6	Leaf stem ratio	63	5.83
7	Root nodules/plant	50	4.63
8	Crude protein yield/plant/day (g)	43	3.98
9	Number of leaves/plant	36	3.33
10	Dry matter yield/plant (g)	21	1.94
11	Plant height (cm)	12	1.11
12	Number of branches/plant	11	1.02
13	Root volume (ml)	5	0.46
14	Root length (cm)	4	0.37
15	Leaf area (cm <sup>2</sup> )	4	0.37
16	Chlorophyll content index	4	0.37
17	Stem diameter (mm)	3	0.28
18	Green fodder yield/plant (g)	1	0.09
19	Days to flower initiation	0	0
20	Days to harvest	0	0

The lower cluster mean values for days to flower initiation (106.67) and days to harvest (113.67) were found in cluster V, plant height (123.87 cm) in cluster IX, number of root nodules per plant (72.58), number of leaves per plant (55.67), root length (45.93 cm), chlorophyll content index (32.43), root volume (9.33 ml), fresh root weight (8.33 g), crude protein yield per plant (2.35 g), green fodder yield per plant per day (0.64 g) and dry matter yield per plant per day (0.12 g) and crude protein yield per plant per day (0.02 g) in cluster VII, leaf area (117.44 cm<sup>2</sup>), green fodder yield per plant (88.84 g), dry matter yield per plant (17.56 g), number of branches per plant (4.67) and crude protein yield per plant per day (0.02 g) in cluster III, stem diameter (4.04 mm) in cluster VI, dry root weight (1.77 g) and leaf stem ratio (0.53) in cluster VIII.

Therefore, the crosses between genotypes of cluster VI, II, IX, V, VI, III, VII, VIII may be expected to generate wide range of variation for yield and other traits. Such segregates may be superior yielding than the parents.

The percentage contribution towards genetic divergence by all the characters is presented in Table 3. The trait green fodder yield per plant per day (26.64%) contributed maximum to genetic divergence by taking 288 times and ranked first followed by crude protein yield per plant (18.5%) by 200 times, fresh root weight (14.99%) by 162 times, dry root weight (8.7%) by 94 times, dry matter yield per plant per day (7.40%) by 80 times, leaf stem ratio (5.83%) by 63 times, nodules per plant (4.63%) by 50 times, crude protein yield per plant per day (3.98%) by 43 times, number of leaves per plant (3.33%) by 36 times, dry matter yield per plant (1.94%) by 21 times, plant height (1.11%) by 12 times, number of branches per plant (1.02%) by 11 times.

Whereas, magnitude of genetic divergence was less than one percent for root volume (0.46%), root length (0.37%), leaf area (0.37%), chlorophyll content index (0.37%), stem diameter (0.28%) and green fodder yield per plant (0.09%). Days to flower initiation and days to harvest had no contribution towards divergence.

The present research exhibited a high level of genetic diversity among 47 genotypes, which they were grouped into nine distinct clusters based on D<sup>2</sup> statistic. The estimates of intra- and inter-cluster D<sup>2</sup> values for nine clusters revealed that the genotypes of the same cluster have little genetic divergence from each other with respect to aggregate effects

of 20 characters under study while much more genetic diversity was observed between the genotypes of different clusters. Since, high or optimum genetic divergence is required between the parents of hybridization plan for obtaining high frequency of desirable recombinants, the chances of obtaining good segregants in the segregating generations. It would be logical to attempt crosses between the diverse genotypes belonging to clusters separated by large inter-cluster D<sup>2</sup> values. This clearly showed presence of wide variation from one cluster to another in respect of cluster mean for nine clusters, which indicate that genotypes having distinctly different mean performance for various characters were separated into different clusters.

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