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Variability and multivariate analysis in rice bean (*Vigna umbellata* (Thumb) Ohwi and Ohashi)

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Abstract
A field trial of 54 diverse genotypes of rice bean (*Vigna umbellata* (Thumb) Ohwi and Ohashi) was conducted to assess the magnitude of genetic variability, heritability, genetic advance and genetic diversity. The analysis of variance indicated the prevalence of sufficient genetic variation among the genotypes for all the ten traits. High heritability coupled with high phenotypic coefficient of variation (PCV) and high genetic advance as per cent of mean (GA%) were observed for days to 50% flowering, plant height at maturity, seed yield per plant and seed yield per hectare which indicated that response to selection would be very high for these yield components. Mahalanobis' D^2 analysis resulted 10 diverse clusters. Two traits viz,, 1000 seed weight, and days to maturity were contributed more than 83 per cent towards total genetic divergence.

Keywords: Rice bean, genetic variability, heritability, genetic divergence

Introduction
Apart from the traditional tropical legumes like chickpea, pigeonpea, mung bean, lentil and peas etc. rice bean (*Vigna umbellata* (Thumb) Ohwi and Ohashi) is one of the legume so identified and gaining attention as supplementary food crop in India (Chandel and Singh, 1984) [5]. In India rice bean is known by various common names like Ghurush,
Meth, Paumia, Shiltong, Sitamash, Rajmung, Khasiamung in various regions. It is also known as Japanese rice bean, climbing mountain bean and the Jerusalem pea etc. Rice bean is native of South East Asia (Burkill, 1935) [3] and grown in India, Burma, Malaysia, China, Korea, Indonesia and Phillipines. It is also cultivated to a limited extent in West Indies, U.S.A. Queensland (Australia) and in East Africa (Burkill, 1935) [3]. Rice bean is truly diploid species with 2n =22 (Sarbhoy, 1978) [13]. In India, rice bean is distributed mainly to the tribal regions of North-Eastern hills, Western and Eastern Ghats in Peninsular India, often hilly tracts.
This is emerging pulse crop with high nutritional qualities. It is rich in protein (20-24%), fat (0.6%), having 59 per cent carbohydrate and 5.2% fiber (Chauhan 1981) [7]. The amino acid profile of rice bean has been reported to have the highest amount of methionine, lysine, histidine and stands top with respect to cysteine, arginine, leucine, tryptophan, tyrosine and valine content among all legumes of worlds economic importance (Duke, 1981) [8]. Because of these facts, the nutritional quality of rice bean is better than traditional pulse (Chandel *et al.* 1978 a & b). The total starch content of rice bean varieties is higher than that of green gram and black gram. It is used as a food, fodder, green manure and cover crop (Thomas *et al.* 1983) [14]. It's distribution pattern indicates it's adaptive polymorphism for diverse distributional range with climatic variation ranging from humid sub tropical to warm cool temperate climate. It is moderately drought tolerant and photo-thermo-sensitive in terms of flowering and reproduction.
The morphological characterization of germplasm is needed to understand the genetic variation since a wide range of genetic variation among parents is essential for hybridization programmes. Nature and magnitude of genetic variability and heritability in a population as genetic and non-genetic factors is pre-requisites in any successful hybridization programme to get desirable segregants. Arunachalam (1981) [2] stated that multivariate analysis using Mahalanobi's "D^2" statistic is a powerful tool to know the clustering pattern to establish the relationship between genetic and geographical divergence and to determine the role of different quantitative characters towards total genetic divergence. Hence, the present experiment was planned on variability analysis along with genetic divergence using 54 genotypes of rice bean.

Material and methods

The experimental material comprised of 54 diverse rice bean genotypes collected from Plant Breeder, AICRP on Underutilized Crops, Mahatma Phule Krishi Vidyapeeth, Rahuri (Table 1). The material was evaluated in randomized block design with two replications at All India Co-ordinated Research Project on Underutilized Crop field, Department of Botany, Mahatma Phule Krishi Vidyapeeth, Rahuri during *kharif -2012*. Each plot consisted of two row plot of 3.0 m length with inter and intra row spacing of 30 cm and 15 cm, respectively. All the recommended agronomical package of practices and plant protection measures were followed timely to raise a good crop.

The observations were recorded on five randomly selected competitive plants for ten traits viz., days to 50 per cent flowering, days to maturity, plant height, length of pod, number of pods per cluster, number of seeds per pod, number of branches per plant, seed yield per plant, 1000 seed weight and seed yield per hectare. The genotypic and phenotypic coefficient of variation was estimated as per Burton (1952) [4], while heritability in broad sense and expected genetic advance were estimated as per Allard (1960) [1]. Genetic diversity was calculated using Mahalanobis (1936) [10] D^2 statistic and genotypes were grouped into clusters by Tocher's method as described by Rao (1952) [12].

Results and discussion

Analysis of variance revealed highly significant differences among the genotypes for all the ten characters indicating the existence of sufficient variability in the material studied. The experimental material showed wide range of phenotypic variation for days to 50% flowering, plant height at maturity (cm), seed yield per plant (g) and seed yield per hectare (q) as revealed by high values of coefficient of range.

Variability Analysis: The values of phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV), in most of the cases (Table 2). However, low differences were also observed between PCV and GCV for most of the cases, which revealed that these all traits were comparatively less influenced by the environments. The values of GCV and PCV were highest for seed yield per plant followed by seed yield per hectare, plant height at maturity and days to 50% flowering indicating the presence of wide variation for these traits to allow selection for individual traits. Moderate estimates of GCV and PCV were observed days to maturity, number of pods per cluster, number of seeds per pod, number of branches per plant and 1000 seed weight, while low estimates of GCV and PCV was observed for length of pod indicated narrow genetic variability for this characters. These results are in agreement with the findings of Chaudhari *et al.*, (2000) [6].

The coefficient of variation indicated only the extent of variability present for different characters and did not indicate the heritable portion. To obtain the heritable portion of variability, it was essential to know the heritability estimates for different traits (Burton, 1952) [4]. Johnson *et al.* (1955) [9] suggested that the heritability estimate along with genetic advance is more useful than the heritability alone in predicting the resultant effect of selection. In the present study, the estimates of high heritability coupled with high genetic advance as per cent of mean was observed for days to 50% flowering, days to maturity, plant height at maturity, seed yield per plant and seed yield per hectare indicated preponderance of additive gene action and selection pressure could profitably be applied on these characters for improving the seed yield (Panse, 1957). On the other hand, high to moderate heritability along with low GCV and low genetic gain were observed for length of pod, number of pods per cluster, number of seeds per pod and number of branches per plant, which indicated that these four traits were regulated by non-additive gene action and presence of high genotypic x environment interaction.

Multivariate Analysis: Multivariate analysis using Wilk's 'JT criterion was carried out to test the differences among 54 genotypes for aggregate of 10 characters. The value of V-statistic (2673.87) which follows X^2 distribution for 583 degrees of freedom showed highly significant differences among the genotypes for aggregate of 10 characters. Thus, one can proceed for further diversity analysis. The "D" values computed for 1431 pairs ranged from 4.03 (between LRB-456 and RBL-50) to 109.20 (between RRBG-11-07 and LBR-470) indicated the presence of high genetic diversity among the genotypes for all the traits.

On the basis of "D" values, the genotypes were grouped into 10 clusters so that genotypes within a cluster had smaller D^2 values among themselves than those belonging of different clusters (Table 3). The cluster IV was largest having 22 genotypes. Likewise, cluster I, II, III and VIII comprised of 11, 7, 6 and 3 genotypes, respectively. The cluster V, cluster VI, cluster VII, cluster IX and cluster X had monogenotypic. The genotypes included in the monogenotypic clusters possess wide variation from rest of the genotypes as well as from each other indicating the genetic diversity in their constitution. The clustering pattern of genotypes showed that their genetic origin was totally independent. Murty and Arunachalam (1966) [11] also stated that genetic drift and selection in varied environments could cause greater diversity than geographic distance. Further, free exchange of seed materials among the different regions consequently causes characters constellations because of the human interference and material may lose its individuality.

In general, intra cluster distances were lower than the inter cluster distances (Table 4). Thus, the genotypes included within a cluster tended to diverse less from one another. The intra cluster distance was ranged from (10.87 in cluster I) to (16.74 in cluster IV). The maximum inter-cluster distance (D) was observed between cluster VIII and IX (D= 103.71) followed by that between cluster III and VIII (D=89.70), while the closest proximity was noticed between cluster V and VII (D=11.19). The genotypes belonging to the clusters separated by high statistical distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregates. In this context, genotypes from cluster III (LRB-458, LRB-467, LRB-465, LRB-456, LRB-480 and LRB-478), cluster V (RRBG-11-13), cluster VII (RRBG-11-02), cluster VIII (RRBG-11-23, RRBG-11-23-3 and RRBG-11-07) and cluster IX (LRB-464) could be selected as parents in hybridization programme.

The clustering pattern could be utilized in selection of parents for crossing and deciding the best cross combinations which may generate the highest possible variability for various traits. In the present study, cluster IV was the best for number of branches per plant and seed yield per hectare. The cluster V was good for number of pods per cluster, and seed yield per hectare while cluster VI was good for length of pod. The cluster VII differed from other clusters (Table 5) in respect of days to 50% flowering and days to maturity, while cluster VIII was the best for plant height, number of seeds per pod,

seed yield per plant and seed yield per hectare. The cluster IX had desirable rating for 1000 seed weight and seed yield per hectare in early maturing genotypes in comparisons to the cluster I, II, III, VI and X.

An assessment of contribution of different characters towards total genetic divergence (Table 5) was showed a very wide range of contribution. Out of 10 characters, 1000 seed weight (55.35%) contributed highest for genetic divergence. It was followed by days to maturity (27.67%), length of pod (5.24%), plant height at maturity (3.77%) and days to 50 per cent flowering (3.00).

Hence, selection of divergent parents based on these five traits would be useful for hybridization programme followed by isolation of desirable transgressive segregants in rice bean. While other character contributed very less in genetic diversity viz., seed yield per plant (1.54%), seed yield per hectare (1.47), number of branches per plant (0.91%) and number of pods per cluster (0.56%) contributed least in genetic diversity followed by number of seeds per pod (0.49%) each. Similar findings were also reported by Chaudhari *et al.*, (2000) [6].

Overall, it can be concluded that high heritability along with high GCV and high genetic gain were observed for days to 50% flowering, plant height at maturity, seed yield per plant and seed yield per hectare which might be attributed to additive gene action in their inheritance and phenotypic selection could be effective. Maximum contribution of 1000 seed weight (g), followed by days to maturity, length of pod and plant height at maturity were observed on total genetic divergence. Hence due consideration should be given to these traits while imposing selection for amenability in seed yield per hectare in rice bean.

Table 1: List of rice bean genotypes used

Sr. No.	Genotypes	Sr. No.	Genotypes	Sr. No.	Genotypes
1.	RRBG-11-02	19.	RRBG-11-35	37.	LRB-464
2.	RRBG-11-03	20.	RRBG-11-36	38.	LRB-465
3.	RRBG-11-04	21.	RRBG-11-37	39.	LRB-467
4.	RRBG-11-05	22.	RRBG-11-37-1-2	40.	LRB-470
5.	RRBG-11-07	23.	RRBG-11-39	41.	LRB-472
6.	RRBG-11-11	24.	RRBG-11-40	42.	LRB-477
7.	RRBG-11-13	25.	RRBG-11-40-1-3	43.	LRB-478
8.	RRBG-11-14	26.	LRB-319	44.	LRB-480
9.	RRBG-11-16	27.	LRB-325	45.	LRB-481
10.	RRBG-11-18	28.	LRB-447	46.	LRB-482
11.	RRBG-11-20	29.	LRB-448	47.	LRB-484
12.	RRBG-11-23	30.	LRB-455	48.	LRB-487
13.	RRBG-11-23-3	31.	LRB-456	49.	RBL-1 (C)
14.	RRBG-11-25	32.	LRB-457	50.	RBL-6 (C)
15.	RRBG-11-27	33.	LRB-458	51.	RBL-35 (C)
16.	RRBG-11-30	34.	LRB-459	52.	RBL-50 (C)
17.	RRBG-11-32	35.	LRB-460	53.	Chandrapur local
18.	RRBG-11-34	36.	LRB-463	54.	Bhandara local

Table 2: Phenotypic range, coefficient of range, phenotypic and genotypic coefficient of variation, heritability, genetic advance and genetic advance expressed as per cent of mean for various characters in rice bean

Sr. No.	Character	Range	CD at 5%	Mean ± S.E.m	GCV %	PCV %	Heritability (b.s.) (%)	Genetic advance	G.A. as % of mean
1.	Days to 50% flowering	55.50 - 121.50	2.834	88.268 ± 0.989	34.08	34.12	99.78	61.9	70.13
2.	Days to maturity	101.50 - 179.00	3.548	135.231 ± 1.239	24.83	24.86	99.72	69.07	51.07
3.	Plant height at maturity (cm)	55.50 - 177.00	6.194	115.833 ± 2.164	36.28	36.38	99.46	86.34	74.53
4.	Length of pod (cm)	6.70 - 9.66	0.212	7.845 ± 0.074	9.14	9.24	97.91	1.46	18.62
5.	Number of pods per cluster	2.16 - 5.12	0.251	3.380 ± 0.087	22.91	23.20	97.56	1.58	46.58
6.	Number of seeds per pod	6.08 - 10.02	0.415	7.971 ± 0.145	15.20	15.42	97.15	2.46	30.86
7.	Number of branches per plant	2.10 - 5.95	0.376	4.199 ± 0.131	21.50	21.96	95.88	1.82	43.37
8.	1000 seed weight (g)	35.90 - 70.00	0.642	49.859 ± 0.224	14.78	14.79	99.81	15.17	30.42
9.	Seed yield per plant (g)	1.73 - 16.24	1.287	7.085 ± 0.449	65.42	66.04	98.12	9.46	133.49
10.	Seed yield per hectare (q)	3.83 - 35.56	1.613	15.432 ± 0.563	64.28	64.49	99.35	20.37	131.99

Table 3: Grouping of 54 genotypes of rice bean on the basis of D^2 statistic in various clusters

Cluster Number	Number of genotype included	Genotypes
I	11	LRB-448 (29), RBL-1(49), LRB-487(48), LRB-460 (35), LRB-472(41), LRB-481(45), Chandrapur local (54), LRB-484 (47), LRB-319 (26), LRB-470 (40), Bhandara Local (53)
II	7	LRB-325 (27), LRB-477 (42), LRB-447(28), LRB-455 (30), RBL-6 (50), LRB-463 (36), LRB-482 (46)
III	6	LRB-458 (33), LRB-467 (39), LRB-465(38), LRB-456 (31), LRB-480 (44), LRB-478 (43)
IV	22	RRBG-11-18 (10), RRBG-11-37-1-2 (22), RRBG-11-03 (2), RRBG-11-40 (24), RRBG-11-04 (3), RRBG-11-30 (16), RRBG-11-14 (8), RRBG-11-20(11), RRBG-11-25 (14), RRBG-11-27 (15), RBL-50 (52),RRBG-11-36(20), RRBG-11-32 (17), RBL-35 (51), RRBG-11-16 (9), RRBG-11-05 (4), RRBG-11-40-1-3 (25), RRBG-11-35 (19), RRBG-11-11 (6), RRBG-11-37 (21), RRBG-11-34 (18), RRBG-11-39 (23).
V	1	RRBG-11-13 (7)

VI	1	LRB-457 (32)
VII	1	RRBG-11-02 (1)
VIII	3	RRBG-11-23 (12), RRBG-11-23-3 (13), RRBG-11-07 (5)
IX	1	LRB-464 (37)
X	1	LRB-459 (34)

( ) denote serial number of genotype as per table1

Table 4: Average inter and intra- cluster distance (D and D^2) values in rice bean

Cluster Distances	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X
Cluster I	10.87 (118.15)	24.18 (584.67)	23.98 (575.04)	61.10 (3733.21)	54.64 (2985.53)	15.93 (253.76)	54.85 (3008.52)	73.93 (5465.64)	40.30 (1624.09)	41.14 (1692.50)
Cluster II		11.21 (125.66)	44.38 (1969.58)	56.47 (3188.86)	56.56 (3199.04)	28.11 (790.17)	55.91 (3125.92)	63.39 (4018.19)	61.46 (3777.33)	21.03 (442.26)
Cluster III			12.93 (167.18)	73.68 (5428.74)	62.70 (3931.29)	25.18 (634.03)	63.66 (4052.59)	89.70 (8046.09)	20.75 (430.56)	61.91 (3832.85)
Cluster IV				16.74 (280.22)	21.46 (460.53)	63.26 (4001.82)	21.78 (474.36)	26.95 (726.30)	86.28 (7444.23)	56.92 (3239.89)
Cluster V					0 (0.0)	55.92 (3127.04)	11.19 (125.21)	40.29 (1623.28)	72.79 (5298.38)	62.67 (3927.53)
Cluster VI						0 (0.0)	58.59 (3432.78)	74.92 (5613.01)	39.08 (1527.25)	45.42 (2062.98)
Cluster VII							0 (0.0)	41.40 (1713.96)	74.50 (5550.25)	60.89 (3707.59)
Cluster VIII								15.76 (248.38)	103.71 (10755.76)	58.33 (3402.39)
Cluster IX									0 (0.0)	79.31 (6290.08)
Cluster X										0 (0.0)

Table 5: Cluster means for different characters in rice bean

Cluster Means	Days to 50% flowering	Days to maturity	Plant height (cm)	Length of pod (cm)	Number of pods per cluster	Number of seeds per pod	Number of branches per plant	1000 seed weight (g)	Seed yield per plant (g)	Seed yield /ha. (q)
Cluster I	58.95	102.14	78.47	7.37	2.57	6.90	3.55	54.50	2.86	6.39
Cluster II	58.57	102.21	72.21	7.44	2.67	6.80	3.21	46.54	2.49	5.59
Cluster III	57.33	102.00	78.57	7.43	2.72	6.93	3.63	62.49	3.03	6.67
Cluster IV	117.89	168.05	154.85	8.13	4.08	9.01	4.98	45.86	11.23	24.29
Cluster V	118.50	172.00	159.60	8.55	4.20	9.30	4.40	52.75	11.50	24.15
Cluster VI	56.00	102.00	92.80	9.25	3.45	8.20	3.30	55.25	3.10	7.05
Cluster VII	121.50	174.00	144.80	7.35	3.65	7.80	4.40	52.45	8.95	19.65
Cluster VIII	117.67	167.17	163.93	8.95	4.08	9.55	4.53	37.62	12.98	28.32
Cluster IX	62.00	102.50	63.70	8.15	2.90	7.25	3.70	70.00	3.05	7.25
Cluster X	59.50	102.50	55.50	6.85	3.15	6.05	4.60	40.00	3.00	6.50
% Contribution towards total genetic divergence	3.00%	27.67%	3.77%	5.24%	0.56%	0.49%	0.91%	55.35%	1.54%	1.47%
Number of times ranked I^{st}	43	396	54	75	8	7	13	792	22	21

Authors' contribution

Conceptualization of research (GAS, SSD); Designing of experiments (GAS, SSD, VPC); Contribution of experimental material (GAS, SSD, VPC); Execution of field/lab experiments and data collection (GAS, SSD, VPC); Analysis of data and interpretation (GAS, SSD, NMM); Preparation of manuscript (SSD, VPC).

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