



Research Article

RICEBEAN [*Vigna umbellata* (Thunb.) Ohwi and Ohashi] LANDRACES OF NAGALAND IN DIFFERENT ENVIRONMENTS

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Abstract: Stability of yield and its attributes were assessed for 13 landraces genotypes of Rice bean over six environments during Kharif season 2016 and 2017, on six different growing seasons, to determine the quantitative responses of different Rice bean genotypes at six different environments. The combined analysis of variance revealed highly significant differences among Genotypes (G), Environment (E) and interactions of Genotypes and environments (G x E) for most of the studied traits. The joint regression analyses of variances due to environment (linear) were highly significant for characters like Days to 50% flowering, number of pods per plant, 80% maturity, 100 seed weight and seed yield per plant under study, which indicated the genetic control of response to the environment. The variance due to GxE (linear) was significantly different for 50% flowering, pod length, number of seeds per pod and 100 seed weight and non-significant for days to primary branches, pods per cluster, number of pods per plant, plant height, number of primary branches per plant, number of pods per plant, number of seeds per pod, 80% maturity and seed yield per plant. It indicated the differential response of varieties to various growing season. Varieties RbnG3, RbnG5, RbnG8, RbnG9 and RbnG12 showed higher seed yield, regression coefficient equivalent to unity and deviation from regression equivalent to zero. It indicated that these varieties were suitable for cultivation on a wide range of environments as these had greater stability along with high yield.

Keywords: Genotype X Environment, Stability parameters, Stable genotypes, Yield

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Introduction

Ricebean is a multipurpose grain legume crop mainly cultivated for food, fodder and green manure specifically by the poor farmers in the marginal areas of South Asia and South East Asia. In India its distribution is mainly confined to tribal regions of North-Eastern hills, Western and Eastern Ghats in peninsular India, often in hill tracts [1]. Rice bean, a leguminous crop and also known as climbing mountain bean, mambi bean and oriental bean, is native to south-east Asia [2]. In Nagaland, rice bean is a traditional and indigenous crop, cultivating since time immemorial and considered as minor legumes grown by subsistence farmers of Nagaland. It is grown under diverse conditions with no additional input, which thrives well in rainfed condition which is generally grown as mixed crop in jhum cultivation, inter crop with maize and cultivated along rice bunds and terrace. All cultivated varieties of rice bean in Nagaland are landraces which have disseminated from one village to another and from generation to generation through an informal distribution system, with farmers solely responsible for management and seed supply. Location specific staple genotypes are an important factor for our changing environment and are needed to evaluate for their performances over varied location and environments. Stable performance of Rice bean genotypes across contrasting environment is essential for the successful selection of stable and high yield genotypes. Therefore, there is a necessity to generate relevant information so as to how different genotypes and their altered in different Environment and to examine the role of Genotype X environment interaction through stability analysis in order to identify stable genotype contributing towards stable yield. It is thus, necessary to evaluate landraces genotypes for their stability in production and to monitor their performances which will get a great boost towards an attempt to serve as source material for future breeding programme.

Although rice bean is grown in diverse environment in Nagaland, there is inadequate information on the stability and response of different genotypes in different environment. Therefore, the present research studies were conducted to know genotype-environment interaction and to identify stable and high yielding Rice bean genotypes under changing environments. The results of present research may be useful both for breeders as well as farmers to select suitable genotype for sustainable Rice bean production.

Materials and Methods

The present study was undertaken during Kharif, season 2016 and 2017. Experiment was carried out at Department of Plant Breeding and Genetics, SASRD, Medziphema, Nagaland. The materials used are thirteen landraces genotypes of Rice bean. These genotypes are arranged in a randomized block design (RBD) with three replications. The Genotypes were sown on 1st July, 1st August and 15th August Kharif 2016 and 1st June, 15th June and 1st July in Kharif 2017 in a plot size of 3m x 1m with 1m row-to-row spacing and 50cm plant to plant spacing. Observations were recorded on five randomly selected plants from each genotype in all the three replications for days to 50% flowering, primary branches, pods per cluster, number of pods per plant, pod length, number of seeds per pod, plant height, 80% maturity, 100 seed weight and seed yield per plant. The data were statistically analyzed and the genotypes were assessed for their stability of performance across environments following the method [3]. This method was followed to estimate the three parameters of stability namely mean, regression coefficient (bi) and mean squared deviation (s²di) for each genotype, using SPAR-2 (Statistical Package for Agricultural Research) developed at the Indian Agricultural Statistics Research Institute, New Delhi [4].

Results and Discussion

The combined analysis [Table-1] indicated the presence of significant G x E interactions for all the characters studied. Higher magnitude of mean squares due to environments indicates considerable differences between environments for all the characters and that these characters were greatly influenced by environments; thereby suggesting the large differences between environments along with greater part of genotypic response was a linear function of environments i.e., the environments created by sowing dates over years was justified and had linear effects. These results are in agreement with the earlier findings of Dillion *et al.* (2009) [9] and Jai Dev *et al.* (2009) [13]. The joined regression analyses of variances [Table-2] due to environment (linear) were highly significant for characters like number of days to 50% flowering, number of pods per plant, Plant height, 80% maturity, 100 seed weight and seed yield per plant under study, which indicated the genetic control of response to the environment. The variance due to GxE (linear) was significantly different for days to 50% flowering, number of pods per plant, plant height, 80% maturity and seed yield and non-significant for primary branches, pods per cluster, pod length, number of seeds per pod, 100 seed weight and protein content. It indicated the differential response of varieties to various growing season. These findings are in agreement with the findings of Patil and Narkhede (1995) [18] for 100 seed weight, pods per plant and seed yield. Kalpande *et al.* (1996) [14] for yield and yield components, Manivannan *et al.* (1999) for seed yield [15], Tofu *et al.* (2002) for days to 50% flowering, days to maturity, plant height and 100 Seed weight and Singh *et al.* (2003) for yield and its components in mung bean [21,22]. Senthilkumar and Chinna (2012) also had the same opinion on these traits [20]. Gupta *et al.* (1991) carried out stability analysis of 30 genotypes of mungbean in 6 environments for seven characters viz, days to maturity, plant height, number of branches/plant, number of pods/plant, seeds/pod, 100 seed weight and seed yield yield/plant [12]. The analysis of variance for stability revealed significant difference among genotypes, environment and GEI for all the characters studied. The mean values for yield and its components, regression coefficient (bi), and deviation from regression (S_{2di}) for 13 genotypes over six environments are presented in [Table-2]. Further, the stable genotypes identified for wider environments and specific (either favourable or poor) environments with high per se performance (over general mean) for seed yield per plant are presented in [Table-3] and [Table-4].

Days to 50% flowering

Varieties RbnG1, RbnG3, RbnG5, RbnG7, RbnG12 possessed high mean values, regression coefficient near unity along with deviation from regression equivalent/near to zero. These genotypes exhibited stability in performance. From the Environmental indices it was observed that E5 was the most favourable one and E3 unfavourable. RbnG6, RbnG9 and RbnG11 possessed high mean values over general mean regression and coefficient equivalent greater than unity with non significant deviation from regression equivalent to zero was found to be highly stable and suitable for favourable environment. Among the Genotypes, RbnG4, RbnG7, RbnG13 having average mean with regression coefficient less than unity and non significant deviation from zero found to be adapted to unfavourable environment. The genotype RbnG1, RbnG3, RbnG4, RbnG10, RbnG12 and RbnG13 might be considered superior for days to 50% flowering, because they gave high mean value above the general mean, besides their stability.

Number of primary branches per plant

Genotypes, RbnG10 had higher number of primary branches per plant, regression coefficient of unity and deviation from regression-near to zero, which shows average stability and well adapted to all the environments. Genotypes RbnG8, RbnG4 and RbnG13 showed regression coefficient more to unity, deviation from regression near to zero and had average number of primary branches per plant over general mean and considered to be stable and specially adapted to favourable environments. Genotypes RbnG5 showed regression coefficient less to unity and deviation from regression to zero and considered for unfavourable environments. From the Environment index, E6 was the most favourable and E1 the least unfavourable. The genotype RbnG4, RbnG6, RbnG8, RbnG10 and RbnG13 might be considered superior for primary branches, because they gave

high mean value above the general mean, besides their stability.

Number of pods per cluster

Stability of number of clusters per pod indicated that variety RbnG6 had higher number of cluster per pod, regression coefficient equivalent to unity and deviation from regression near to zero which shows stable and well adapted to all environments. RbnG5, RbnG10 and RbnG13 shows more than one regression coefficient and deviation from regression near zero with high mean, more than unity and so considered stable for favourable environment. Genotype RbnG3, RbnG and RbnG8 showed less to unity regression coefficient and deviation from regression equivalent to zero along with average number of clusters per plant over general mean and stable for unfavourable environments. From the Environment index it was observed that E6 was the most favourable and E1 was unfavourable. The genotype RbnG1, RbnG3, RbnG5, RbnG8, RbnG10 and RbnG13 might be considered superior for pods per cluster, because they gave high mean value above the general mean, besides their stability.

Number of pods per plant

Genotypes RbnG9 and RbnG11 showed regression coefficient equivalent to unity, deviation from regression equivalent to zero and these varieties possessed highest number of pods per plant over general mean and well adapted to all environments. Genotypes RbnG3, RbnG4, RbnG10 exhibited more than one regression coefficient, deviation from regression near to zero and adapted to favourable condition. Genotypes RbnG1 and RbnG13 exhibited regression coefficient less to unity and deviation from regression near to zero and showed high mean and considered below average stability and adapted specially for unfavourable environment. Genotypes RbnG2 and showed regression coefficient equivalent to unity, deviation from regression near to zero and these varieties possessed lower number of pods per plant over general mean and considered average stability adapted poorly to all the environments. E4 is considered for maximum number for pods per plant and E3 for minimum number of pods per plant. The genotype RbnG1, RbnG3, RbnG4, RbnG5, RbnG8 and RbnG13 might be considered superior because they give high mean value for number of seeds per pod above the grand mean, besides their stability. These results are in agreement with De Rocha *et al.* (2007) [8] and El-Shaieny *et al.* (2015) on cowpea [10].

Pod length

RbnG13 showed high mean and exhibited regression coefficient equivalent to unity, deviation from regression equivalent to zero and show average stability and well adapted to all environments. Genotype RbnG3, RbnG4, RbnG6 and RbnG10 had regression coefficient more to unity with high mean, deviation from regression more to unity and non significant deviation and specially adapted for favourable environments. RbnG7 and RbnG8 showed high mean, regression coefficient less to one, deviation from regression near to zero and had longer pod length which shows below average stability and specially adapted to unfavourable environment. The genotype RbnG2, RbnG3, RbnG5, RbnG9 and RbnG10 might be considered superior because they are longer than the mean length besides their stability. Similar results were reported by Akande and Balogun (2009) [5].

Number of seeds per pod

Genotypes RbnG3 and RbnG4 had higher number of seeds per pod, regression coefficient equivalent to unity and deviation from regression equivalent to zero which shows stability and well adapted to all environments. RbnG5 ($\mu=5.96$, $B_i=3.20$, $S_{2di}=0.49$), RbnG7 ($\mu=5.73$, $B_i=2.15$, $S_{2di}=0.445$) and RbnG13 ($\mu=6.13$, $B_i=1.87$, $S_{2di}=0.25$) had high mean seed per pod and regression coefficient more to unity, deviation from regression equivalent to zero, which shows below average stability and adapted to favourable environments condition. Genotypes RbnG2, RbnG9 and RbnG12 had low mean, regression coefficient less to unity, deviation from regression equivalent to zero. It shows below average stability and adapted to unfavourable environments. Similar findings were reported by Senthilkumar and Chinna (2012) [20] and Nath and Dasgupta (2017) [17]. E6 was the most favourable and E3 unfavourable for number of seeds per pod.

Table-1 Combined (pooled) analysis of variance for studied traits of 13 genotypes under six environments

SOV	df	Days to 50% flowering	Primary branches	Pods/cluster	No. of pods/plant	Pod length (cm)
Env	5	11836.09*	10.12*	10.018*	3535*	50.26*
Rep (Env)	12	279.07	0.36	0.379	100.52	1.83
Genotype	12	3451.22*	3.46*	4.94*	1983.90*	27.13*
Env x Gen	60	567.82*	0.280*	0.373*	16.48*	3.35*
Error	144	158.63	0.132	0.151	24.148	0.86

SOV	df	No. of seeds/pod	Plant height (cm)	80% Maturity	100 Seeds weight (gm)	Protein content (%)	Seed yield/plant (gm)
Env	5	31.34*	52171.07*	7102.75*	95.88*	228.16*	779.30*
Rep (Env)	12	1.026	782.97	17.95	1.69	8.03	20.14
Genotype	12	36.79*	15021.48*	317.33*	912.77*	246.44*	411.47*
Env x Gen	60	1.323*	265.32*	85.61*	7.21*	15.75*	35.02*
Error	144	0.513	95.082	3.054	0.615	3.86	2.13

* Significant at 0.05 level of probability

Table-2 Joint regression analysis of variance for the studied character [* Significant at 5% level]

SOV	df	50% flowering	Primary branches	Pods per cluster	No. of pods per plant	Pod length (cm)
Genotype (g)	12	105.48*	0.22	0.57	351.13*	2.206*
Environment (e)	5	11836.09*	10.12	10.01	3535.006*	50.26*
Genotype x Environment	60	567.82*	0.83	0.37	16.48*	2.18
Environment + (Genotype x Environment)	65	3219.31*	0.17	0.14	95.71*	0.255
Environment (linear)	1	7187.78*	5.66	3.8	2169.63*	1.69
Genotype x Environment (linear)	12	30.47*	0.15	0.2	103.38*	0.42
Pooled Deviation	52	15.7	0.07	0.056	54.06*	0.187
Pooled Error	156	41.65	0.03	0.036	4.85	0.217

SOV	df	No. of seeds/pod	Plant height (cm)	80% Maturity	100 Seeds weight(gm)	Protein content (%)	Seed yield/plant (gm)
Genotype (g)	12	8.31*	2794.33*	174.53*	297.74*	50.53*	56.23*
Environment (e)	5	31.34*	52171.07*	21338.90*	95.88*	228.16*	779.30*
Genotype x Environment	60	1.32	265.32*	1031.84*	7.21*	15.75*	35.02*
Environment+(Genotype x Environment)	65	0.396	1419.36*	229.66*	4.67	1	30.75
Environment (linear)	1	4.85	60397.88*	11035.64*	81.66*	0.98	327.73*
Genotype x Environment (linear)	12	0.488	714.99*	127.42*	6.87	0.33	29.69*
Pooled Deviation	52	0.289	447.70*	45.44*	2.69	1.15	25.29*
Pooled Error	156	0.131	9.17	56.82	0.23	0.98	0.13

Table-3 Mean and stability parameters of 13 genotype over six Environment

Genotype	50%flowering			Primary branches			pods/ cluster			No. of pods/plant			Pod length (cm)		
	Mean	bi	S ² di	Mean	bi	S ² di	Mean	bi	S ² di	Mean	bi	S ² di	Mean	bi	S ² di
RbnG1	96.89	0.95	57.83	2.82	1.55	0.09	3.02	1.46	0.14	61.63	0.28	43.08	7.52	-0.74	0.21
RbnG2	96.89	1.4	64.79	2.3	0.23	0.04	2.56	-0.15	0.06	39.98	1.66	40.97	8.46	0.54	0.23
RbnG3	100.5	1.02	59.3	2.58	0.25	0.15	2.96	0.78	0.06	52.4	1.21	52.26	8.28	2.89	0.23
RbnG4	94.06	0.94	65.77	2.86	1.46	0.05	3.22	0.36	0.09	57.16	1.2	24.92	7.73	1.68	0.3
RbnG5	90.78	1.06	63.9	2.5	0.06	0.05	2.78	1.68	0.06	54.81	1.85	197.5	9.42	-0.03	0.22
RbnG6	91.78	1.1	43.13	2.73	0.93	0.13	2.5	1.07	0.09	49.41	1.49	95	7.72	4.6	0.36
RbnG7	97.89	0.71	55.35	2.61	1.43	0.12	2.36	0.66	0.06	52.64	-0.5	71.17	7.4	0.55	0.72
RbnG8	83.61	0.49	73.45	2.66	1.82	0.08	3	0.42	0.13	59.86	-0.36	58.64	7.58	0.59	0.34
RbnG9	93.61	1.31	48.77	2.28	1.33	0.26	2.77	2.72	0.08	40.14	1.1	7.49	8.57	0.37	0.47
RbnG10	95.67	0.92	47.01	2.84	1.02	0.05	3.18	1.25	0.1	58.93	2.05	25.56	8.3	3	0.28
RbnG11	96.33	1.1	54.32	2.63	0.23	0.11	2.33	-0.35	0.12	36.63	1.12	17.91	8.95	-2.63	1.04
RbnG12	96.78	1.07	58.34	2.68	1.3	0.09	2.46	1.26	0.09	45.18	1.16	70.58	8.09	1.11	0.37
RbnG13	96.89	0.87	53.65	2.83	1.31	0.04	2.98	1.8	0.08	57.33	0.69	60.71	7.78	1.02	0.44
genotypic mean	94.47	0.995	-	2.64	0.106	-	2.78	0.997	-	51.24	0.996	-	8.14	0.996	-
S.E(bi)	-	0.651	-	-	0.163	-	-	0.142	-	-	1.027	-	-	0.152	-

Genotype	No. of seeds/pod			Plant height (cm)			80% maturity			100 seed weight (gm)		
	Mean	bi	S ² di	Mean	bi	S ² di	Mean	bi	S ² di	Mean	bi	S ² di
RbnG1	6.45	2.32	0.57	138.18	0.998	149.206	133.11	1.200	64.827	3.93	0.431	-0.127
RbnG2	3.82	0.16	0.51	98.07	0.725	278.117	128.83	1.232	66.824	21.5	0.924	6.832*
RbnG3	5.77	1.06	0.45	121.96	0.351	479.899	133.39	1.105	60.765	10.06	0.382	0.06
RbnG4	6.93	0.92	0.43	140.33	1.143	231.408	132.39	1.152	73.972	3.97	1.715	0.012
RbnG5	5.96	3.20	0.49	148.18	0.978	284.057	125.72	1.173	61.291	18.01	1.184	3.947*
RbnG6	6.18	1.26	0.693	138.12	1.540	1641.84	124.67	1.015	60.787	12.73	2.218	1.126
RbnG7	5.73	2.15	0.445	100.28	0.383	67.256	127.89	0.860	80.740	11.88	2.854	5.291*
RbnG8	6.43	-0.55	0.182	154.77	0.802	1388.92	121.17	-0.246	288.32	11.83	-0.986	1.753
RbnG9	3.76	0.86	0.341	116.22	1.311	256.759	131.39	1.147	238.97	21.19	0.153	0.800
RbnG10	6.29	-0.31	0.281	167.59	1.700	343.164	132.72	1.072	83.881	4.4	0.185	0.4846
RbnG11	3.63	-0.14	0.244	108.09	1.143	217.836	131.67	1.068	67.781	21.03	1.798	10.525*
RbnG12	4.59	0.16	0.565	122.96	0.900	509.912	132.61	1.190	62.780	19.03	1.770	0.915*
RbnG13	6.13	1.87	0.256	135.33	1.021	91.105	135.94	1.028	118.57	3.36	0.368	0.338
genotypic mean	5.51	0.997	-	130.01	1.000	-	130.12	1.000	-	11.76	1.000	-
S.E(bi)	-	0.843	-	-	0.294	-	-	0.223	-	-	0.670	-

Genotype	Crude protein (%)			Seed yield/plant (gm)		
	Mean	bi	S ² di	Mean	bi	S ² di
RbnG1	20.69	1.685*	1.726	26.62	1.430	8.948
RbnG2	18.46	0.447	1.744	27.02	0.400	20.286
RbnG3	21.24	-0.218	2.874	29.66	0.932	10.093
RbnG4	12.60	0.089	1.396	28.03	3.064	43.024
RbnG5	17.25	6.010	2.954	31.37	1.061	29.926
RbnG6	12.73	2.690	1.222	27.77	1.493	47.485
RbnG7	14.76	-1.446	4.178	26.84	1.943	45.732
RbnG8	20.30	1.912	4.758	37.82	0.056	32.825
RbnG9	14.18	0.915	1.000	29.93	0.171	22.324
RbnG10	14.24	2.360	1.007	28.12	2.167	50.463
RbnG11	13.92	1.566	1.004	28.13	-1.265	6.878
RbnG12	14.52	-1.506	1.933	31.61	0.828	7.002
RbnG13	17.95	-1.507	2.014	26.01	0.716	5.622
genotypic mean	16.37	1.00	-	29.15	1.000	-
S.E(bi)	-	0.419	-	-	0.967	-

Table-4 Environment indices for yield and quality components for Six Environments

Characters		Env1	Env2	Env3	Env4	Env5	Env6
50%flowering	Ij	3.02	-3.37	-18.6	12.94	3.74	2.27
Primary branches	Ij	-0.06	-0.4	-0.28	0.18	0.25	0.31
Pods/cluster	Ij	-0.06	-0.23	-0.33	0.21	0.18	0.22
No.of pods/plant	Ij	2.19	-11.29	-0.08	4.3	3.29	1.59
Pod length(cm)	Ij	0.05	-0.31	-0.02	0.07	0.06	0.16
No.of seeds/pod	Ij	0.003	-0.38	-0.27	0.06	0.21	0.38
Plant height (cm)	Ij	3.47	-39.54	-38.7	36.77	23.9	14.1
80% maturity	Ij	9.35	-9.76	-22.91	7.91	11.01	9.35
100 seeds weight (gm)	Ij	-0.45	-1.05	-0.92	-0.23	1.7	0.94
Protein content (%)	Ij	-0.46	-1.1	-1.08	-0.21	1.72	0.98
seed yield/plant (gm)	Ij	1.39	-1.11	-3.2	-1.61	1.65	2.89

Ij- environment index

Table-5 Classification of genotypes for different characters based on stability parameters

S	Characters	Genotypes stable over all environments (bi=1), (S ² di=0)	Genotypes stable for favourable environments (bi<1), (S ² di=0)	Genotypes stable for poor Environments (bi>1), (S ² di=0)
1	50%flowering	RbnG1, RbnG5 and RbnG10	RbnG6, RbnG9 and RbnG11	RbnG4, RbnG7, RbnG8 and RbnG13
2	Primary branches	RbnG10	RbnG1, RbnG4, RbnG8, RbnG12 and RbnG13	RbnG5
3	Pods/cluster	RbnG6	RbnG10	RbnG3, RbnG4, RbnG7 and RbnG8
4	No. of pods/plant	RbnG3, RbnG4	RbnG10	RbnG1, RbnG13
5	Pod length (cm)	RbnG13	RbnG3, RbnG6, RbnG10	RbnG7, RbnG8
6	No. of seeds/pod	RbnG3, RbnG4	RbnG1, RbnG5, RbnG7, RbnG13	RbnG2, RbnG9, RbnG12
7	Plant height (cm)	RbnG1, RbnG4, RbnG5, RbnG13	RbnG9, RbnG10	RbnG2, RbnG7, RbnG11
8	80% maturity	RbnG6, RbnG10, RbnG11	RbnG1, RbnG3, RbnG4, RbnG5 and RbnG12	-
9	100 seeds weight (gm)	RbnG8, RbnG12	RbnG4 and RbnG6	RbnG1, RbnG3, RbnG9, RbnG10 and RbnG13
10	Crude protein (%)	RbnG9	RbnG1, RbnG6, RbnG11	RbnG2, RbnG4
11	Seed yield/plant (gm)	RbnG3 and RbnG5	RbnG1, RbnG4, RbnG6 and RbnG10	RbnG8 and RbnG9

The genotype RbnG3, RbnG4, RbnG5, RbnG7, RbnG8, RbnG10 and RbnG13 might be considered superior because they gave high mean value above the general mean, besides their stability. These results are in agreement with those obtained from Dahiya *et al.* (2007) and Singh *et al.* (2007), [6,23].

Plant height

Genotypes RbnG1, RbnG4, RbnG5, RbnG13 had high mean, regression coefficient equivalent to unity, deviation from regression equivalent to zero, which shows average stability and well adapted to all environments. Genotypes RbnG9 and RbnG10 had high mean, regression coefficient more to one and deviation from regression equal to zero which shows average stability and specially adapted to favourable environments. Genotypes RbnG2, RbnG7, RbnG11 had low mean, regression coefficient less to unity and deviation from regression equivalent to zero which shows below average stability and adapted to unfavourable environment. E4 was observed to be favourable and E2 unfavourable for plant height. The genotype RbnG1, RbnG4, RbnG5, RbnG10 and RbnG13 might be considered superior because they gave high mean value above the general mean, besides their stability. The genotype RbnG1, RbnG4, RbnG5, RbnG10 and RbnG13 might be considered superior for plant height, because they gave high mean value above the general mean, besides their stability.

Days to 80%Maturity

Varieties RbnG6, RbnG10 and RbnG11 had regression coefficient equal to unity and non significant deviation from linearity, hence these varieties were found to be more stable than the other varieties and could perform relatively better in wide range of environments. Variety RbnG1, RbnG3, RbnG4, RbnG5 and RbnG12 have high general mean and had regression coefficient more to unity and non significant deviation. Hence this variety could be preferred for favourable condition. E5 was observed to be favourable and E2 unfavourable for days to 80% maturity. The genotype RbnG1, RbnG3, RbnG4, RbnG10, RbnG11 and RbnG12 might be considered superior for 80% maturity, because they gave high mean value above the general mean, besides their stability.

100 seed weight

Genotypes RbnG8 and RbnG12 had higher 100 seed weight, regression coefficient equivalent to unity and deviation from regression equivalent to zero. It shows average stability and well adapted to all the environments. Genotypes RbnG6, RbnG4 had moderate 100 seed weight, regression coefficient more than one and Deviation from regression equivalent to zero which is adaptable to favourable environment condition. Genotypes RbnG1, RbnG3, RbnG9, RbnG10 and RbnG13 had low 100 seed weight, regression coefficient less to one and deviation from regression near to zero, which shows below average stability and

specially adapted to unfavourable environments. It is observed that, E5 produced maximum seed weight and E1 minimum 100 seed weight. The genotype RbnG5, RbnG6, RbnG8, and RbnG9 might be considered superior because they gave high mean value above the general mean, besides their stability. Similar results were reported by Akande and Balogun (2009).

Seed yield per plant

Genotypes RbnG3 and RbnG5 showed higher seed yield per plant [Fig-2], regression coefficient equivalent to unity and deviation from regression equivalent to zero, which shows average stability and well adapted to all environments. Genotypes RbnG8, RbnG9 also had regression coefficient less to unity and significant deviation from regression near to zero and can be considered as below average stability and adapted for unfavourable condition. Genotypes RbnG1, RbnG4 RbnG6 and RbnG10 had regression coefficient more than unity, deviation from regression near to zero, with high mean yield and adapted to favourable environments. The genotype RbnG3, RbnG5, RbnG8, RbnG9 and RbnG12 might be considered superior because they gave high mean value above the general mean, besides their stability. Similar results were reported by Dahiya *et al.* (2007) and Singh *et al.* (2007).

Protein content

ANOVA indicated that a G x E interaction was highly significant for protein content [Table-1]. Joint regression analysis was continued further to estimate G x E for protein content which exhibited significant interactions in the pooled analysis [Table-2]. The Eberhart's and Russel ANOVA showed that genotype, environment and G x E were significant [3]. Crude protein content in Rice bean genotypes varied between 12.36 and 21.24 percent [Fig-1]. This study is in agreement with Rodriguez, *et al.* (1991) [19], reported that seeds of rice bean had 17.26% to 21.42% protein content. The genotypes RbnG9 ($\mu=14.18$, $bi=0.915$, $S2di=1.000$), show average mean, regression coefficient near to unity and deviation from regression equivalent to zero. These genotypes can be considered as stable for crude protein across the environments. Genotypes, RbnG1 ($\mu=20.33$, $bi=1.685$, $S2di=1.726$), RbnG6 ($\mu=12.23$, $bi=2.69$, $S2di=1.22$) and RbnG11 ($\mu=13.15$, $bi=1.566$, $S2di=1.004$) indicates high mean, regression coefficient more than one

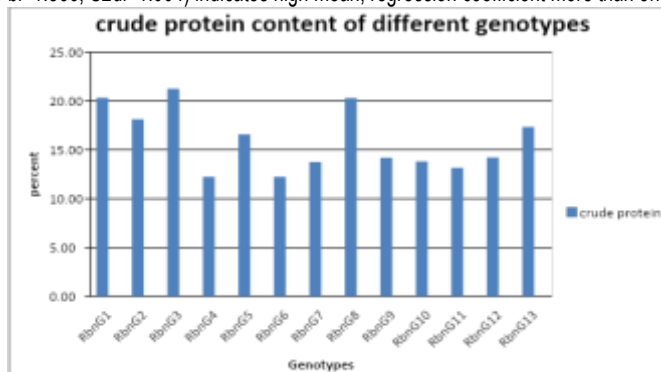


Fig-1 Crude protein content of different genotypes

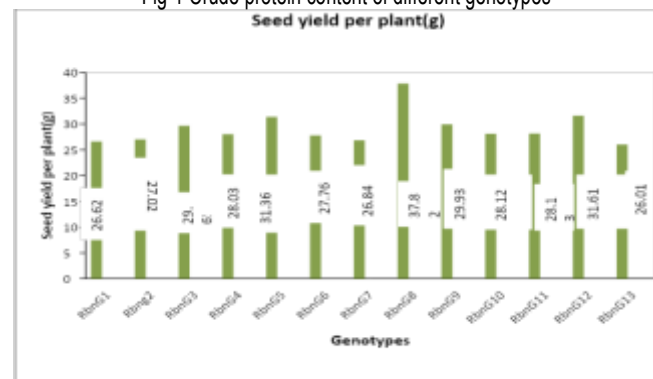


Fig-2 Mean performance of seed yield per plant

and deviation from regression near to zero and can be considered as stable for

crude protein content under favourable environment. RbnG2 ($\mu=18.13$, $bi=0.44$, $S2di=1.74$) and RbnG4 ($\mu=12.23$, $bi=0.089$, $S2di=1.396$) showed regression coefficient less to zero and deviation from linearity near to zero, these genotypes can be considered for unfavourable environment. All other genotypes are found to be not stable. Chaudhari *et al.*, (2013), based on their study on 36 genotypes of cowpea under four seasons observed that magnitude of genotype x environment linear and pooled deviation from linearity was high for protein content and found none of the genotype are found stable. Similar findings were reported by Senthilkumar and Chinna (2012) also could not identify any single variety stable for all the traits. From the result [Table-5], it is also exhibited that genotypes RbnG4, RbnG10 shows stability in eight characters, RbnG1 and RbnG3 shows stability in four characters, RbnG6 shows stability in six characters, RbnG5 and RbnG8 shows stability in five characters, this stability in landraces will provide opportunities for breeders for further crop improvement and other related research in the future. The genotype RbnG1, RbnG2, RbnG5, RbnG8 and RbnG13 might be considered superior for protein because they gave high mean value above the general mean, besides their stability. The genotype RbnG3, RbnG5, RbnG8, RbnG9 and RbnG12 are considered stability for seed yield per plant. Wilson (2004) [26] suggested the independent manipulation of these two variables, and it could be achieved through the selection of individual lines those present either intermediate grain yield or protein content values or mean values above that of the experimental means. The results indicated that the selection of genotypes that combine high protein content and grain yield will not be a hard task, because the genotypes presenting the highest protein contents also showed the higher yields in our assays, so there is a wide scope for selection of these genotypes as parents for improvements. High protein line such as RbnG1, RbnG2, RbnG5, RbnG8 and RbnG13 could be employed in backcross breeding programs; RbnG3, RbnG5, RbnG8, RbnG9 and RbnG12 can be used as recurrent parents in order to simultaneously increase yield and protein content, as it was suggested by Wilcox and Cavins (1995) in their studies on soyabeans [25].

Conclusion

The study identified considerable degree of genotypic differences and stability for yield in Rice bean genotype tested under various environments. The partitioning of mean squares (environments + genotype x environments) showed that environments (linear) differed significantly and were quite diverse with respect to their effects on the performance of genotypes for seed yield and majority of yield components. Further, the higher magnitude of mean squares due to environments (linear) as compared to genotype x environment (linear) exhibited that linear response of environments accounted for the major part of total variation for majority of the characters studied. 50 % flowering, Primary branches, pods per cluster, Pod length, number of seeds per pods, number of pods per plant, plant height, 80% maturity and 100 seed weight were identified as important stable components traits in rice bean genotypes. Genotypes RbnG1, RbnG3 RbnG4, RbnG5, RbnG6, RbnG8 and RbnG10 revealed stability in different character and this stability in landraces will provide opportunities for breeders for high protein content Genotypes such as RbnG1, RbnG3 and RbnG8 could be employed in backcross breeding programs. The genotype RbnG1, RbnG2, RbnG3 might be considered superior because they gave high mean value above the general mean; besides their stability can be used as recurrent parents in order to simultaneously increase yield and protein content.

Application of research: The findings can be put for further investigation in breeding programmes and analysed for further documentation and improvement in Landraces of Rice bean in Nagaland.

Research Category: Genetics and Plant Breeding

Abbreviations: RbnG -Nagaland Rice bean genotype, E- Environment

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Study area / Sample Collection: Tuensang, Wokha and Dimapur district

Cultivar / Variety / Breed name: *Vigna umbellata* (Thunb.) Ohwi and Ohashi

Conflict of Interest: None declared

Ethical approval: This article does not contain any studies with human participants or animals performed by any of the authors.

Ethical Committee Approval Number: Nil

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