



Co-efficient of variation, heritability, genetic advance and variability for ricebean (*Vigna umbellata* (Thunb.) genotypes under mid hill conditions of Uttarakhand

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Abstract: The present investigation was carried out to estimate the genetic parameters for ten traits in ricebean genotypes. Fourteen genotypes of ricebean (*Vigna umbellata* (Thunb.)) were collected from different regions of country were evaluated for yield and its components. The study revealed that the phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all traits. The value of PCV and GCV was higher for seed yield/plant, 100 seed weight and number of pods/plant. Heritability values were high for all the traits except leaflet size and pod length. High genetic advance was observed for days to 50% flowering, number of pods and seeds /plant, days to maturity, suggest that scope for improvement of these characters through selection. High heritability coupled with high genetic advance was registered for 50% flowering, number of pods and seeds /plant indicate that the genetic variance for these traits are probably owing to their high additive gene effect and thus there is better scope for improvement of these traits through direct selection. Therefore selection based on these characters will bring the desired improvement in seed yield of ricebean. With respect to mean performance of genotype, PRR-2, PRR-1 and PRR-2011- 1 was found superior among all the genotypes.

Keywords: Genetic Advance, GCV, Heritability, PCV

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. It is mainly cultivated in India, China, Korea, Japan, Myanmar, Malaysia, Indonesia, Philippines, Java, Fiji, Bangladesh, Sri Lanka and Nepal (Purseglove, 1974; Rachie and Roberts, 1974). It is an important crop of mid Himalayan region. In India its distribution is mainly confined to the tribal region of the north-eastern hills and the western and eastern ghats in peninsular region, often in hilly tracts. However its cultivation and production is limited and restricted to small and marginal areas. Therefore ricebean is regarded as underutilized crop. This underutilized crop has recently gained attention as an additional grain legume/pulse crop which keeps great potential to solve the food and nutritional problem. In the marginal areas resource poor farmers cultivates the ricebean. Therefore this crops is directly related with the population who is really suffers frequent food shortage and many nutritional disorders. Mostly it is cultivated in the non irrigated and uncultivated land which otherwise goes to waste. In this sense cultivation of ricebean in such areas is considered important contribution to food and nutritional security

and to utilize uncultivated marginal land and conserving biodiversity. The potential productivity of ricebean has been found superior over other pulse crops, such as greengram and blackgram in mid altitude, particularly Himalayan region, beyond 1500 m above mean sea level where other pulse crops like blackgram and green gram cannot be grown successfully. However, under these conditions, ricebean gives reasonably good seed yield because of its better cold tolerance ability and better adaptation to acidic soil condition (Dutta *et al.*, 2000 and Shukla *et al.*, 2014). The nutritive value of ricebean is exceptionally high. The protein contents of seeds vary from 14-24% and the amino acids, methionine and tryptophane are considerable high (Chandel *et al.*, 1978). It provides sizable amounts of important minerals such as Ca, P, Mg, K, Fe, Zn, Cu and Mn.

This crop has been left as a neglected one due to lack of attention and absence of any kind of scientific breeding. Although it's nutritional quality and other associated benefits qualifies this crop for intensive research, and development efforts for increased and sustained production. However, little research work on its qualities can enhance its properties according to our requirements and this crop which is highly adaptive to all sorts of marginal areas and soils can rise as a great source of edible nutrients for the poor people residing

in those areas. 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). 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 ricebean.

MATERIALS AND METHODS

The present investigation was carried out during *kharif*, 2011 at the Research Block of Department of Crop Improvement, G.B. Pant University of Agriculture and Technology, Hill Campus, Ranichauri, Tehri Garhwal, Uttarakhand. The experimental site is located at 10 km away from Chamba (Rishikesh-Gangotri Road) at an altitude of about 2100 m above mean sea level, lying between 30°15' N latitude and 78° 30' E longitude under mid hill zones of Uttarakhand, India. The experimental materials for the present investigation comprised of 11 diverse entries of ricebean including three checks named PRR-1, PRR-2 and RBL-6. The crop was sown on second week of June, 2011 in silty clay loam soil having slightly acidic PH (5.5 to 5.6) in Randomized Complete Block Design (RCBD) with three replications under rainfed condition. The replications were located in three adjacent terraces. Each genotype in each replication was represented by a plot of four rows of 3m length with a spacing of 30 cm between rows and 15 cm between plants within row. All cultural practices were adopted to raise the normal healthy crop. Observations were recorded on ten randomly selected plants in each entry and replication for ten characters *viz.*, field emergence percent, days to 50% flowering, days to maturity, stem thickness (mm), leaflet size (cm), number of pods per plant, number of seeds per pod, pod length (cm), 100 seed weight (g), seed yield per plant (g). Data were subjected to statistical analysis of ANOVA using STPR software model developed by University Computer Center. The statistical analysis for all the characters was done by the method recommended by

Cochran and Cox (1992). The genetic parameters *viz.* phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were estimated as per formula given by Burton and Devane (1953).

$$\text{Genotypic coefficient of variability (GCV)} = \sqrt{V_g} \times 100 / \bar{x}$$

$$\text{Phenotypic coefficient of variability (PCV)} = \sqrt{V_p} \times 100 / \bar{x}$$

Where,

V_g = Genotypic variance,

V_p = Phenotypic variance and

\bar{x} = General mean of character.

Broad sense heritability was estimated based on the ratio of genotypic variance to the phenotypic variance and was expressed in percentage (Hanson *et al.*, 1956).

$$\text{Heritability (h}^2\text{)} = V_g / V_p \times 100$$

Where V_g = Genotypic variance

V_p = Phenotypic variance

The expected genetic advance resulting from selection of five percent superior individuals worked out as suggested Johnson *et al.* (1955).

$$\text{Genetic advance} = h^2 \times V_p \times K$$

h^2 = heritability in broad sense

V_p = Phenotypic standard deviation

K = Selection differential at 5% selection intensity ($K = 2.06$)

RESULTS AND DISCUSSION

Analysis of variance revealed significant (5% level) difference among the fourteen genotypes for all the ten traits under study and indicating the presence of substantial genetic variability in ricebean. The genetic parameters *viz.* phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), heritability and genetic advance are presented in (Table- 1). The estimate of genotypic and phenotypic coefficient of variation provides a better comparison of the characters for the extent of genetic variation. As expected, the PCV values were greater than the GCV values for all the characters indicating considerable influence of environment on the expression of these characters under field conditions. Similarly greater values of PCV than GCV for different characters were also reported by Khan *et al.* (2015) in cowpea and

Table 1. Estimation of heritability, genetic advance, GCV and PCV for field parameters of different genotypes of ricebean.

S.N.	Characters	Heritability (%)	Genetic Advance	Coefficient of variation (%)	
				Genotypic	Phenotypic
1.	Field germination (%)	0.94	9.10	5.58	5.74
2.	Days to 50% flowering	0.97	9.88	5.72	5.79
3.	Days to maturity	0.94	10.34	3.15	3.24
4.	Stem thickness (mm)	0.74	0.823	9.38	10.86
5.	Leaflet size (cm)	0.42	0.39	4.05	6.24
6.	No. of pods/plant	0.77	7.58	16.12	18.25
7.	No. of seeds/pod	0.68	1.46	12.78	15.48
8.	Pod length(cm)	0.49	0.79	6.46	9.17
9.	Seed yield/plant (g)	0.93	3.66	20.58	21.23
10.	100 seed weight (g)	0.98	2.27	18.47	18.58

Table 2. Mean performance of different genotypes of ricebean for field parameters.

Entries	Field Germination (%)	Days to 50% flowering	Days to maturity	Stem thickness (mm)	Leaflet size (cm)	No. of pods/plant	No. of seeds/pod	Pod length (cm)	Seed yield/plant (g)	100 seed weight (g)
PRR-2011-1	86.00	88.66	165.66	4.99	7.57	31.43	6.64	8.83	11.99	6.22
PRR-2011-2	80.66	82.66	160.66	5.16	6.85	31.26	6.34	8.43	8.69	5.52
PRR-2011-3	81.33	79.33	157.33	5.57	6.72	25.93	6.05	8.30	9.19	6.42
RBHP-30	79.66	79.66	157.66	4.79	7.36	30.63	5.55	7.77	6.99	4.49
RBHP-35	73.33	90.33	168.33	4.81	7.07	21.80	5.36	7.53	6.34	5.39
BRS-1	80.33	84.66	162.66	4.77	7.02	26.16	6.65	8.22	8.83	5.83
IC-563980	83.33	91.00	169.00	6.14	7.75	18.96	6.06	8.23	8.49	8.18
IC-141077	85.33	82.66	168.33	5.20	6.78	27.83	6.51	8.56	8.36	4.78
LRB-460	71.66	90.33	169.33	4.42	7.31	20.06	6.96	8.73	6.87	5.15
RBHP-43	83.00	88.66	160.66	4.87	7.06	24.70	7.23	8.78	8.53	5.40
VRB-3	78.33	75.33	167.66	4.66	7.46	19.96	6.26	7.91	7.91	7.73
PRR-1	84.66	81.00	153.33	4.68	7.08	28.46	8.11	9.72	11.60	6.16
PRR-2	87.00	87.66	158.66	4.75	7.87	30.26	8.50	9.53	12.36	7.51
RBL-6	85.33	86.33	165.66	4.14	7.08	24.93	7.80	7.85	8.75	5.38
RANGE	71.66 -87.00	75.33 -91.0	153.33 169.33	4.14 -6.14	6.7 -7.87	8.96 -31.43	5.36 -8.50	7.53 -9.72	6.34 -12.36	4.49 -8.18
GM	81.42	84.88	163.21	4.92	7.21	25.88	6.71	8.46	8.92	6.01
SEM	0.63	0.45	0.69	0.15	0.19	1.28	0.33	0.31	0.268	0.072
CD(%)	1.82	1.30	1.99	0.43	0.54	3.69	0.95	0.89	0.75	0.20
CV(%)	1.35	0.90	0.73	5.28	4.57	8.53	8.68	6.38	5.04	1.99

Arshad *et al.* (2003) in chickpea. Wide range of PCV was observed and it ranged from 3.24% for days to maturity to 21.23% for seed yield/plant. Number of pods/plant (18.25%), number of seeds/pod (15.48%), Seed yield/plant (21.23%) and 100 seed weight (18.58%) registered high PCV values that suggested favourable effect of environment in the expression of these characters. These results indicated that the material under study provide ample scope for improvement through selection in these characters. Lakshmana *et al.* (2010) 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) evaluated greengram 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) in cowpea reported high PCV values for grain yield/plant (34.93%), number of pods/plant (34.13%) and 100 seed weight (22.49%).

High value of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) recorded for the Seed yield/plant (21.23%, 20.58%) followed by 100 seed weight (18.58%, 18.47%), number of pods/plant (18.25%, 16.12%) and number of seeds/pod (15.48%, 12.78) respectively and narrow range of difference between phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was observed for these characters indicating less influence of environment on the phenotypic expression of these characters and they are mostly governed by genetic factor. So, the selection based on phenotypic performance would be effective for improvement of these characters. These results are in accordance with the findings of Ahmad and Rabbani (1992), who studied the genetic variability in ricebean 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) in mungbean and Lakshmana *et al.* (2010) in ricebean and Khan *et al.* (2015) in cowpea.

Knowledge on the heritability is important to a plant breeder since it indicates the possibility and extent to which improvement is possible through selection. The estimate of heritability in broad sense for ten traits studied, ranged from 0.42 for leaflet size to 0.93 for seed yield. The broad sense heritability estimates were higher for all the characters except leaflet size (0.42) and pod length (0.49). It indicates that the character expressing higher heritability estimate are less influenced by environment and such characters also indicate that they are under influence of more number of fixable factors Vaghela *et al.* (2009). Burton (1952) suggested that genotypic coefficient of variation along with heritability estimate would exhibit a better picture of genetic gain expected through phenotypic selection. Seed yield/plant (20.58%, 0.93%), 100 seed weight

(18.47%,0.98%), number of pods/plant (16.12%, 0.77%) recorded high estimate of GCV coupled with heritability. 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) in ricebean, Dodwad *et al.* (1998) in greengram, Vaghela *et al.* (2009) in chickpea and Khan *et al.* (2015) in cowpea. High estimate of genetic advance was observed for days to maturity (10.34), days to 50% flowering (9.88), field germination (9.10), number of pods/plant (7.58) and seed yield/plant (3.66), suggesting that these characters were governed by additive gene action and selection pressure could profitably applied on these characters for yield improvement. Lakshmana *et al.* (2010) in ricebean also observed high value of genetic advance for germination percent (11.85), days to maturity (10.92) and days to 50% flowering (9.66).

The mean performance of some selected genotypes in respect of characters investigated in the present study is presented in (Table- 2). Maximum field emergence was recorded for genotypes PRR-2 and PRR-2011-1, whereas minimum for genotype LRB-460. Genotype VRB-3 showed the minimum days to 50% flowering followed by PRR-2011-3. The highest number of pods per plant were recorded in the genotype PRR-2011-1 followed by PRR-2011-2 while lowest for IC-563980. The maximum number of seeds/pod was recorded in the genotype PRR-2 and minimum for RBHP-35. Genotype PRR-1 showed the maximum pod length followed by and PRR-2 and PRR-2011-1 whereas minimum for RBHP-35. The mean performance for 100 seed weight was ranged from 4.49 – 8.18g. The highest weight was recorded for genotype IC-563980 and the minimum for the genotype RBHP-30. The mean value for seed yield/plant was ranged from 6.34 to 12.36g and maximum value was recorded for genotype PRR-2 followed by PRR-2011-1 and PRR-1. A considerable variation among the genotypes has also been observed in clusterbean by Rai *et al.* (2012). Compared to the performance of check varieties genotype PRR 2011-1 appeared to be better over one check variety RBL-6. Likewise genotype PRR 2011-2 and RBHP-30 for number of pods/plant, IC-563980 and VRB-3 for seed weight were much better compared to three check varieties.

Conclusion

The experimental studies revealed substantial amount of genetic variability among the genotypes under study. The study indicates that the seed yield per plant, days to 50% flowering and number of pods per plant exhibited high magnitude of heritability coupled with high genetic advance and greater GCV which indicate the predominance of additive gene action in controlling these characters and simple directional selection may be effective to improve these characters. Crossing between the genotype showing better mean

performance in respect of no. of pods/plant and the genotypes showing better seed weight may help in generating a new genotype with better expression for these traits.

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