

GENETIC VARIABILITY IN RICE BEAN (*VIGNA UMBELLATA* THUNB.) FOR IMPORTANT QUANTITATIVE CHARACTERISTICS

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SUMMARY

The current experiment was conducted in the Instructional-Cum-Research Farm, Assam Agricultural University, Jorhat, Assam during *Rabi* 2018 to study the genetic variability and yield performance of fourteen rice bean genotypes grown in Randomized Block Design with two replications. The observations were recorded for twenty-six quantitative characters *viz.*, plant height, primary branches per plant, secondary branches per plant, stem diameter, stem length, seed yield per plot, leaf length, leaf breadth, leaf area, leaf-stem ratio, 100 seed weight, pod length, pod breadth, seed length, seed breadth, seeds per pod, specific gravity of seeds, days to 50% flowering, days to maturity, green forage yield per plant, dry matter yield per plant, productive racemes per plant, pods per raceme, crude protein %, crude fibre % and ash %. The analysis of variance revealed that there was significant difference among all the genotypes for all the characters. The estimates of genotypic coefficient of variation and phenotypic coefficient of variation were observed to be high for stem length, leaf-stem ratio, productive racemes per plant and seed yield per plant. High heritability coupled with high genetic advance as per cent of mean was observed for stem length, leaf area, 100 seed weight, pod length, seed breadth, leaf-stem ratio, productive racemes per plant and seed yield per plant indicating the preponderant influence of additive gene effects.

Key words : Rice bean, genetic variability, genotypic coefficient of variation, phenotypic coefficient of variation, heritability

Rice bean (*Vigna umbellata* Thunb.) is a warm season vine legume. It is also known as red bean and climbing mountain bean. It is a multipurpose legume, once in a while considered as neglected and underutilised (Joshi *et al.*, 2008). Though rice bean is least important than cowpea and mung bean, it is locally important contributor to human and animal nutrition (Joshi *et al.*, 2008; Tomooka *et al.*, 2011). Originated from Indo-China, it was presumably domesticated in Thailand and neighbouring areas (Tomooka *et al.*, 2011). It is normally found in India, central China and in the Indochinese Peninsula. It is currently cultivated in tropical areas of Asia, Fiji, Australia, tropical Africa, the Indian Ocean Islands as well as in the Americas (USA, Honduras, Brazil and Mexico).

The rice bean plant as a whole is completely edible and is very useful as feed for livestock. The rice bean seeds can be used as fodder and vegetative portion can be used as feed directly. Also rice bean is a lean period crop that supports the farmers with

continuous fodder supply to the animals all round the growing season (Janjal and Mehta, 2019). Rice bean is also cultivated for green manure, it can also be used as a cover crop, prevents soil erosion and improves soil fertility by its nitrogen fixing ability (Ecoport, 2014). Most importantly rice bean has an essential role in improvement of human, animal and soil health as it is a good source of protein, essential amino acids, essential fatty acids and minerals (Mohan and Janardhanan, 1994). It contains up to 24% protein and at vegetative stage it contains 14-19% protein which is at par with cowpea and black gram. Also it is one of the most important pulse crop that is grown all over India.

Rice bean has a lot of scope and variability and has gained importance recently due to its high nutritional quality. Therefore, for developing high yielding varieties genetic improvement of the crop is necessary which points towards gaining knowledge on the genetic parameters. Estimation of the genetic parameters will help in effective selection and

development of high yielding varieties. Therefore, in this research programme detailed study on the crop was done to observe the extent of genetic variability in rice bean genotypes.

MATERIALS AND METHOD

Eleven rice bean genotypes collected from different regions of North-East India along with three check varieties *viz.*, Bidhan Ricebean-1, Bidhan Ricebean-2 and Shyamalima were used for the study. The genotypes used in the current investigation are presented in Table 1.

TABLE 1
List of the genotypes

S. No.	Genotypes	Place of collection
1.	JCR-07-7	Manipur
2.	JCR-08-7	Mizoram
3.	JCR-8-2	Mizoram
4.	JCR-14-1	Assam
5.	JCR-14-3	Assam
6.	JCR-16-1	Manipur
7.	JCR-16-2	Manipur
8.	JCR-16-4	Manipur
9.	JCR-18-1	Arunachal Pradesh
10.	JCR-18-2	Arunachal Pradesh
11.	JCR-18-3	Arunachal Pradesh
12.	Bidhan Ricebean-1	BCKV, Kalyani
13.	Bidhan Ricebean-2	BCKV, Kalyani
14.	Shyamalima	AAU, Jorhat

Observations recorded

Five plants were randomly chosen from each plot for every genotype and were tagged for recording observations on the following characters *viz.*; plant height (cm), number of primary and secondary branches per plant, stem diameter(cm), stem length (cm), leaf length (cm), leaf breadth (cm), leaf area (cm²), leaf-stem ratio, 100 seed weight (gm), pod length (cm), pod breadth (cm), seed length (cm), seed breadth (cm), seeds per pod, specific gravity, days to 50% flowering, days to maturity, green forage yield per plant (gm), dry matter yield per plant(gm), productive racemes per plant, pods per raceme, crude protein percentage, crude fibre content (%), ash content(%) and seed yield per plant (gm).

Data analysis

Analysis of variance and all the genetic parameters including genetic variance, phenotypic

variance, genotypic coefficient of variation, phenotypic coefficient of variation, heritability and genetic advance was calculated by using computer software OPSTAT.

$$\text{Genetic variance } \sigma^2_g = \frac{\text{MSg} - \text{MSer}}{r}$$

Where, MSg = Mean square due to genotype

MSe = Mean square due to error

r = number of replications

Phenotypic variance (σ^2_p) = $\sigma^2_g + \sigma^2_e$

Where, σ^2_e = error variance or error mean square (MSe)

$$\text{Genotypic coefficient of variation (GCV)} = \sqrt{\frac{\sigma^2_g}{x}}$$

$$\text{Phenotypic coefficient of variation (PCV)} = \sqrt{\frac{\sigma^2_p}{x}} \times 100$$

Where, x = grand mean for phenotypic traits

$$\text{Heritability } h^2 = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Expected genetic advance (GA) = $k \cdot \sigma_p \cdot h^2$

Where, k = standardized selection differential (k = 2.06 at 5% selection intensity)

σ_p = Phenotypic standard deviation

$$h^2_{bs} = \text{Heritability in broad sense} = \frac{\sigma^2_g}{\sigma^2_p}$$

$$\text{Genetic advance as percent of population mean} = \frac{\text{GA}}{x} \times 100$$

Where, X = Mean of base population

RESULT AND DISCUSSION

The results of analysis of variance for different yield attributing characters have been presented in Table 2. The results indicated that there were significant differences among the rice bean genotypes that were used in the present study. This indicated that there was real difference among the genotypes under study. Shitiri *et al.* (2018) reported wide range of genetic variability among the genotypes for all the characters

TABLE 2
Analysis of variance for forage and grain yield characters in ricebean

Source of variation	d. f.	Mean squares												
		Plant height (cm)	Primary branches/plant	Secondary branches/plant	Stem diameter (cm)	Stem length (cm)	Leaf length (cm)	Leaf breadth (cm)	Leaf area (cm ²)	100-Seed weight (g)	Pod length (cm)	Pod breadth (cm)	Seed length (cm)	Seed breadth (cm)
Replication	1	3.148	0.070	0.756	0.001	3.036	0.778	0.039	82746.87	0.128	0.223	0.000	0.000	0.000
Genotypes	13	384.657**	0.351**	0.902*	0.010**	20.825**	3.383**	0.518**	551621.31**	4.557**	4.658**	0.008**	0.027**	0.010**
Error	13	8.556	0.020	0.241	0.001	1.515	0.205	0.040	24824.34	0.173	0.112	0.001	0.002	0.001
CD (5%)		6.384	0.311	1.062	0.095	2.659	0.980	0.432	343.900	0.900	0.724	0.078	0.087	0.065
CV (%)		3.122	4.933	8.090	8.154	12.581	4.830	5.379	5.335	5.515	3.727	6.741	5.500	7.861

Source of variation	d. f.	Mean squares									
		Seeds/pod	Specific gravity	Leaf stem ratio	Productive racemes/plant	Pods/raceme	Days to 50% flowering (days)	Days to maturity (days)	Green forage yield (g)	Crude protein (%)	Crude fibre (%)
Replication	1	0.006	0.000	0.036	0.103	0.103	3.571	8.035*	55.723	0.070	0.001
Genotypes	13	2.376**	0.002*	0.189**	61.475**	0.787**	111.054**	191.442**	468.421**	6.909**	0.972**
Error	13	0.109	0.000	0.017	1.399	0.090	2.417	1.574	22.933	0.435	0.051
CD (5%)		0.712	0.044	0.278	2.555	0.648	3.359	2.710	10.345	1.424	0.489
CV (%)		4.220	1.644	9.307	7.183	4.709	1.542	0.857	4.060	4.428	1.924

*Significant at 5% probability level, **Significant at 1% probability level.

which included days to 50% flowering, primary branches per plant, pods per cluster, pod length, number of seeds per pod, plant height and 100 seed weight in rice bean. Janjal and Mehta (2019) reported wide range of variation for all the yield attributing characters which included plant height, number of primary branches per plant, stem diameter, leaf area, dry matter yield per plant, leaf-stem ratio, crude protein% and green forage yield per plant in rice bean.

The assessment of phenotypic and genotypic coefficient of variation, heritability in broad sense and expected genetic advance (as% of mean) for all the characters has been presented in Table 3. The magnitude of phenotypic coefficient of variation (PCV) was observed to be higher than the genotypic coefficient of variation (GCV) in the present study, showing us the role of environmental influence on the traits. Pandey *et al.* (2015), Lakshmana *et al.* (2010), Janjal and Mehta (2019) and Shitiri *et al.* (2019) also observed higher PCV as compared to GCV in rice bean genotypes showing the influence of environment on the characters.

High GCV estimates were observed for stem length, leaf-stem ratio, productive racemes per plant and seed yield per plant. Moderate estimates of GCV were observed for plant height, primary branches per plant, stem diameter, leaf length, leaf breadth, leaf area, 100 seed weight, pod length, pod breadth, seed length, seed breadth, seeds per pod, green forage yield per plant, dry matter yield per plant and crude protein %. This indicated that there was sufficient amount of genetic variability among these characters which can be exploited by breeding procedure for the improvement of these traits. Low estimates of GCV were observed for secondary branches per plant, specific gravity, pods per raceme, days to 50% flowering, days to maturity, crude fibre % and ash %. Janjal and Mehta (2019) also observed high GCV for leaf-stem ratio and moderate GCV for stem diameter and plant height in rice bean. Borah and Khan (2000) also observed low GCV for days to 50% flowering in cowpea. Dodake and Dahat (2011) observed low GCV for days to maturity in rice bean. Sawant *et al.* (2019) observed moderate estimate of GCV for seeds per

TABLE 3
Estimates of genetic parameters for various characters in ricebean

Characters	Range	Mean \pm SE	GCV (%)	PCV (%)	h ² b.s (%)	GA (% of mean)
Plant height (cm)	77.53-129.00	93.68 \pm 2.96	14.63	14.96	95.64	29.48
Primary branches/plant	2.20-3.60	2.92 \pm 0.14	13.91	14.76	88.83	27.01
Secondary branches/plant	5.00-7.20	6.07 \pm 0.49	9.45	12.44	57.71	14.79
Stem diameter (cm)	0.38-0.60	0.54 \pm 0.04	11.97	14.48	68.32	20.39
Stem length (cm)	5.44-18.02	9.78 \pm 1.23	31.76	34.16	86.43	60.82
Leaf length (cm)	7.41-12.27	9.39 \pm 0.45	13.42	14.26	88.52	26.01
Leaf breadth (cm)	3.08-4.80	3.72 \pm 0.20	13.13	14.19	85.63	25.04
Leaf area (cm ²)	2020.30-3702.60	2953.51 \pm 157.57	17.37	18.17	91.38	34.21
100 seed weight (g)	5.90-11.30	7.55 \pm 0.41	19.60	20.36	92.66	38.86
Pod Length (cm)	7.21-12.27	8.99 \pm 0.33	16.77	17.17	95.29	33.72
Pod Breadth (cm)	0.45-0.67	0.54 \pm 0.03	10.61	12.57	71.25	18.45
Seed Length (cm)	0.59-0.94	0.73 \pm 0.04	15.27	16.23	88.52	29.61
Seed Breadth (cm)	0.29-0.51	0.38 \pm 0.03	17.82	19.48	83.71	33.59
Seeds per pod	6.25-10.00	7.81 \pm 0.33	13.62	14.26	91.24	26.81
Specific Gravity	1.20-1.29	1.23 \pm 0.02	1.97	2.56	58.97	3.11
Leaf-stem ratio	1.08-1.89	1.38 \pm 0.129	21.19	23.14	83.83	39.97
Productive racemes/plant	8.35-26.45	16.46 \pm 1.18	33.28	34.04	95.54	67.01
Pods/raceme	5.20-7.25	6.37 \pm 0.30	9.26	10.39	79.45	17.00
Days to 50% flowering (days)	85.00-114.00	100.78 \pm 1.55	7.31	7.47	95.73	14.74
Days maturity (days)	131.00-164.00	146.25 \pm 1.25	6.66	6.71	98.36	13.61
Green forage yield/plant (g)	96.05-141.35	117.94 \pm 4.78	12.65	13.28	90.66	24.82
Crude protein (%)	12.90-18.15	14.88 \pm 0.65	12.08	12.87	88.16	23.37
Crude fibre (%)	9.45-12.40	11.75 \pm 0.22	5.77	6.08	90.00	11.28
Ash (%)	7.30-9.45	8.30 \pm 0.22	5.94	6.54	82.66	11.13
Seed Yield/plant (g)	5.50-15.50	11.42 \pm 1.31	30.62	32.70	87.63	59.04
Dry matter yield/plant (g)	22.80-35.55	28.20 \pm 1.99	14.54	16.17	80.91	26.96

pod. Devi *et al.* (2018) also observed low estimate of GCV for days to 50% flowering and moderate estimate of GCV for leaf length, seeds per pod, pod breadth and seed length in rice bean. Singh *et al.* (2019) observed moderate estimates of GCV for pod length, seeds per pod and 100 seed weight and low estimates of GCV for days to 50% flowering and days to maturity in rice bean.

High PCV estimates were observed for stem length, 100 seed weight, leaf-stem ratio, productive racemes per plant and seed yield per plant. Moderate PCV estimates were observed for plant height, primary branches per plant, secondary branches per plant, stem diameter, leaf length, leaf breadth, leaf area, pod length, pod breadth, seed length, seed breadth, seeds per pod, pods per raceme, green forage yield per plant, dry matter yield per plant and crude protein %. Low PCV estimates were observed for specific gravity, days to 50% flowering, days to maturity, crude fibre % and ash %. Devi *et al.* (2018) also observed low estimate of PCV for days to 50% flowering, leaf breadth and seed length in rice bean. Sawant *et al.* (2019) observed moderate estimate of PCV for seeds per pod. Singh *et al.* (2019) observed moderate PCV for pod length, seeds per pod and primary branches per plant and low estimates of PCV for days to 50% flowering and days to maturity in rice bean.

The heritability estimates of the genotypes in the present study were found the highest for the traits *viz.*, plant height, primary branches per plant, stem length, leaf length, leaf breadth, leaf area, 100 seed weight, pod length, seed length, seed breadth, seeds per pod, leaf-stem ratio, productive racemes per plant, days to 50% flowering, days to maturity, green forage yield per plant, dry matter yield per plant, crude protein %, crude fibre %, ash % and seed yield per plant. Moderate heritability was observed for stem diameter, pod breadth and pods per raceme. Low heritability was observed for secondary branches per plant and specific gravity. Dash (2012) observed high heritability for days to 50% flowering and dry matter yield per plant in rice bean. Pandey *et al.* (2015) observed heritability to be high for days to 50% flowering, days to maturity and 100 seed weight in rice bean. Devi *et al.* (2018) observed high heritability for 100 seed weight, days to 50% flowering and seeds per pod in rice bean. Singh *et al.* (2019) observed heritability to be high for 100 seed weight, pod length and plant height in rice bean. Shitiri *et al.* (2019) also observed heritability to be high for days to 50% flowering, pod length, seeds per pod, plant height and 100 seed weight in rice bean.

Genetic advance as per cent of mean was observed to be high for characters *viz.*, stem length, leaf area, 100 seed weight, pod length, seed breadth, leaf-stem ratio, productive racemes per plant and seed yield per plant. Moderate estimates of genetic advance were observed for plant height, primary branches per plant, stem diameter, leaf length, leaf breadth, seed length, seeds per pod, green forage yield per plant, dry matter yield per plant and crude protein %. Low estimates of genetic advance were observed for secondary branches per plant, pod breadth, specific gravity, pods per raceme, days to 50% flowering, crude fibre% and ash %. Gupta *et al.* (2009) observed similar results in his study on rice bean. He found genetic advance estimates high for 100 seed weight. Janjal and Mehta (2019) observed high genetic advance estimate for leaf-stem ratio in rice bean. Shitiri *et al.* (2019) observed high genetic advance estimate for 100 seed weight. Devi *et al.* (2018) observed low estimate of genetic advance for days to 50% flowering. Singh *et al.* (2019) observed genetic advance to be high for 100 seed weight and pod length.

High heritability coupled with high genetic advance was observed for characters *viz.*, stem length, leaf area, 100 seed weight, pod length, seed breadth, leaf-stem ratio, productive racemes per plant and seed yield per plant. This also shows that there was predominance of additive gene action. High heritability coupled with moderate genetic advance was observed for plant height, primary branches per plant, leaf length, leaf breadth, seed length, seeds per pod, green forage yield per plant, dry matter yield per plant and crude protein %. Kumari *et al.* (2017) also observed high heritability coupled with high genetic advance for seed yield and 100 seed weight. Shitiri *et al.* (2019) observed high heritability coupled with high genetic advance for 100 seed weight. Singh *et al.* (2019) observed high heritability coupled with high genetic advance for 100 seed weight and pod length.

The mean performances of fourteen genotypes for twenty-six yield attributing characters are presented in Table 4. On the basis of mean performance of the genotypes with respect to the characters, some promising genotypes were identified which have been represented in Table 5.

Among all the rice bean genotypes which were evaluated under the present study, JCR-18-2, JCR-07-7, JCR-14-1 and JCR-14-3 were observed to have high green forage yield, more leaf area, higher number of primary branches per plant and more number of secondary branches per plant. JCR-18-2, JCR-07-7 and JCR-14-1 showed good response with respect to

TABLE 4
Mean performance of ricebean genotypes for forage yield characters

S. No.	Genotype	PH	PB	SB	SD	SL	LL	LB	LA	100SW	Pod L	Pod B	Seed L	Seed B
1.	JCR-07-7	107.28	3.50	7.00	0.60	13.56	7.41	3.40	3576.00	7.95	9.59	0.50	0.80	0.34
2.	JCR-08-7	88.25	2.90	5.90	0.39	9.31	11.13	4.10	3092.85	6.60	7.32	0.48	0.61	0.33
3.	JCR-8-2	96.70	3.00	6.10	0.61	9.70	8.61	3.80	3155.25	6.40	8.28	0.52	0.69	0.38
4.	JCR-14-1	106.08	3.40	6.90	0.57	11.58	9.25	4.16	3406.65	7.30	8.37	0.60	0.71	0.41
5.	JCR-14-3	99.35	3.20	6.60	0.59	11.69	9.70	3.64	3451.25	8.65	12.18	0.45	0.92	0.33
6.	JCR-16-1	90.55	3.00	5.90	0.56	9.43	8.71	3.59	3014.25	6.30	9.06	0.61	0.80	0.47
7.	JCR-16-2	77.53	2.20	5.00	0.57	5.44	12.27	4.81	2020.30	7.65	8.30	0.47	0.61	0.31
8.	JCR-16-4	84.73	2.60	5.70	0.59	7.65	9.37	3.52	2563.50	9.80	8.82	0.68	0.68	0.51
9.	JCR-18-1	88.09	2.80	5.80	0.43	8.01	10.06	4.55	2854.50	7.50	9.44	0.56	0.84	0.44
10.	JCR-18-2	129.00	3.60	7.20	0.57	18.02	10.34	3.44	3702.60	11.30	12.27	0.55	0.95	0.45
11.	JCR-18-3	98.65	3.10	6.50	0.60	10.71	9.61	3.08	3230.75	5.90	8.67	0.61	0.78	0.49
12.	Bidhan RB-1 (NC)	84.73	2.70	5.80	0.56	7.27	8.13	3.19	2712.35	7.55	7.21	0.53	0.60	0.32
13.	Bidhan RB-2 (NC)	79.60	2.40	5.20	0.55	7.23	7.81	3.52	2115.75	6.50	8.09	0.51	0.66	0.30
14.	Shyamalima (LC)	81.10	2.50	5.50	0.43	7.38	9.11	3.30	2453.15	6.35	8.28	0.53	0.63	0.37
	Mean	93.68	2.92	6.07	0.54	9.78	9.39	3.72	2953.51	7.55	8.99	0.54	0.73	0.38
	C.D (5%)	6.32	0.31	1.06	0.09	2.65	0.98	0.43	343.90	0.90	0.72	0.07	0.08	0.06

Table 4. Contd...

S. No.	Genotype	S/P	SG	L:S	Prod R/plt	Pods/R	D50F	DM	GFY	CP%	CF%	Ash%	SY	DMY
1.	JCR-07-7	8.90	1.27	1.89	17.85	6.95	110.00	160.00	137.15	17.20	11.74	8.05	12.00	35.10
2.	JCR-08-7	6.30	1.21	1.23	10.70	5.40	99.00	145.00	111.95	13.30	11.80	8.45	8.50	26.10
3.	JCR-8-2	7.20	1.23	1.19	9.95	6.10	103.50	149.50	124.10	18.10	11.62	7.30	10.00	29.40
4.	JCR-14-1	7.50	1.23	1.81	21.00	6.45	105.00	155.50	136.80	15.20	12.03	8.25	15.50	32.65
5.	JCR-14-3	10.00	1.20	1.78	23.45	7.10	107.50	153.00	132.50	12.90	12.40	7.70	16.00	31.20
6.	JCR-16-1	8.15	1.23	1.25	18.55	6.80	99.50	146.00	118.25	13.80	12.01	8.75	11.50	28.90
7.	JCR-16-2	7.40	1.25	1.09	15.90	6.20	95.00	131.00	96.05	14.20	12.11	8.15	10.50	22.80
8.	JCR-16-4	7.90	1.27	1.19	12.60	6.60	97.00	138.00	106.05	18.15	12.10	8.50	7.00	23.80
9.	JCR-18-1	8.05	1.30	1.22	14.55	6.90	98.50	142.50	111.90	15.50	11.98	8.55	10.00	26.05
10.	JCR-18-2	9.60	1.27	1.89	26.45	7.25	114.00	164.00	141.35	15.75	9.45	9.45	18.00	35.55
11.	JCR-18-3	7.70	1.20	1.34	22.70	6.50	105.00	151.00	126.90	14.90	11.79	8.75	15.50	30.50
12.	Bidhan RB-1 (NC)	6.25	1.21	1.27	11.50	5.20	98.50	140.50	107.80	13.10	11.58	7.90	9.50	25.70
13.	Bidhan RB-2 (NC)	7.10	1.23	1.11	8.35	5.70	92.00	134.00	97.20	13.25	12.05	8.10	5.50	23.50
14.	Shyamalima (LC)	7.35	1.25	1.16	17.00	6.10	96.50	137.50	103.25	13.05	11.83	8.35	10.50	23.60
	Mean	7.81	1.23	1.38	16.46	6.37	100.78	146.25	117.94	14.88	11.75	8.30	11.42	28.20
	C.D (5%)	0.71	0.04	0.27	2.55	0.64	3.35	2.71	10.34	1.42	0.48	0.48	2.86	4.30

green forage yield, dry matter yield, high number of primary branches, high number of secondary branches and more leaf area. JCR-07-7, JCR-14-1 and JCR-14-3 were observed to have more green forage yield, dry matter yield, high number of primary branches, high number of secondary branches leaf-stem ratio and more stem diameter. JCR-18-2 had highest plant height, JCR-07-7 had high crude protein content and JCR-14-1 and JCR-14-3 had high crude fibre content.

In case of seed yield, JCR-18-2, JCR-18-3, JCR-14-1 and JCR-14-3 were observed to have higher seed yield per plant. JCR-18-2 and JCR-14-3 had longer pods and had more number of seeds per pod. JCR-18-2, JCR-18-1, JCR-07-7 and JCR-16-4 had higher specific gravity. Productive racemes per plant were observed to be high in JCR-18-2. Pods per racemes were observed to be high for JCR-18-2, JCR-18-1, JCR-14-3, JCR-07-7 and JCR-16-1.

Thus, the following genotypes viz., JCR-18-

TABLE 5
List of some genotypes observed superior for various traits in the study

S. No.	Genotype	Character
1.	JCR-18-2	High green forage yield per plant and dry matter yield per plant, tall, late flowering, late maturing, more number of productive racemes per plant, more number of pods per raceme, more 100 seed weight, more leaf area, more pod length, more seed length, more stem length, more number of primary and secondary branches per plant, high ash content and high seed yield per plant.
2.	JCR-07-7	High green forage yield per plant, high dry matter yield per plant, more number of primary branches per plant, more number of secondary branches per plant, greater leaf stem ratio, more stem diameter, more leaf area, more specific gravity, more number of pods per raceme and high crude protein content.
3.	JCR-14-1	High green forage yield per plant, high dry matter yield per plant, more number of primary branches per plant, more number of secondary branches per plant, more stem diameter, more leaf area, more leaf stem ratio, high crude fibre content and seed yield per plant.
4.	JCR-14-3	High green forage yield per plot, more number of secondary branches per plant, more stem diameter, more leaf area, more pod length, more seed length, more number of seeds per pod, more leaf stem ratio, high crude fibre content and high seed yield per plant.

2, JCR-14-3 and JCR-14-1 were the promising genotypes that might be used as breeding material in hybridization programme for development of variety suitable for forage as well as seed. However, testing of these genotypes in one to two or more successive generations for forage yield, seed yield and quality in replicated multi-location trial is must for taking a conclusive decision. Similar findings were also reported in cowpea by Vu *et al.*, (2019), Arya *et al.*, (2020) and in fababean by raiger *et al.*, (2021).

CONCLUSION

This experiment has revealed that there was significant difference among all the genotypes for all the characters. The estimates of GCV and PCV were observed to be high for stem length, leaf-stem ratio, productive racemes per plant and seed yield per plant. High heritability coupled with high genetic advance as per cent of mean was observed for stem length, leaf area, 100 seed weight, pod length, seed breadth, leaf-stem ratio, productive racemes per plant and seed yield per plant. Among all the entries, genotype JCR-18-2 had the highest green forage yield per plant, dry matter yield per plant, days to 50% flowering, days to maturity, productive racemes per plant, pods per raceme, plant height, primary branches per plant, secondary branches per plant, stem length, 100 seed weight, leaf area, pod length, seed length, ash% and seed yield per plant indicating that this entry is superior performer in forage yield and many other component traits. The rice bean genotypes viz., JCR-18-2, JCR-07-7, JCR-14-1 and JCR-14-3 had higher estimates

for several traits indicating the importance of these entries in future rice bean improvement programme. Also the study revealed that Rice bean can be cultivated both in *Kharif* as well as in *Rabi* season.

Future prospects

As fodder crisis is observed during *Rabi* season, genotypes with high green forage yield can be identified to overcome this crisis. Studies can be carried out to identify flowering type rice bean genotypes which can be further used for seed production in *Rabi* season. Also identifying early maturing genotypes will help in development of short duration varieties.

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