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GENETIC DIVERGENCE AMONG RICE BEAN (*VIGNA UMBELLATA* (THUMB) OWHI AND OHASHI) CULTIVARS OF MANIPUR HILLS

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ABSTRACT

Genetic divergence of thirty-one local rice bean cultivars of Manipur hills and genotype $CXM_{12}P_3$ from the N.B.P.G.R, was studied. Based on Mahalanobis D^2 values, the genotypes were classified into five different clusters following Tocher's method. Depending upon the inter-cluster distance, cluster mean value and mean *per se* performance of the best genotype within the cluster, cross combinations involving different selected parents for various breeding objectives were suggested: RBM1 × RBM10 for shorter plant height, early flowering and higher number of seeds per pod, RBM10 × RBM17 for higher primary branches per plant, RBM11 × RBM17 for higher number of pods per plant and grain yield per plant, RBM31 × RBM17 for higher length of pod and seed weight.

Key words : Rice bean, genetic divergence, D^2 statistic

Although rice bean seems to be a very promising grain legume crop for Manipur hills, the rice bean cultivars growing for grain production in the state are mostly of late duration with long trailing growth habit. These cultivars, in fact, are not suitable for scientific crop production under density planting. Attempts are, therefore, being made for developing desirable high yielding rice bean varieties for increased productivity and production under the agro-ecological conditions of Manipur hills. The present investigation aimed at identifying genetically divergent parents which can be utilized in the hybridization programme for rice bean breeding in Manipur.

MATERIALS AND METHODS

Thirty-two rice bean cultivars comprising of 31 local cultivars from five hill districts of Manipur collected through actual visit at farmers field and 1 cultivar collected from the NBPGR, New Delhi-12, were evaluated for eight important agronomic characters in Randomised Complete Block Design with three replications during *kharif* 1993 and 1994 at the Pulses Experimental Farm of the Central Agricultural University, Imphal. Each experimental plot consisted of 6 rows of 4m in length with row to row and plant to plant distances of 50 cm and 40 cm respectively. Observation on flowering initiation was recorded on plot basis while the Characters - plant height at maturity (cm), primary branches per plant, pods per plant, length of pod (cm), seeds per pod, 1000 seed weight (g) and grain yield per plant (g) were recorded from 5 randomly selected competitive plants from each plot.

Yearwise and pooled data were subjected to analysis of variance following Gomez and Gomez [1]. From the pooled data, genetic divergence of the cultivars was studied following Mahalanobis D^2 statistics [2, 3]. Grouping of the genotypes into various clusters was made by Tocher method [4].

RESULTS AND DISCUSSION

Yearwise analysis of variance for eight characters and homogeneity test of their error variances permitted pooled analysis of variance for the two seasons. Significance of variance ratio due to genotypes for all the eight characters in the pooled analysis further revealed the true differences among genotypes themselves. The test of significance for multiple measurements using "V" statistics which utilized Wilk's criterion further confirmed the significant differences among the cultivars (χ^2 = 1210.30 for 248 d.f.). These results indicated adequacy of continuing D^2 analysis in the present studies. The calculated values of D^2 were tested against the tabulated value of χ^2 for 8 degrees of freedom (15.51). Since the tabulated χ^2 value was lower than minimum calculated value of D^2 (38.80) it obviously showed the significance of all D^2 values.

Based on D^2 values, the 32 rice bean cultivars were grouped into 5 clusters by Tocher's method (Table 1). The cluster I included 24 cultivars while the clusters IV and V were monogenotypic. The clustering pattern of cultivars, as they are of the same geographical origin, might have resulted from genetic drift followed by selection [5].

Table 1. Grouping of rice bean cultivars into different clusters by Tocher method

Cluster	Name of genotype	Number of genotypes
I	RBM-2, RBM-3, RBM-4, RBM-6, RBM-7, RBM-8, RBM-9, RBM-12, RBM-13, RBM-14, RBM-15, RBM-16, RBM-18, RBM-20, RBM-21, RBM-22, RBM-23, RBM-24, RBM-25, RBM-26, RBM-27, RBM-28, RBM-29, RBM-30	24
II	RBM-5, RBM-11, RBM-19	3
III	RBM-1, RBM-17, C × $M_{12}P_3$	3
IV	RBM-31	1
V	RBM-10	1

RBM = Rice Bean Manipur

The maximum inter-cluster distance was estimated between cluster III and V which were followed by cluster II and III, cluster I and V and cluster III and IV in order of magnitude (Table 2). Although cluster I had a total of 24 cultivars, the highest intra-cluster distance was recorded from cluster II with only 3 cultivars (Table 2). De *et al.* [6] suggested that genotypes belonging to the clusters separated by high estimated statistical distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregants. Roy and Panwar [7] further suggested that the magnitude of resulting heterosis was largely dependent upon the degree of genetic diversity in the parental lines.

Table 2. Average intra and inter-cluster D^2 values of rice bean cultivars of Manipur

Cluster	I	II	III	IV	V
I	802.9	2358.3	2227.7	1685.7	6491.1
II		894.3	6946.5	1891.8	2903.3
III			347.2	5375.9	147292.9
IV				0.0	2951.3
V					0.0

The magnitude of cluster means, ranges of the means and co-efficient of variations (C.V.) obtained from the means in the clusters for eight agronomic characters are presented in Table 3. Depending upon the inter-cluster distance, cluster mean,

Table 3. Means, ranges and Co-efficient of Variations (C.V.) of rice bean cultivars of Manipur in the clusters for 8 agronomic characters

Agronomic character	Statistical parameters	Clusters				
		I	II	III	IV	V
Plant height (cm)	Mean	177.89	247.60	91.40	249.82	345.45
	Range	134.53-242.26	225.90-281.31	70.53-107.09	250.00-251.00	340.00-350.00
	C.V. (%)	16.94	11.95	20.52	0.32	1.04
Days to flowering	Mean	99.53	105.29	72.34	104.20	98.90
	Range	90.39-105.86	103.89-106.03	57.83-97.60	103.00-105.00	97.00-100.00
	C.V. (%)	3.60	1.15	15.35	0.80	1.36
Primary branches	Mean	7.75	8.48	6.62	9.37	9.40
	Range	5.63-10.76	7.53-9.93	5.73-7.63	9.00-10.00	9.00-10.00
	C.V. (%)	16.62	15.09	14.44	5.30	4.45
Pods per plant	Mean	128.52	216.88	85.63	67.50	144.63
	Range	30.03-207.09	183.63-248.96	69.53-109.63	62.00-72.00	138.00-150.00
	C.V. (%)	32.33	15.07	24.74	5.59	3.64
Length of pod (cm)	Mean	9.09	9.22	7.61	11.11	10.13
	Range	7.48-11.02	8.47-9.65	6.62-8.22	10.50-11.50	10.00-10.30
	C.V. (%)	11.98	7.04	11.37	3.00	1.27
Seeds per pod	Mean	6.01	5.70	6.52	5.57	608
	Range	5.19-7.01	5.31-6.31	6.04-7.33	5.00-6.00	5.80-6.30
	C.V. (%)	8.55	9.46	10.82	7.17	3.16
100 seed weight (g)	Mean	11.65	11.31	7.07	19.71	13.99
	Range	4.43-21.52	10.81-13.83	4.29-10.43	19.00-20.00	13.85-14.10
	C.V (%)	29.79	14.03	23.94	2.09	0.64
Grain yield (g)	Mean	64.59	114.16	33.31	77.73	90.40
	Range	42.06-136.26	90.11-121.20	19.43-54.59	70.00-85.00	85.00-96.00
	C.V. (%)	27.65	15.29	26.18	7.22	5.56

per se performance of the best genotype within the cluster, the following cross combinations for various breeding objectives are suggested : RBM1 × RBM10 for shorter plant height, early flowering and higher number of seeds per pod, RBM10 × RBM17 for higher primary branches per plant RBM11 × RBM17 for higher number of pods per plant and grain yield per plant, RBM31 × RBM17 for higher pod length and seed weight.

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