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Assessment of genetic diversity in ricebean germplasm for yield traits

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ABSTRACT

Genetic diversity was studied in 40 ricebean germlasm accessions collected mostly from the different parts of NW Himalayas using Mahalanobis's D^2 statistics. In the present investigation with non-hierarchical Euclidean cluster analysis, 40 genotypes of ricebean were grouped into two clusters. While cluster II contained only one genotype *i.e* PRR-2007-2, all other genotypes were grouped into cluster I. The maximum contribution towards the genetic divergence was exhibited by pods/cluster (19.10%) followed by plant height (15.77%), seed yield/plant (15.00%) and days to flowering (15%). Lowest contribution towards the genetic divergence was exhibited by seeds per pod (0.13%). Cluster distance observed for cluster II was 10.36 followed by cluster I which was 3.23. Cluster 1 showed maximum cluster mean values for all characters *viz.*, days to flowering, days to maturity, plant height, branches/plant, pods/plant, pod length, 100-seed weight, seeds/pod, clusters/plant, pods/cluster and seed yield/plant, while cluster 2 showed lowest values for all the characters studied. Based on present study, parents for hybridization programme for incorporation of earliness and determinate habit which is the major bottleneck in the popularization of this underutilized pulse can be selected from cluster II whereas for other traits parents can be selected from cluster I.

Key words: Divergence, Genetic variability, Ricebean.

Ricebean [*Vigna umbellata*, (Thunb) Ohwi and Ohashi] is one of the potential pulse and is a multipurpose grain legume crop mainly cultivated for food, fodder and green manure. Grains are used as whole '*dal*' while immature pods and leaves as vegetable. The green fodder contains higher amount of proteins and also used for green manuring. It is largely self-pollinated diploid (2n=22) grown as *kharif* crop. The nutritional quality of ricebean appears to be best among all the traditional pulses due to higher amount of proteins, essential amino acids, essential fatty acids and minerals. It contains about 20% protein which is enriched in essential amino acids like methionine, tryptophan, lysine, tyrosine and valine. Its favourable protein content ensure higher digestibility and therefore make it a fit food item for children, women and older people with weak digestion. In addition it provides sizeable amounts of important minerals such as Ca, P, Mg, K, Fe, Zn, Cu and Mn. Though diverse landraces with different plant and seed morphologies have been locally produced and maintained by farmers, still the genetic improvement of this crop is slow due to inadequate information of genetic stocks and paucity of this information about existing ones. Thus, systematic efforts are needed to characterize the germplasm for their sustainable utilization in breeding programmes as choice of germplasm is an essential and crucial step in any plant breeding program, whether for the development of varieties or to produce hybrids, and can determine the success or failure of the selection process. The study of genetic divergence can assist in the choice of genotypes to be used in breeding programs for the development of new populations.

The selection of suitable diverse parents for hybridization programme is an important feature of any crop improvement strategy for getting desired recombinants. Genetic diversity present in the available lines provides immense value on crop improvement for character(s) of interest. For selecting the parents for hybridization, which are required to be divergent enough for the character(s) of interest, estimation of the genetic distance is most important. Genetic divergence is related to the degree of distance between populations in the set of genetic characters that differ between the populations. Multivariate analysis with "Mahalanobis D^2 statistics (1936)" is a powerful tool to know the clustering pattern to establish the relationship between genetic and geographic divergence and to determine the role of different quantitative characters towards the maximum divergence (Murthy and Arunachalam,1966). It quantifies

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the degree of divergence between biological populations at genotypic level and assess relative contribution of different components to the total divergence both intra and inter-cluster level. The knowledge about the source of genetic diversity for the different characters is of considerable importance, since the prime aim of the plant breeder is to improve the yield and the quality by evolving superior varieties.

Materials and layout of the design: The experiment was conducted in the experimental farm of the Department of Organic Agriculture, CSKHPKV, Palampur, Himachal Pradesh in *kharif*, 2015. The experimental material for the present study consisted of 40 ricebean accessions including 2 checks (PRR-1 and PRR-2). These genotypes along with checks were evaluated for different quantitative traits in RBD design during *kharif,* 2015 with plot size of 3 m x 0.6 m with row to row and plant to plant distance of 30 cm and 10 cm, respectively in three replications. The crop was raised following standard package of practices. The details of genetic stocks are given in Table 1.

Observations recorded: The data was recorded on five random competitive plants for each genotype across replications on branches/plant, days to flowering, pods/ cluster, pods/plant clusters/plant, days to maturity, plant height (cm), pod length (cm), seeds/pod (no.), 100-seed weight (g) and seed yield/plant (g).

Statistical methods: Statistical analysis of the data was done as per Mahalanobis (1936) and using D^2 values, different genotypes were grouped into various clusters following Tocher's method as suggested by Rao (1953). Cluster means of ricebean genotypes falling under different clusters in individuals as well as combined over environments were also calculated.

In the present investigation with non-hierarchical Euclidean cluster analysis, 40 genotypes of ricebean were grouped into two clusters (Fig. 1, Table 2). While cluster II contained only one genotype *i.e.* PRR-2007-2, all other genotypes were grouped into cluster I. The Cluster distance observed for cluster II was 10.36 whereas for cluster I it was 3.23 (Table 3). The higher inter-cluster distance indicated the presence of more genetic diversity among the genotypes included among these clusters. Thus, more heterosis and greater number of useful transgressive segregants can be obtained by hybridization between genotypes from distant clusters. Cluster 1 showed

Table 1: List of germplasm lines of ricebean evaluated under the present study

Genotypes	Source/Pedigree
LRB-478	PAU, Ludhiana
LRB-474	PAU, Ludhiana
LRB-473	PAU, Ludhiana
LRB-476	PAU, Ludhiana
LRB-449	PAU, Ludhiana
LRB-447	PAU, Ludhiana
LRB-475	PAU, Ludhiana
LRB-464	PAU, Ludhiana
LRB-311	PAU, Ludhiana
LRB-498	PAU, Ludhiana
LRB-455	PAU, Ludhiana
IC-395028	NBPGR, New Delhi
IC-538878	NBPGR, New Delhi
IC-23512	NBPGR, New Delhi
IC-538983	NBPGR, New Delhi
IC-419518	NBPGR, New Delhi
IC-359282	NBPGR, New Delhi
IC-524082	NBPGR, New Delhi
IC-421926	NBPGR, New Delhi
IC-538870	NBPGR, New Delhi
UURB-17	UUHF, Ranichauri
UURB-2014-I	UUHF, Ranichauri
PRR-2007-2	UUHF, Ranichauri
RBHP-401	CSKHPKV, Palampur
RBHP-43	CSKHPKV , Palampur
RBHP-38	CSKHPKV , Palampur
RBHP-403	CSKHPKV , Palampur
RBHP-404	CSKHPKV , Palampur
RBHP-405	CSKHPKV , Palampur
RBHP-406	CSKHPKV , Palampur
RBHP-407	CSKHPKV , Palampur
RBHP-408	CSKHPKV , Palampur
RBHP-409	CSKHPKV , Palampur
RBHP-410	CSKHPKV , Palampur
RBHP-411	CSKHPKV , Palampur
RBHP-412	CSKHPKV , Palampur
RBHP-413	CSKHPKV , Palampur
RBHP-414	CSKHPKV , Palampur
PRR-I	UUHF, Ranichauri
PRR-2	UUHF, Ranichauri

Table 2: Grouping of ricebean genotypes into different clusters on the basis of Mahalanobis D^2 analysis

Clusters	Number of genotypes	Genotypes
I	39	LRB-478, LRB-474, LRB-473, LRB-476, LRB-449, LRB-447,LRB-475, LRB-464, LRB-311, LRB-498, LRB-455, IC-395028, IC-538878, IC-23512, IC-538983, IC-419518, IC-359282, IC-524082, IC-421926, IC-538870, UURB-17, UURB-2014-I, RBHP-401, RBHP-43, RBHP-38, RBHP-403, RBHP-404, RBHP-405, RBHP-406, RBHP-407, RBHP-408, RBHP-409, RBHP-410, RBHP-411, RBHP-412, RBHP-413, RBHP-414, PRR-I (C) , PRR-2 (C)
II	1	PRR-2007-2

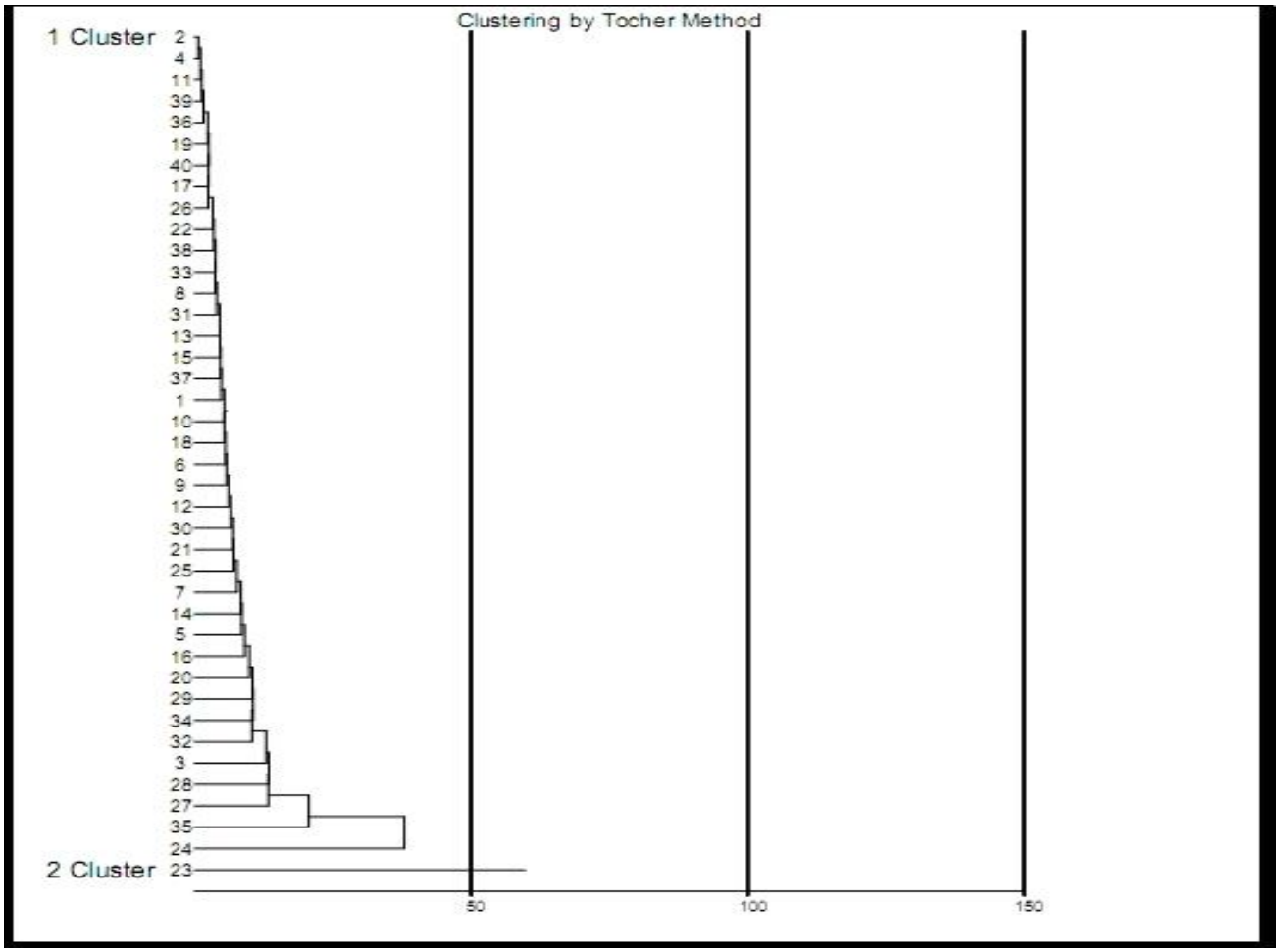

Fig-1: Phenogram of ricebean genotypes generated using Mahalanobis D^2-cluster analysis

maximum cluster mean values for all characters *viz.*, days to flowering, days to maturity, plant height, branches/ plant, pods/plant, pod length, 100-seed weight, seeds/pod, clusters/plant, pods/cluster and seed yield/plant, while cluster II showed lowest values for all the characters studied (Table 4). RBHP-403, RBHP-43, RBHP-413, UURB-17, IC-419518, IC-395028 of cluster I showed higher number of branches/plant and clusters/plant and seed yield/plant. The genotype PRR-2007-2 was earliest and dwarfest genotype among all the genotypes. Thus, hybridization between these genotypes could be effective in future breeding programme in developing early maturing and high yielding varieties of rice bean with more number of branches, clusters and pods per plant.

Based on present study, parents for hybridization programme for incorporation of high yield and other economic traits can be selected from cluster I whereas for earliness can be selected from cluster II(Table 4). Panchta *et al.* (2012) also studied genetic divergence in 65 genotypes using Mahalanobis D^2 statistic and grouped the genotypes into eight clusters whereas Misra *et al.* (2009) devided the ricebean mutagenic population of ricebean into five different clusters.

Table 3: Cluster Distances

	Group 1	Group 2
Group 1	3.23	10.36
Group 2	10.36	0.00

Table 4: Cluster means of two clusters for different traits of ricebean genotypes

	Days flowering	Days to maturity	Plant height	Branches/ plant	Pods/ length	Pod plant	100- seed weight	Seeds/ pod	Clusters/ plant	Pods/ cluster	Seed yield/ plant
Cluster 1	85.74	132.30	154.08	1.88	68.98	9.74	9.67	9.23	22.65	3.01	10.10
Cluster 2	52.00	106.00	90.00	1.70	39.10	5.95	7.26	6.07	11. 80	2.13	3.45

Table 5: Relative contribution (%) of individual trait to the genetic divergence among ricebean genotypes

Traits	No. of times ranked first	Contribution (%)
Days to flowering	117	15.00
Days to maturity	66	8.46
Plant height	123	15.77
Branches/plant	65	8.33
Pods/plant	2	0.26
Pod length	22	2.82
100-seed weight	54	6.92
Seeds/pod	1	0.13
Clusters/plant	64	8. 21
Pods/cluster	149	19.10
Seed yield/plant	117	15.00

The relative contribution of individual trait to the genetic divergence among ricebean genotypes is presented in Table 5. The maximum contribution towards the genetic divergence was exhibited by pods/cluster (19.10%) followed by plant height (15.77%), seed yield/plant (15.00%) and days to flowering (15%). Lowest contribution towards the genetic divergence was exhibited by seeds/pod (0.13%). Similar studies in ricebean were also conducted by Gupta *et al*. (2014) on fifty two genotypes revealing that 100-seed weight and pod yield/ plant were the major contributing characters towards genetic diversity.

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