

Analysis of Genetic Diversity on Rice bean [*Vigna umbellata* (Thunb.) Ohwi and Ohashi] Germplasm in Uttarakhand Region

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Abstract:

The present investigation was conducted during *Kharif*, 2014 at Research Block, Department of Crop Improvement, V.C.S.G. Uttarakhand University of Horticulture and Forestry, College of Forestry, Ranichauri Campus, Tehri Garhwal, Uttarakhand. The experiment included the 28 diverse genotypes of rice bean along with three checks *viz.*, PRR-1, PRR-2 and BRS-1 were evaluated in Randomized Complete Block Design. The characters studied were days to 50 % flowering, days to maturity, plant height, stem thickness, number of primary branches per plant, leaflet size, number of pods per plant, number of seeds per pod, pod length, 100 seed weight and seed yield per plant. The twenty eight genotypes of rice bean were grouped into six clusters irrespective of geographical diversity, indicating no parallelism between geographic and genetic diversity. The cluster pairs exhibiting very high inter-cluster distances were cluster IV and V, cluster II and IV, cluster I and cluster IV, cluster III and IV. Considering cluster mean and genetic distance the crossing of entry of clusters IV with entries of cluster V and those genotypes of cluster II, I and III with the entries of cluster IV would be fruitful for obtaining transgressive segregants for developing high yielding and better quality rice bean varieties.

Keywords: Genetic diversity, yield, rice bean.

Introduction

Rice bean ($2n=24$) varyingly known as climbing mountain bean, mambi bean and haricot bean is a native of South and South East Asia (Ohwi, 1965) and locally known as Naurangi or Rayansh. Rice bean is a self pollinated crop but there is some probability of natural cross pollination (Sastrapradja and Sustarnu, 1977). Rice bean is a underused crop which has recently gained attention as an supplementary grain legume/pulses crop and acquire vast potential due to its high nutritional quality, high grain yield ability and versatile usage such as food, animal feed, cover crop and as soil enriched, it is more tolerant to pest and disease and in storage it is less infected by storage pest (Chatterjee and Dana, 1977). The nutritional quality

of rice bean is magnificent due to the presence of high amount of protein and limiting quantities of amino acids such tryptophan and methionine which rank it as one of the best among the pulses (NAS, 1975). Its seed contain vitamins such as thiamine, riboflavin, niacin, and ascorbic acid (Joshi *et al.*, 2006). A great expanse of diversity present in various quantitative traits among the genotypes of rice bean indicates good scope for amendment in economic traits through conventional breeding. Determination of available genetic variability for important economic traits to develop high yielding varieties is an important function in crop breeding.

The objective of breeding mostly apprehended to evaluate different genotypes of rice bean under high hills, low temperature and rain-fed condition of Himalayas from a set of germplasm collected from different places at hills and plains of India. Furthermore, information on expanse of genetic variability among available genetic resources, the nature of association between various yield attributes and relative importance and direct and indirect influence of each of the factor traits on yield could prove helpful in standardized an effective breeding approach for randomized the productivity of rice bean at specific region of Uttarakhand.

Method and Material

The present research was carried out during *Kharif* 2014 at Research Block of Crop Improvement, College of Forestry, Ranichauri, Tehri Garhwal, Uttarakhand. The research site, College of Forestry, Ranichauri is located at 10 km away from Chamba (Reshikesh-Gangotri road) at an altitude of about 2100 m above mean sea level, lying between 30° 15' N latitude and 78° 30' E longitudes under mid hill zones of Uttarakhand. The field analyses of the genotypes were carried out in the experimental block of Department of Crop Improvement. The experimental materials for the present investigation comprised of 28 diverse entries of rice bean obtained from the Department of Crop Improvement, College of Forestry, Ranichauri. The experiment was conducted in the Randomized Complete Block Design (RBD) during *kharif* season under rainfed condition. The research include 25 entries along with the three check was planted during the first week of June, 2014. The seeds were sown 4-6 cm depth by open furrow with *kutla*. Each furrow was hand operated dribbled with seed and covered with soil immediately. As per the standards, the row to row distance 30 cm x 15 cm between plants was maintained after germination. At the time of harvesting, the crop was cut above the ground with the help of sickles and tied into bundles and tagged. The bundles were allowed to dry under the sunlight for 8-10 days. After that the hand operated threshing of bundles of individual plots was done.

Result and Discussion

The studies of genetic divergence among the 28 genotypes of rice bean germplasm were performed by employing Mahalanobis D^2 statistic as described by Rao (1952).

3.1 Composition of clusters

The twenty eight genotypes of rice bean were grouped into six different non-overlapping clusters as presented in Table 3.1. The cluster V was largest group containing 9 genotypes (IC 394201, IC 524084, IC 524076, IC 538870, IC 421875, IC 137189, IC 524075, IC 419806, IC 524549), followed by cluster VI consisting of 8 genotypes (IC 524085, IC 411730, IC 524522, IC 369282, IC 524082, IC 524074, IC 538983, IC 524070) and cluster III represented by 5 genotypes (LRB 456, LRB 458, PRR 2 ©, LRB 471, PRR 1) whereas cluster II possessed 3 genotypes (LRB 319, LRB 472, LRB 322) and cluster I consisted of 2 genotypes (IC 419489, IC 394537). The cluster IV was represented by only 1 genotype (BRS 1).

Thus, the clustering pattern did not requisite go through any relevance with the geographical origin of the test germplasm as specify in the present study. Also the substantial genetic diversity among the germplasm lines screened indicates that these materials may serve as good source for selecting the diverse parents for hybridization programme aimed as isolating desirable segregates for developing high yielding varieties of finger millet.

Table 3.1 Clustering pattern of genotypes of rice bean on the basis of genetic divergence

| No. of clusters | No. of genotypes | Genotypes |
|-----------------|------------------|---|
| Cluster 1 | 2 | IC 419489, IC 394537 |
| Cluster 2 | 3 | LRB 319, LRB 472, LRB 322 |
| Cluster 3 | 5 | LRB 456, LRB 458, PRR 2©, LRB 471, PRR 1© |
| Cluster 4 | 1 | BRS 1© |
| Cluster 5 | 9 | IC 394201, IC 524084, IC 524076, IC 538870, IC 421875, IC 137189, IC 524075, IC 419806, IC 524549 |
| Cluster 6 | 8 | IC 524085, IC 411730, IC 524522, IC 369282, IC 524082, IC 524074, IC 528983, IC 524070 |

3.2 Intra-and Inter cluster genetic distance ($\sqrt{D^2}$)

The estimates of intra- and inter-cluster distance represented by D^2 values have been given in Table 3.2. The intra-cluster distances ranged from 19.453 (cluster VI) to 43.369 (cluster III). The maximum inter-cluster distance was observed between cluster IV and V (200.266), followed by cluster II and IV (156.869), cluster I and IV (154.054) and cluster III and IV (152.162). The inter-cluster distance between cluster III and VI and cluster IV and VI were also high. The clusters with higher inter-cluster distances indicated that the genotypes included in those clusters had high genetic variation and hybridization between genotypes of these cluster may result heterotic hybrids because of convergence of diverse genes scattered in parents to progeny. The

minimum estimates for inter-cluster distance was recorded between cluster V and VI (37.084). The clusters with lowest inter-cluster distances indicated that genotypes present in these cluster pairs were genetically close to each other. The crosses between genotypes belonging to clusters separated by low inter cluster distance were likely to throw promising recombinants in the segregating generations. Diversity of genotypes belonging to clusters with maximum inter-cluster distance for hybridization had also been proposed by Vavilapalli *et al.* (2014) and Nagalaxmi *et al.* (2010) in cowpea.

Table 3.2 Inter and Intra cluster distance $\sqrt{D^2}$ values among genotypes of rice bean

| | I | II | III | IV | V | VI |
|-----|---------------|---------------|---------------|-------------|---------------|---------------|
| I | 28.341 | 83.171 | 95.813 | 154.054 | 63.07 | 65.629 |
| II | | 40.668 | 75.476 | 156.869 | 69.53 | 75.605 |
| III | | | 43.369 | 152.162 | 144.097 | 139.387 |
| IV | | | | 0.00 | 200.266 | 117.252 |
| V | | | | | 26.724 | 37.084 |
| VI | | | | | | 19.453 |

3.3 Cluster means

The intra-cluster group means for eleven characters given in Table 3.3 revealed the marked differences between the clusters in respects of cluster means for different characters. Cluster I, having 2 genotypes, showed highest cluster for stem thickness (5.577 mm) and number of primary branches (3.483) but exhibited lowest cluster mean for days to 50% flowering (83.000), number of pods per plant (19.533) and 100 seed weight (6.083g). Cluster II exhibited average cluster mean for all characters but had lowest cluster mean for plant height (66.222cm). The 5 entries of cluster III were responsible for highest cluster mean for pod length (7.993cm), number of pods per plant (30.075), leaflet size (6.937cm), number of seeds per pod (7.473) and seed yield per plant (10.115g) but also exhibited lowest cluster mean for days to maturity (152.333 days) and stem thickness (3.279mm). The cluster IV having monogenotypic, resulting highest cluster mean for days to maturity (160.33 days), plant height (88.967cm) and 100 seed weight (10.050g) but this cluster were characterized by low mean for number of primary branches (2.800). Cluster V having highest number of genotypes (9) and showed lowest mean for leaflet size (5.998cm), number of seeds per pod (5.652) and seed yield per plant (7.142g). Cluster VI having 8 genotypes, exhibited highest cluster mean for days to 50% flowering (94.167 days) and days to maturity (60.333 days) but it showed lowest cluster mean for pod length (5.868cm).

On the ground of above results it is perceptible that cluster III had maximum cluster means for most of desirable characters *viz.*, pod length, number of pods per plant, leaflet size,

number of seeds per pod and seed yield per plant. Similar results have also been observed by Das *et al.* (2001) in soybean and Bakiyarani *et al.* (2000) in cowpea.

Table 3.3 Intra cluster group means for various components of yield in rice bean

| S. No. | Characters | Cluster Means | | | | | |
|--------|---------------------------|---------------|---------|---------|---------|---------|---------|
| | | I | II | III | IV | V | VI |
| 1. | Days to 50 % flowering | 83.000 | 85.556 | 86.200 | 90.000 | 93.037 | 94.167 |
| 2. | Days to maturity | 156.667 | 159.889 | 152.333 | 160.333 | 158.963 | 160.333 |
| 3. | Plant height (cm) | 83.250 | 66.222 | 79.260 | 88.967 | 69.852 | 75.700 |
| 4. | Stem thickness (mm) | 5.577 | 3.684 | 3.279 | 4.133 | 5.013 | 5.287 |
| 5. | Pod length (cm) | 7.282 | 7.183 | 7.993 | 7.950 | 6.051 | 5.868 |
| 6. | No. of pods per plant | 19.533 | 25.003 | 30.075 | 23.070 | 19.896 | 19.640 |
| 7. | Leaflet size (cm) | 6.230 | 6.862 | 6.937 | 6.917 | 5.998 | 6.203 |
| 8. | No. of primary branches | 3.483 | 2.889 | 3.340 | 2.800 | 2.974 | 2.833 |
| 9. | No. of seeds per pod | 6.083 | 5.833 | 7.437 | 6.233 | 5.652 | 5.692 |
| 10. | 100 seed weight (gm) | 6.040 | 6.939 | 6.959 | 10.050 | 6.385 | 7.605 |
| 11. | Seed yield per plant (gm) | 8.125 | 8.526 | 10.115 | 8.280 | 7.142 | 7.333 |

3.4 Contribution of different characters to total divergence

The percentage contribution of eleven characters towards total genetic divergence is listed in Table 3.4. The maximum contribution towards expression of genetic divergence was exhibited by 100 seed weight (27.78%) followed by pod length (17.20%), stem thickness (12.96%) and plant height (11.38%). Seed yield per plant (7.41%), number of seeds per pod (6.35%), days to 50% flowering and leaflet size (5.03%) also played considerable role in conditioning the genetic divergence. Days to maturity (3.44%), number of pods per plant (2.12%) and number of primary branches (1.32%) exhibited low contribution towards total genetic divergence. These were considered to be the most important characters for the genetic diversity. The observation is accordance with the result obtained by Raje and Rao (2001) in mung bean, Ushakumari *et al.* (2002), Borah and Khan (2002), Venkatesan (2004), Nagalaxmi *et al.* (2010) in cowpea, Singhal *et al.* (2010) in horse gram, Gokulakrishna *et al.* (2012) in mung bean; and Vavilapalli *et al.* (2014) in cowpea

In present investigation, an assessment of the contribution of different characters indicated that 100 seed weight, pod length, stem thickness, and plant height had maximum contribution to genetic divergence as these traits appeared maximum times highest *viz.*, 105, 65, 49 and 43, respectively.

Table 3.4 Contribution of different plant growth and seed yield characters to total divergence in rice bean

| S. No. | Characters | Number of times appearing first in ranking | Percent contribution |
|--------|---------------------------|--|----------------------|
| 1. | Days to 50 % flowering | 19 | 5.03 |
| 2. | Days to maturity | 13 | 3.44 |
| 3. | Plant height (cm) | 43 | 11.38 |
| 4. | Stem thickness (mm) | 49 | 12.96 |
| 5. | Pod length (cm) | 65 | 17.20 |
| 6. | No. of pods per plant | 8 | 2.12 |
| 7. | Leaflet size (cm) | 19 | 5.03 |
| 8. | No. of primary branches | 5 | 1.32 |
| 9. | No. of seeds per pod | 24 | 6.35 |
| 10. | 100 seed weight (gm) | 105 | 27.78 |
| 11. | Seed yield per plant (gm) | 28 | 7.41 |

Conclusion

From the above research, it is assume that the high inter-cluster distances, cluster means and means performance of genotypes, crossing of entries of cluster IV (BRS-1 (c)) with entries of cluster V (IC-394201, IC-524084, IC-524076, IC-538870, IC-421875, IC-137189, IC-524075, IC-419806 and IC-524549). Similarly, crossing of promising genotypes belonging cluster II (LRB 319, LRB 472 and LRB 322), cluster I (IC-419489 and IC-394537) and cluster III (LRB 456, LRB 458, PRR-2, LRB 471 and PRR-1) with high yielding genotypes of cluster IV (BRS-1) would also be fruitful for obtaining transgressive segregants for developing high yielding and better quality rice bean varieties.

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