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## Genetic variability for yield and related traits in rice bean landraces (*Vigna umbellata* (Thunb.) Ohwi and Ohashi) of Nagaland in different environments

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**Abstract**

The study was carried out to estimate different genetic parameters in rice bean landraces of Nagaland. Thirteen genotypes of rice bean were evaluated for yield and its components in the cropping seasons of 2016-2017 across six environments represented by different sowing dates. In each cropping season the genotypes were arranged in Randomized Block Design (RBD) with three sowing dates. The study revealed that phenotypic coefficient variation (PCV) was higher than genotypic coefficient of variation (GCV) for all the traits in all the six environments. High PCV and GCV was observed for number of pods per plant, number of seeds per pod, plant height, 100 seed weight and seed yield/plant, indicating the role of these characters for effective selection. The study also revealed that heritability in broad sense was high for days to flowering, pod length, number of pods per plant, number of seeds per pod, plant height, 80% maturity and 100 seed weight indicating that the variation observed was mostly under genetic control and less influenced by environment. Overall high to moderate heritability with high genetic advance was observed for pod length, number of seeds per pod and 100 seed weight indicating additive gene control of these traits across the six environments and thus there is better scope for improvement of these traits through direct selection. On the basis of mean performance of all the genotypes, RbnG1, RbnG3, RbnG4, RbnG5, RbnG8, RbnG10 and RbnG13 was found promising among all the genotypes. The genotype RbnG8 was observed to be earliest genotype among all the genotypes studied. The best environment studied was Env4 and Env6.

**Keywords:** Heritability, genetic advance, GCV, PCV, rice bean

**Introduction**

Rice bean [*Vigna umbellata* (Thunb) Ohwi & Ohashi = *Phaseolus calcaratus* Roxb.] is considered to be native of Indo-China (Tamooka *et al.* 1991) [18]. It is a multipurpose grain legume crop mainly cultivated for food, fodder and green manure. In North Eastern Region Rice bean is grown predominantly under rainfed condition in mixed cropping system, shifting cultivation or in the kitchen garden particularly in Assam, Meghalaya, Manipur, Mizoram, Arunachal Pradesh and Nagaland and also in the hill region of North Bengal and Sikkim. Rice bean distribution pattern indicates great adaptive polymorphism for diverse environments, with its distribution ranging from humid tropical to sub-tropical to sub-temperature climate. In the North Eastern region of India, rice bean is an important component of the 1.7 million ha area of shifting cultivation (Sarma *et al.* 1995) [16] for upliftment of the socio economic condition of farmers. Rice bean is known by different local names in different areas of Nagaland. It is popularly known as *Naga dal*. Area under cultivation is too low compared to other crops and hence low production and productivity. It is mostly cultivated for household consumption and the surplus is sold in the market during peak season period for additional income. Rice bean is included in the diet of local people which is consumed as dal, cooked with other vegetables or eaten as sprouts for salads and chutneys. Owing to its important and immense potential of this crop, not much work has been done for the improvement of this crop. For the effective selection of superior genotype to use in hybridization programme for the development of superior varieties, proper study of genetic variability due to genetic and non-genetic causes and other genetic parameters is necessary (Prasad *et al.*, 2012) [14]. So, the main objective of present investigation was to estimate the genetic variability, heritability, and genetic advance for different important economic characters in a set of diverse genotypes of rice bean across different environment.

**Materials and Methods**

Thirteen genotypes of rice bean [*Vigna umbellata* (Thunb.) Ohwi and Ohashi] were collected from different district of Nagaland, viz, Tuensang, Wokha and Medziphema.

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Thirteen genotypes were evaluated in the cropping seasons of 2016 and 2017. In each cropping season the genotypes were arranged in Randomized Block Design (RBD) with six sowing dates. 1<sup>st</sup> week July and 1<sup>st</sup> July, 2<sup>nd</sup> week July and 1<sup>st</sup> week August 2016 and 1<sup>st</sup> week June, 2<sup>nd</sup> week June in 2017. Observations were recorded on 5 randomly selected plants for days to 50% flowering primary branches, pods per cluster, number of pods per plant, pod length (cm), number of seeds per pod, plant height (cm), 80% maturity, 100 seed weight (g) and seed yield per plant (g). The mean values were used for statistical analysis. Analysis of variance was done according to procedure given by Panse and Sukhatme (1987). The genotypic, phenotypic and environmental coefficients of variation were estimated by following method of Burton and DeVane (1953) [2]. Heritability in broad sense and genetic advance was calculated by the formula given by Burton and DeVane (1953) [2] and Johnson (1955) [6].

### Results and Discussion

The analysis of variance (Table 1) revealed significant genotypic differences for all the characters studied across the environments, indicating the presence of substantial genetic variability in rice bean. Mean squares were significant for all the characters studied. It is evident from analysis of variance that sufficient genetic variability exists among genotypes for all the characters studied and hence desirable improvement can be brought through selection in these different characters. The estimates of phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance are presented in Table 2.

### Phenotypic coefficient of variations

The result from the findings indicated that primary branches (31.49%), pods per cluster (47.78%), number of pods per plant (69.27%), Pod length (31.59%), plant height (68.77%) and seed yield per plant (46.12%) reported high PCV. Low PCV was recorded for number of seeds per pod (8.02%). Moderate for 50% flowering, 80% maturity and 100 seed weight. High estimates of PCV for these characters indicated that sufficient genetic variability existed in the experimental material and therefore, selection might bring desirable improvement in these characters. Lakshmana *et al.* (2010) [9] also studied genetic variability in ricebean and reported high PCV values for number of pods/plant (7.41%), number of seeds/pod (8.64%). Dodwad *et al.* (1998) [5] evaluated green gram for pod and seed characters and registered high PCV values for pods/plant (33.42%) and 100 seed weight (29.03%). Pal *et al.* (2014) [13] in cowpea reported high PCV values for grain yield/plant (34.93%), number of pods/plant (34.13%) and 100 seed weight (22.49%).

### Genotypic coefficient of variation

From the results finding it is recorded that primary branches (30.72%), pods per cluster (47.13%), number of pods per plant (68.96%), pod length (31.38%), plant height (68.65%) and Seed yield per plant (45.68%) exhibited high GCV. These results are in accordance with the findings of Ahmad and Rabbani (1992) [1], who studied the genetic variability in rice bean and also reported high GCV and PCV for yield/plant (19.27, 20.07) and 100 seed weight (24.62, 24.80). Similarly high values of GCV and PCV for number of pods/plant, number of seeds/pod, 100 seed weight and seed yield/plant were also reported by Lavanya (2006) [10] in Mungbean and Lakshmana *et al.* (2010) [9] in ricebean and Khan *et al.* (2015) [7] in cowpea. High estimates of GCV coupled with high

heritability for number of pods/plant, seed yield/plant and 100 seed weight were also reported by Ahmad and Rabbani (1992) [1] in rice bean. Dodake and Dahat (2011) [4] experimented on 50 genotypes of rice bean and reported high genotypic and phenotypic coefficient of variation for seed yield per plant and pods per plant.

### Heritability

The heritability (bs) was computed for each of the characters by the variance components for estimating their relative magnitudes of genotypic and phenotypic variability contributed through environmental factors.

The result (Table 2) indicated that the heritability estimates were observed high for 50% flowering (85.29%), Number of pods per plant (99.08%), pod length (98.67%), number of seeds per pods (93.89%), plant height (99.65%), 80% maturity (93.97%), 100 seed weight (97.74%) and seed yield per plant (91.70%). Low heritability was recorded for primary branches (43.78%). A low heritability estimates were also obtained in field bean by Coyne (1968) for seed yield and yield components.

### Genetic advance

Due to masking influence of environment upon characters concerned, values of genetic advance exhibited high fluctuations. Therefore, to attain relative comparison of the characters in relation to environment genetic advance as percentage of mean was calculated to predict the genetic gain (Table 2).

The highest estimate of genetic advance as percentage of mean was recorded for 50% flowering (35.33%), number of pods per plant (72.45%), plant height (83.54%), 80% maturity (36.51), 100 seed weight (62.02%) and seed yield per plant (27.16%). Similar results were observed by Kumar *et al.* (1997) [8] on genetic advance as percent of mean for number of pods per plant and seed yield per plant in rice bean. Majid *et al.* (1982) [11] studied black gram and found highest GA and GA% for number of pods per plant suggesting that the direct selection for the character would be effective for the improvement of yield.

High heritability coupled with high genetic advance mean was recorded for 50% flowering, number of pods per plant, plant height, 80% maturity, 100 seed weight and seed yield per plant. This indicated that this character can be improved upon by selection since the character is under control of additive gene effect. For rest of the characters either the estimate of heritability or genetic advance was low to moderate and, therefore selection may not be useful in improving these traits as these characters are highly influenced by the environment. Similar findings were reported by Pal *et al.* (2018) that 100 seed weight exhibited high heritability along with almost high genetic advance and number of pods/plant, the heritability estimates were low to high in different environments coupled with high estimates genetic advance. Dodake and Dahat (2011) [4] observed high heritability coupled with high genetic advance for seed yield per plant and pods per plant characters indicating additive gene action and emphasized the effectiveness of selection for the improvement of these traits. Similar results were observed for plant height, number of pods per plant, number of seeds per pod and grain yield per plant indicating these characters would be best for phenotypic selection by Rahim *et al.* (2010) [15].

### Mean response of Rice bean genotypes to different environments

The mean performance of different characters of the thirteen genotypes under six environments is presented in Table 3. The six environments give significant differences in photoperiod, temperature and precipitation, all of which have a profound effect on growth and development of this crop. It is revealed that, the mean number of days required to 50 per cent flowering and 80% maturity were greatly influenced by different dates of sowing. The genotype RbnG5, RbnG6 and RbnG8 recorded less number of days for 50 per cent flowering and 80% maturity across the six environments. RbnG1, RbnG3, RbnG7 and RbnG13 recorded the maximum days to flowering across the six environments. Env 4 and Env5 recorded the maximum number of days to flowering and

maturity for all the genotypes followed by Env 1 and Env 6. Env2 and Env3 recorded the minimum days to flowering for all the genotypes and maturity. These findings are in conformity with findings of Singh *et al.* (2006) [17] in rice bean. From the results, it is observed that, seed yield per plants were affected across the six environments. The maximum seed yield per plant was produced by the genotype RbnG5, RbnG8 and RbnG12 followed by RbnG4 and RbnG5. The maximum seed yield was recorded in Env1, Env 4, Env 5 and Env 6 and decreased drastically for Env2 and Env3. This might be due to the availability of more congenial growing conditions of photoperiod, temperature etc., in optimum sowing environment i.e. Env 4, Env 5 and Env 6 as compared to other sowing dates Env 2 and Env 3.

**Table 1:** Analysis of variance (Mean squares) for yield and its component traits in six different Environments

Sources of Variation	Df	Days to 50% flowering	Primary branches	Pods per cluster	No. of pods per plant	Pod length (cm)	No. of seeds per pod
Env	5	4312.674*	3.3901	2.287	1280.298*	1.022	25.577*
Rep (Env)	12	14.974	0.0721	0.0602	20.069	0.103	0.055
Genotype	12	316.469*	0.661*	1.717*	1249.443*	6.528*	33.046*
Error	144	2.488	0.034	0.045	11.524	0.088	0.074

  

Sources of Variation	Df	plant height (cm)	80% maturity	100 seeds weight (g)	seed yield per plant (g)	plant height (cm)
Env	5	40530.13*	7102.756*	46.789*	211.088*	40530.13*
Rep (Env)	12	39.083	17.957	0.637	5.184	39.083
Genotype	12	7968.33*	317.338*	906.983*	177.575*	7968.33*
Error	144	27.796	3.054	0.538	3.439	27.796

\* Significant at 0.05 level of probability

**Table 2:** Genetic parameters for seed yield and its components in rice bean

Characters	Mean	Min	Max	PCV %	GCV %	h2bs (%)	GA	GA as % of mean
50% flowering	94.470	80.33	103.33	19.520	18.825	85.296	5.160	35.332
Primary branches	2.640	2.2	3.6	31.499	30.724	43.78	0.534	1.630
Pods/cluster	49.985	2.4	3.6	47.757	47.137	63.59	0.590	2.661
No. of pods/plant	51.240	30.63	68.8	69.277	68.960	99.085	0.510	72.456
Pod length (cm)	8.138	6.75	9.54	31.591	31.380	98.670	0.280	5.225
Number of seeds/pod	5.513	3.1	7.33	8.029	8.021	93.89	0.379	11.828
Plant height (cm)	130.05	84.13	252.53	68.774	68.654	99.652	0.312	83.542
80% maturity	130.115	120	148	13.752	13.686	93.97	0.103	36.508
100 seed weight (gm)	12.532	4	26.8	18.490	18.485	97.74	0.450	62.019
seed yield/plant (gm)	29.150	22.6	46	46.122	45.681	91.70	6.361	27.168

**Table 3:** Mean performance of different characters of the thirteen genotypes under six environments

Geno-types	50% flowe-ring	Primary branches	Pods/ cluster	No. of pods/plant	Pod length (cm)	Number of seeds /pod	Plant height (cm)	80% maturity	100 seed weight (g)	seed yield/ plant(g)
RbnG1	96.889	2.822	3.022	61.633	7.522	6.450	138.178	133.222	3.933	26.622
RbnG2	93.333	2.300	2.556	39.978	8.456	3.822	98.067	128.722	21.500	27.022
RbnG3	100.50	2.578	2.956	52.400	8.276	5.767	121.956	133.333	10.056	29.656
RbnG4	94.056	2.856	3.222	57.156	7.729	6.933	140.333	132.278	3.967	28.033
RbnG5	90.778	2.500	2.778	54.811	9.418	5.956	148.178	125.611	18.011	31.367
RbnG6	91.778	2.733	2.500	49.411	7.718	6.178	138.122	124.556	12.733	27.767
RbnG7	97.889	2.611	2.356	52.644	7.400	5.733	100.278	127.889	11.878	26.844
RbnG8	83.611	2.656	3.000	59.856	7.577	6.433	154.767	121.056	11.833	37.822
RbnG9	93.611	2.278	2.767	40.144	8.574	3.756	116.222	131.278	21.189	29.933
RbnG10	95.667	2.844	3.178	58.933	8.296	6.289	167.589	132.611	4.400	28.122
RbnG11	96.333	2.633	2.333	36.633	8.954	3.633	108.089	131.778	21.033	28.133
RbnG12	96.778	2.678	2.456	45.183	8.091	4.589	122.956	132.722	19.033	31.611
RbnG13	96.889	2.833	2.978	57.333	7.781	6.128	135.333	135.833	3.356	26.011

### Conclusion

Days to 50% flowering, primary branches, pods per cluster, number of pods per plant, pod length, seeds per pod, plant height, 100 seed weight and seed yield per plant are contributing phenotypic traits for yield and these can be use as

an indices for breeding programme. Mean performances identified superior genotypes for different traits. The maximum seed yield per plant was produced by the genotype RbnG5, RbnG8 and RbnG12. The estimates of phenotypic and genotypic coefficient of variation were the highest for

Pods per plant, number of seeds per pod, plant height and 100 seed weight. The heritability estimates were found to be very high for 50% flowering, number of pods per plant, pod length, number of seeds per pods, plant height, 80% maturity, 100 seed weight and seed yield per plant. Low heritability was recorded for primary branches. It can be concluded that the traits and genotype identified will provide scope for improvement through selection.

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