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GENETIC DIVERGENCE IN FODDER RICEBEAN (*VIGNA UMBELLATA*)

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SUMMARY

Eighty-five ricebean genotypes were analyzed for genetic divergence which resulted in six clusters having maximum inter-cluster distance between cluster II and VI and least between clusters I and V. Maximum intra-cluster distance was exhibited by cluster VI followed by cluster IV. 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.

Key words : Genetic divergence, D^2 analysis, cluster analysis, ricebean, fodder yield

Foliage of ricebean (*Vigna umbellata*) is of high value nutritive animal fodder. It belongs to the family of peas and beans and hence it is rich in protein which is at par with cowpea and blackgram. Therefore, it plays an important role in dairy and meat production being an important source of protein, energy, fiber and micronutrients.

Planning and execution of the breeding objectives largely depend upon the extent of genetic variability. Breeding programme primarily aims at improving the yield components and the pre-requisite for its success is the knowledge of nature and degree of divergence in the existing germplasm. Hence, information on genetic diversity was used to identify putative genotypes, which may be used as parents in various breeding strategies.

MATERIALS AND METHODS

The experiment was laid out in randomized complete block design with three replications having plot size 3 x 0.9 m and keeping row to row distance 30 cm. The experiment was conducted at Seed Breeding Farm, Department of Plant Breeding and Genetics, JNKVV, Jabalpur (M. P.), India. The germplasm consisted of 85 genotypes. Sowing of seeds of each genotype was done in **kharif** 2015 in each replication. At 50 per cent flowering stage, five competitive plants were tagged from each replication of each germplasm and data were recorded for days to flower initiation, days to 50 per cent flowering, plant height (cm), number of leaves per plant, leaf area (cm^2), number of branches, stem diameter (mm), root length (cm), root volume (ml), root nodules, fresh root weight (g), dry root weight (g), green fodder yield per plant (g), green fodder yield per plant per day (g), dry fodder yield per plant (g), dry fodder yield per plant per day (g), crude protein yield per plant (g), crude protein yield per plant per day (g) and leaf : stem ratio. Estimation of degree of divergence was analyzed by Mahalanobis (1936) D^2 statistics between different pairs of genotypes. While method suggested by Rao (1952) was followed for computing D^2 values and for determining group constellations.

RESULTS AND DISCUSSION

The analysis of variance showed highly significant differences within the population for all the 19 characters studied. This suggested that the genotypes under investigation consisted of appreciable amount of diversity and also indicated that this material

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TABLE 1
Cluster composition based on D^2 statistics in ricebean genotypes

Cluster No.	No. of genotypes	Genotypes
I	72	JRO 15-2, JRBJ 07-1, JRO 15-5, BFRB-3, BFRB 3-1, KRB 86, KRB 99, KRB 99-1, BFRB 52, BFRB 6-1, BFRB 7, BFRB 7-1, KRB 102, KRB 136-1, KRB 167, BFRB 8-1, JRB 6, BFRB 9, KRB 19-1, BFRB 16, KRB 128, KRB 235, KRB 239, KRB 239-1, KRB 239-2, JRB 06-1-1, JRB 06-2, JRB 06-2-1, JRB 06-3, JRB 06-5-1, JRB 06-7, JRB 06-8-1, JRB 06-11, JRB 06-10, JRB 06-114, JRB 04-1, JRB 07-1, JRB 07-2, JRB 07-2-2, JRB 07-2-3, JRB 07-4-1, JRB 07-4-2, JRB 07-33, JRB 07-33-2, JRB 07-35-1, JRB 07-35-2, JRB 07-38-2, JRB 07-39-2, JRB 07-42-1, JRB 07-43-2, JRB 07-43-3, JRB 07-43-4, JRB 07-48-1, JRB 07-49-1, JRB 07-50-1, JRB 07-50-2, JRB 07-51-1, JRB 07-28-2, JRB 07-22, JRB 07-22-1, JRB 08-6-2, JRB 10-1, JRB 10-2-1, JRB 11, JRB 12, JRB 13, JRB 14-1, JRB 14-2, JRBJ 15, BL 6, JRBJ 16, BIDHAN 2
II	3	JRB 08-6, JRB 08-6-1, JRB 07-4
III	3	JRB 06-4, JRB 06-4-1, KRB 136
IV	3	JRO 15-1, JRO 15-4, JRO 15-3
V	1	JRB14
VI	3	JRO 15-6, KRB 86-1, JRB 07-35-3

was appropriate for estimation of further analysis. On the basis of D^2 values, the 85 genotypes were grouped into six clusters following Tocher's method. The cluster I, the largest cluster, was polygenotypic (72 genotypes) followed by clusters II, III, IV and VI, with three genotypes each and cluster V with one genotype. Significant amount of variability can be inferred from the pattern of group constellation (Table 1 & Fig. 1). This revealed that pattern of clustering of genotypes did not depend upon its geographical origin. It means the genotypes from same geographical origin do not group together i. e. genetic constituent of the genotypes is dominant. Clustering between genetic diversity and geographical diversity was in agreement with Roquib and Das (1995), Singh *et al.* (1999) and Basavaprabhu *et al.* (2013).

The inter- and intra-average distance among six clusters were computed and presented in Table 2 & Fig. 2. The highest inter-cluster divergence was observed between genotypes of clusters II and VI (D^2=1364.11) followed by clusters V and VI (D^2=1302.31), clusters III and VI (D^2=1269.89), clusters IV and VI (D^2=1157.10), whereas least inter-cluster divergence was observed between genotypes of clusters I and V (D^2=485.21). The intra-cluster distance was highest in the cluster VI (404.87) followed by cluster IV (291.03). It can be observed that the intra-cluster distance is much less than the inter-cluster distance, indicating homogeneity within the clusters and heterogeneity between the clusters.

TABLE 2
Average intra (diagonal and bold) and inter-cluster distance (D^2) values in ricebean

Clusters	I	II	III	IV	V	VI
I	**159.81**	556.94	491.33	630.43	485.21	1149.75
II		**166.21**	1034.76	913.93	996.44	1364.11
III			**85.67**	657.66	729.02	1269.89
IV				**291.03**	926.88	1157.10
V					**0.00**	1302.31
VI						**404.87**

Analysis of cluster mean (Table 3) revealed that cluster VI had highest mean value for green fodder yield per plant (1.445 kg), number of leaves per plant (1249.34), plant height (235.17 cm), days to 50 per cent flowering (161), number of branches per plant

TABLE 3
Cluster mean for characters in ricebean

Cluster	Days to flower initiation	Days to 50% flowering	Plant height (cm)	No. of leaves/ plant	Leaf area (cm^2)	No. of branches/ plant	Stem diameter (mm)	Root length (cm)	Root volume (ml)	Nodules/ plant	Fresh root weight (g)	Dry root weight (g)	Green fodder yield/ plant	Green fodder yield/ plant/ day (g)	Dry matter yield/ plant (g)	Dry matter yield/ plant/ day (g)	Crude protein yield/ plant (g)	Crude protein yield/ plant/ day (g)	Leaf : stem ratio
I	141.34	143.19	182.97	276.99	32.51	6.07	5.71	52.54	17.58	125.03	12.17	3.32	261.63	1.72	48.60	0.34	6.84	0.05	0.61
II	150.78	150.78	174.36	445.24	30.34	6.09	4.76	29.96	10.47	97.25	9.48	1.95	817.89	5.02	157.96	1.05	25.11	0.17	0.74
III	141.56	141.56	160.10	279.30	27.57	5.92	6.69	58.11	47.18	483.61	21.18	8.16	205.69	1.31	37.93	0.27	5.12	0.04	0.60
IV	110.00	108.78	208.47	455.39	37.15	6.22	7.40	75.56	38.78	51.40	19.22	9.67	434.74	3.66	51.65	0.75	12.35	0.11	0.68
V	143.00	143.00	205.02	485.75	28.86	7.49	5.73	30.82	80.43	90.40	6.42	1.49	246.55	1.58	45.72	0.32	5.84	0.04	0.60
VI	126.67	161.00	235.17	1249.34	35.04	11.33	6.22	54.02	28.98	139.03	16.46	5.59	1445.78	10.57	29.29	0.20	4.46	0.03	0.75

(11.33), green fodder yield per plant per day (10.57) and leaf : stem ratio (0.75). Where as leaf area, stem diameter, root length, fresh root weight and dry root weight was highest in cluster IV. Cluster II had highest mean value 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 V had maximum root volume of 80.43 ml, however, cluster III had maximum mean value for nodules per plant (483.61). Difference in relative contribution of different characters (Table 4) for genetic divergence (D^2) was highest for dry root weight (30.00%) followed by dry matter yield per plant (12.94%), nodules per plant (12.69%), crude protein yield per plant (11.88%), root volume (11.37%), green fodder yield per plant (5.29%), fresh root weight (3.5%), root length (2.41%), green fodder yield per plant per day (1.62%), number of leaves per plant (1.57%), days to flower initiation (1.54%), leaf : stem ratio (1.32%), dry matter yield per plant per day (1.23%) and leaf area (1.09%), whereas magnitude of genetic divergence was less than one per cent for stem diameter (0.78%), plant height (0.62), number of branches per plant (0.11) and days to 50 per cent flowering (0.03%). Crude protein yield per plant per day had no contribution towards divergence. Roquib and Das (1995) analyzed different clusters to identify genotypes for crop improvement in ricebean and found 50 per cent flowering had a more profound effect on genetic divergence than other characters under study. It was reported that days to maturity, days to flowering and plant height contributed more towards divergence in ricebean. Nagalakshmi *et al.* (2010) also reported days to 50 per cent flowering in cowpea as important trait towards divergence.

From the present investigation, it can be concluded that parent line selected 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 also 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 could be used to achieve desired segregants for the crossing programme and could broaden the genetic base of future genotypes.

TABLE 4
Per cent contribution of characters towards divergence in ricebean

S. No.	Characters	Times ranked 1st	Per cent contribution of traits towards divergence
1.	Dry root weight (g)	1071	30.00
2.	Dry matter yield/plant (g)	462	12.94
3.	Nodules/plant	453	12.69
4.	Crude protein yield/plant (g)	424	11.88
5.	Root volume (ml)	406	11.37
6.	Green fodder yield/plant (g)	189	5.29
7.	Fresh root weight (g)	125	3.5
8.	Root length (cm)	86	2.41
9.	Green fodder yield/plant/day (g)	58	1.62
10.	No. of leaves/plant	56	1.57
11.	Days to flower initiation	55	1.54
12.	Leaf : stem ratio	47	1.32
13.	Dry matter yield/plant/day (g)	44	1.23
14.	Leaf : area (cm2)	39	1.09
15.	Stem diameter (mm)	28	0.78
16.	Plant height (cm)	22	0.62
17.	No. of branches/plant	4	0.11
18.	Days to 50% flowering	1	0.03
19.	Crude protein yield/plant/day (g)	0	0

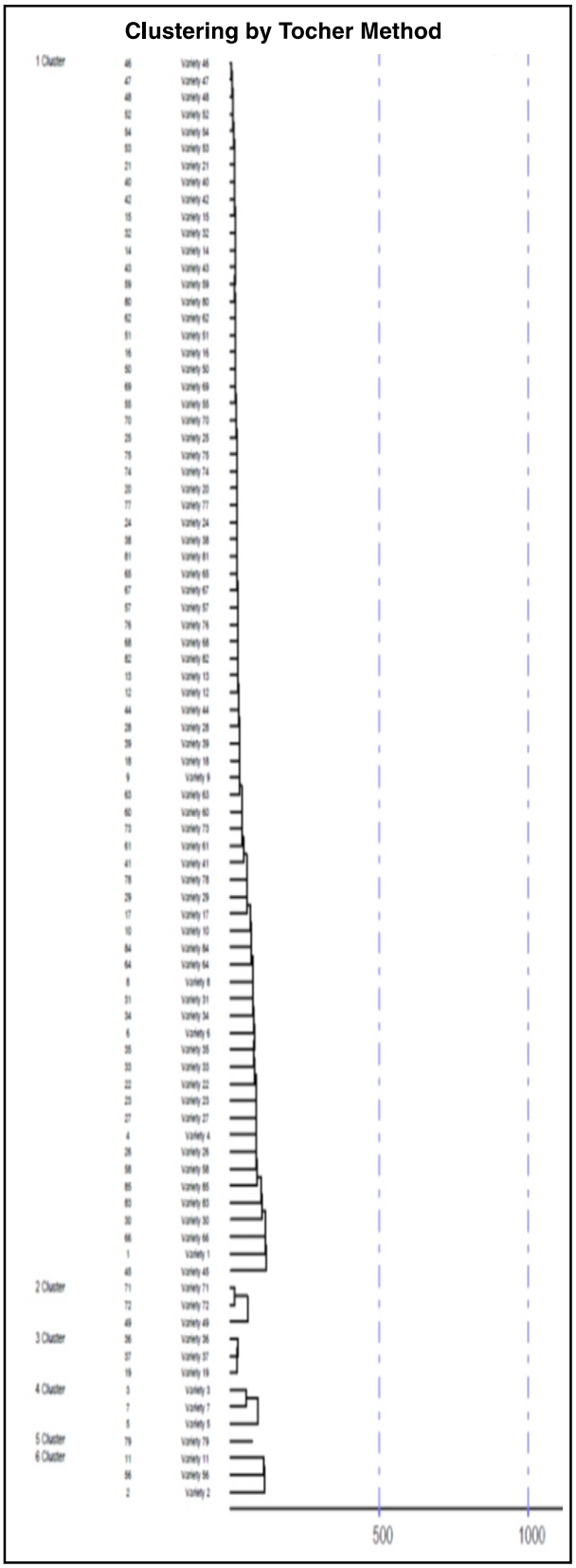

Fig. 1. The dendrogram showing the clustering pattern of 85 genotypes of ricebean.

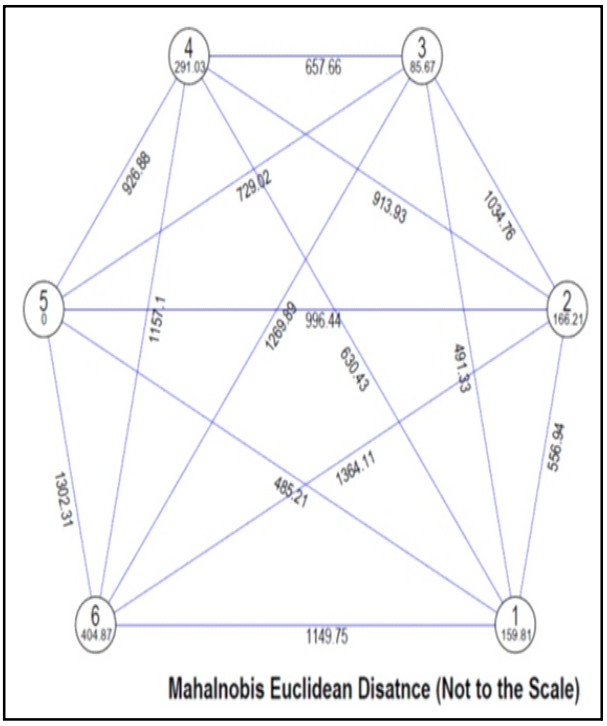

Fig. 2. Cluster diagram showing average intra- and inter-cluster D^2 values of genotypes.

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