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Genetic divergence, path coefficient and cluster analysis of ricebean (*Vigna umbellata*) genotypes in the mid-altitudes of Meghalaya

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ABSTRACT

One hundred and twenty germplasm of ricebean [*Vigna umbellata* (Thunb) Ohwi and Ohashi] were evaluated during 2015-16 and 2016-17 to study the yield related traits in ricebean in the mid-altitudes of Meghalaya. Luxuriant ricebean growth with a wide spectrum of variability for plant height, number of branches per plant, days to flowering, number of pods per plant and 100 seed weight was observed. The genotypic variance was moderate to high for the said characters which resulted in moderate to high heritability and genetic advance values. Grain yield/plant was positively and significantly correlated with number of clusters per plant, number of pods per plant and 100 seed weight. Moderate to high heritability and the genetic advance of these plant characters vis-a-vis their positive association and direct positive effect on grain yield/plant suggested for their consideration during selection of high yielding genotypes. All the tested ricebean genotypes could be grouped into seven distinct clusters. An analysis of the percentage contribution of individual characters towards genetic diversity revealed that 100-seed weight and days to 80% maturity, days to 50% flowering were the major characters contributing to genetic diversity in ricebean. Based on the results we found genotype CHAK HAWAI-2 may be used as parent for developing long pod with bold seed cultivar. Genotype Chak Hawai-31 may be used as parent for developing high yielding genotypes. Genotype BKSB-23 had less bold seed but, high yield and may be used as parent for developing small seed and high yielding variety.

Key words: Genetic divergence, Path coefficient, Chester analysis, Meghalaya, Ricebean

Ricebean [*Vigna umbellata* (Thunb) Ohwi and Ohashi], previously *Phaseolus calcaratus* is an under-exploited or neglected tropical legume crop of *Leguminosae* family. The rice bean plants are annual crop which usually grows in spreading habit. The plant height extends up to 30 cm- 200 cm. Plants are hairy on leaf, stem, pod etc. and produce profuse branching. The leaves are tri-foliate with broader and long leaflets. Flowers are borne in clusters, bright yellow colour. The pods are 7.5-12.5 cm long having 6-10 cylindrical, distinct hilum seeds. The seed is of different colour like yellow, greenish yellow, brown, black. The major rice bean cultivating countries are India, Nepal, Myanmar, Thailand, Laos and Southern China. The crop is mainly cultivated by subsistence farmers on hilly areas of Nepal, Northern India and parts of South East Asia. In India, the distribution of rice bean is mainly concentrated in North Eastern hill regions and Western and Eastern Ghats. It can be grown in wider climacteric conditions and can tolerate extreme environments with low economic inputs (Dwivedi 1996). The rice bean is often cultivated as an intercrop with maize (*Zea mays*), sorghum (*Sorghum bicolar*) or cowpea (*Vigna ungui culata*).

In India, ricebean is widely grown in the hill regions and is an excellent source of dietary protein. It is cultivated in rotation/intercropping with cereals and therefore important as a nitrogen fixer for maintaining soil fertility. However, the productivity of rice bean is very low due to different stresses. A large number of high yielding cultivars have been released for most of the important crop plants to meet the requirements of diverse agro-climatic conditions, agronomic practices and preferences of the consumers. However, rice bean exhibits recalcitrance to such efforts, as it has been not possible to achieve a quantum jump in their productivity.

In spite of the large collections of diverse germplasm made over the years, very few have found their way into rice bean improvement programs. A tendency to add desirable characters in the already popular and in-use local cultivars have been responsible for the repeated use of a few lines as the background material in the breeding programs. So, it is

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imperative to further explore the genetic diversity available in this crop for better utilization of genetic resources in yield improvement.

For exploring the suitability of ricebean in this region, it is necessary to estimate the genetic variability of different plant characters of economic importance and their heritability. The association pattern among various traits and their direct and indirect effect on yield would be useful to ascertain the selection criteria for high yielding genotypes. For further crop improvement with desired character combinations, it is required to hybridize diverse parents and for this, a measure of genetic diversity in the available genotypes is required. The objective of this study was to characterize ricebean genotypes, study yield attributing components, their heritability and genetic advance.

MATERIALS AND METHODS

One hundred and twenty genotypes of ricebean were evaluated during rainy season in two consecutive years of 2015 and 2016 at the experimental farm of ICAR Research Complex for NEH Region, Umiam, Meghalaya. The experiment was laid out in a randomized block design (RBD) with three replications, with a spacing of 45 × 20 cm, and a gross plot size was measuring 3m × 4.5 m. The recommended agronomic practices and plant protection measures were followed to ensure a normal crop growth. Observations were recorded for 23 quantitative traits on five randomly selected plants in each treatment across all replications. Mean values were taken for analysis of variance as per Panse and Sukhatme (1978). Phenotypic and genotypic variances of the genotypes were estimated as described by Burton and Devane (1953), heritability as described by Hanson *et al*. (1956) and the genetic advance was estimated using the formula suggested by Johnson *et al*. (1955). The genotypic and phenotypic correlation coefficient and path coefficient were estimated as suggested by Dewey and Lu (1959). The data were subjected to analysis of genetic divergence through D^2 statistic (Mahalanobis 1936) to measure genetic divergence as suggested by Rao (1952), while Tocher's method was used to form clusters.

RESULTS AND DISCUSSION

Genetic variability, heritability and genetic advance

Response to selection for quantitative traits is directly proportional to the function of its heritability, genetic advance and its genotypic variance. Heritability enables the vegetable breeder to recognize the genetic differences among traits and genotypic variance reveals the potential for improvement of a particular trait. Analysis of variance (Table 1) revealed that genotypic differences were significant for all the characters except terminal leaf length, pod width, seed length and seed width.

The estimates of range, mean, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance are presented in Table 2. A considerable range of variation was observed for all the traits under study indicating enough scope for bringing about improvement in the desire direction. Maximum plant height (169.7 cm) was observed in genotype LRGP 40 from Nagaland, while minimum (36.7 cm) in genotype Chak Hawai-14 from Manipur. The number of pods per plant ranged from 10.7–75. A range of 3-9.7 was observed among genotypes for number of seeds per pod. Data on 100 seed wt. (gm) among genotypes varied from 6.4 to 52.4 whereas for pod length (cm) a range of 7-13 was observed.

The highest genotypic coefficient of variation was observed for 100 seed weight (64.4 gm) followed by petiole length of terminal leaf (45.7 cm), number of seed per plant

Table 1 Analysis of variance for yield and other traits in ricebean

Source of variation	D.F.	Plant height at 50% flowering	Plant height at maturity	Days 50% flowering	Days 80% maturity	Terminal leaf length (cm)	Terminal leaf width (cm)	Petiole length of the terminal leaf	Leaf length (cm)
Replicate	2	1880.7	1335.8	36.2	60.8	0.6	1.1	4.9	18.1
Genotypes	119	2440.1***	2720.6***	58.7***	234.3***	6.0	2.1***	8.4***	29.9
Error	238	702.20	703.2	9.9	11.0	5.0	0.8	2.3	25.9
Source of variation	D.F.	Leaf width (cm)	Petiole length of leaf (cm)	Primary branch length (cm)	No. of clusters/ plant	No. of pods/ plant	No. of branches	Peduncle length (cm)	No. of seeds/pod
Replicate	2	0.5	30.4	86.9	8.1	31	0.55	2.7	2.1
Genotypes	119	3.2**	43.0***	1108.1***	32.9***	569.8***	0.94***	13.3***	7.8***
Error	238	2.0	19.3	522.3	11.5	154.5	0.36	5.9	1.4
Source of variation	D.F.	No. Of seed/ plant	Yield/plant (gm)	100 Seed Wt.	Pod length (cm)	Pod width (cm)	Seed length (cm)	Seed width (cm)	
Replicate	2	23876.9	242.1	4	0.5	0.5	0.02	11.88	
Genotypes	119	61411.9***	598.1***	220.4***	3.2***	0.7	0.07	13.88	
Error	238	17524.2	139.6	1.5	0.8	0.6	0.007	5.6	

Table 2 Genetic parameters for variation in ricebean

Character	Max.	Min.	GCV	PCV	h² (Broad Sense)	Gen. Adv. as % of Mean
Plant height at 50% flowering	151.7	33	25.9	30.7	0.7	45
Plant height at maturity	169.7	36.7	24.2	28.1	0.7	42.9
50% flowering	72.7	44	7	7.7	0.8	13.1
80% maturity	141	103	7.3	7.5	1	14.7
Terminal leaf length (cm)	17.2	12	12	29.1	0.2	10.2
Terminal leaf width (cm)	5.3	1.1	26.1	33.5	0.6	41.9
Petiole length of the terminal leaf (cm)	12	1.3	45.7	53.8	0.7	79.8
Leaf length (cm)	40.8	3.8	10.8	29.9	0.1	8.1
Leaf width (cm)	9.2	2.3	9	14.6	0.4	11.3
Petiole length of leaf (cm)	25.2	5.3	16.2	21.8	0.6	24.7
Primary branch length (cm)	110.7	10.3	23.8	32.7	0.5	35.6
No. of clusters/plant	25	4	19.5	24.3	0.6	32.4
No. of pods/plant	75	10.7	29.8	35	0.7	52.5
No. of branches	4.7	1	15.4	19.7	0.6	24.8
Peduncle length (cm)	16.6	4.8	15.3	20.7	0.6	23.4
No. of seeds/pod	9.7	3	19.8	22	0.8	36.7
No. of seed/Plant	816.7	18.3	45.1	53.3	0.7	78.5
100 Seed weight (g)	52.4	6.5	64.4	64.6	1	52.1
Pod length (cm)	13	7	8.8	10.3	0.7	15.5
Pod width (cm)	1.3	0.5	13.6	69.4	0	5.5
Seed length (cm)	1.3	0.5	18.8	19.8	0.9	36.8
Seed width (cm)	0.8	0.3	38.8	313.8	0	9.9
Yield/plant (g)	80.5	2.1	42.7	48.8	0.8	77.1

(45.1 g), pield per plant (42.7 g) and low genotypic variance was obtained for pod length (8.8 cm), 80% maturity (7.3), days to 50% flowering (7.0). Highest phenotypic coefficient of variation variance was also observed for pod width (69.4) followed by 100 seed weight (64.6), petiole length of terminal leaf (53.8), number of seed/plant (53.3) and lowest phenotypic coefficient of variation was observed for pod length (10.3 cm), days to 50% maturity (7.7), days to 80% maturity (7.5). 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, Arshad *et al*. (2003) in chickpea and Pandey *et al*. (2015) in ricebean.

In the crop improvement programme, a study of heritability provides knowledge of the extent of the contribution of genotype to the phenotypic variation which serves as a useful guide to the breeder. A wide range of heritability (1.0- 0.0) was observed for the characters under study. High values of heritability were observed for 100 seed weight and 80% maturity (1.0) followed by seed length (0.9) and days to 50% flowering, number of seed per pod, yield per plant (0.8), low value of heritability was recorded for terminal leaf length (0.2), leaf length (0.1), pod width and seed width (0.0). High heritability for 100 seed wt. and yield per plant was also observed by Gupta *et al*. (2013). 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) and Pandey *et al*. (2015) in ricebean, Dodwad *et al*. (1998) in greengram, Vaghela *et al*. (2009) in chickpea and Khan *et al*. (2015) in cowpea. The value of genetic advance varied from 48.6 to 0.0, maximum high genetic advance was recorded for the character number of seed per plant (48.6) followed by plant height at maturity (46.0), plant height at 50% flowering (41.8) and yield per plant (22.3) whereas, the low genetic advance exhibited for characters seed length (0.3), terminal leaf length (0.2), seed width (0.1) and pod width (0.0). Low genetic advance for 50% flowering was also observed by Gupta *et al*. (2013).

Correlation coefficients and path coefficient analysis

Genotypic and phenotypic correlations were estimated among twenty three traits in 120 genotypes and these indicated the inherent association between any two variables, which might have occurred due to the pleiotropic action of genes, linkage or more likely both. Grain yield per plant was positively and significantly correlated with clusters per plant,

Table 3 Genotypic correlation coefficients among the twenty three characters of ricebean

Charac-ters	Plant height at 50% maturity	Plant height at maturity	Days to 50% flowering	Days to 80% maturity	Termi-nal leaf length (cm)	Terminal leaf width (cm)	Petiole length of ter. Leaf length (cm)	Leaf length (cm)	Leaf width (cm)	Petiole length of leaf length (cm)	Primary branch length (cm)	No. of clusters/ plant	No .of pods/plant	No .of branches	Peduncle length (cm)	No .of s eeds/pod	No. Of seed/ plant	100 Seed Wt. (gm)	Pod length (cm)	Pod width (cm)	Seed length (cm)	Seed width (cm)
2	0.946***																					
3	-0.346 ***	-0.344 ***																				
4	0.498 ***	-0.495 ***	0.744***																			
5	0.061	0.106 *	-0.121 *	-0.097																		
6	-0.291 ***	-0.291 ***	0.408 ***	0.497 ***	0.279***																	
7	-0.144 **	-0.140 **	0.200 ***	0.239***	0.282 ***	0.629 ***																
8	0.208 ***	0.214***	-0.208 ***	-0.126 *	0.063	-0.074	0.003															
9	0.211 ***	0.212 ***	-0.003	0.024	0.009	0.1284*	0.033	0.332***														
10	0.327 ***	0.358 ***	-0.104 *	-0.139**	0.008	-0.048	0.051	0.287***	0.566 ***													
11	0.641 ***	0.665 ***	-0.258 ***	-0.418***	0.087	-0.397 ***	-0.225 ***	0.161**	0.158**	0.227***												
12	0.096	0.108 *	-0.117 *	-0.173***	0.117 *	-0.148**	0.034	0.111 *	0.125 *	0.257***	0.151**											
13	0.176 ***	0.190 ***	-0.131 *	-0.254***	0.106 *	-0.250 ***	-0.025	0.030	0.061	0.253***	0.256***	0.842***										
14	0.052	0.031	-0.032	-0.039	0.112 *	-0.0251	-0.017	0.037	0.059	0.074	0.213***	0.427***	0.345***									
15	0.334 ***	0.350 ***	-0.234***	-0.264***	-0.019	-0.226 ***	0.100	0.095	0.069	0.358 ***	0.199***	0.316***	0.392***	0.046								
16	0.566 ***	0.634 ***	-0.583 ***	-0.707 ***	0.107 *	-0.428 ***	-0.202 ***	0.217 ***	0.12 *	0.269 ***	0.569***	0.186***	0.241***	0.114*	0.396***							
17	0.377***	0.421 ***	-0.344 ***	-0.502 ***	0.141 **	-0.429 ***	-0.137**	0.123 *	-0.028	0.257***	0.514***	0.541***	0.709***	0.329***	0.388***	0.532***						
18	-0.570 ***	-0.593 ***	0.554***	0.687 ***	-0.069	0.481 ***	0.234***	-0.211 ***	0.020	-0.112*	-0.515***	0.001	-0.134*	-0.062	-0.409***	-0.783***	-0.496***					
19	-0.129 *	-0.168 **	0.209***	0.199 ***	-0.011	0.255 ***	0.170 **	0.009	0.102	0.120 *	-0.114*	0.175***	0.029	0.133*	-0.038	-0.156**	-0.239***	0.484***				
20	-0.188 ***	-0.208 ***	0.122 *	0.185 ***	-0.032	0.086	0.036	-0.04	0.119 *	0.040	-0.144**	0.001	-0.043	0.046	-0.097	-0.196***	-0.147**	0.253***	0.144**			
21	-0.542 ***	-0.592 ***	0.622***	0.739 ***	-0.114 *	0.445 ***	0.207 ***	-0.195 ***	0.013	-0.154 **	-0.489***	-0.086	-0.185**	-0.010	-0.373***	-0.780***	-0.549***	0.826***	0.494***	0.250***		
22	-0.141 **	-0.155 **	0.082	0.125 *	-0.049	0.050	0.207 ***	-0.059	-0.005	0.019	-0.100	0.009	-0.004	-0.032	0.004	-0.206***	-0.078	0.188***	0.211***	0.066	0.1763**	
23 (y/ plant)	-0.037	-0.012	0.155 **	-0.081	0.136 **	0.051	0.207 ***	-0.015	0.101	0.272***	0.100	0.655***	0.706***	0.302***	0.143**	-0.066	0.577***	0.271***	0.241***	0.065	0.178***	0.163**

Table 4 Genotypic path coefficient showing direct and indirect effect of observed characters on grain yield/plant in ricebean

Character	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22
Plant height at 50% maturity	-0.029	-0.027	0.010	0.014	-0.002	0.008	0.004	-0.006	-0.006	-0.010	-0.019	-0.003	-0.005	-0.002	-0.010	-0.016	-0.011	0.017	0.004	0.006	0.016	0.004
Plant height at maturity	0.057	0.061	-0.021	-0.030	0.007	-0.018	-0.009	0.013	0.013	0.022	0.040	0.007	0.012	0.002	0.021	0.039	0.026	-0.036	-0.010	-0.013	-0.036	-0.009
Days to 50% flowering	-0.016	-0.016	0.045	0.034	-0.006	0.018	0.009	-0.009	0.000	-0.005	-0.012	-0.005	-0.006	-0.002	-0.011	-0.026	-0.016	0.025	0.010	0.006	0.028	0.004
Days to 80% maturity	-0.014	-0.014	0.021	0.029	-0.003	0.014	0.007	-0.004	0.001	-0.004	-0.012	-0.005	-0.007	-0.001	-0.008	-0.020	-0.014	0.020	0.006	0.005	0.021	0.004
Terminal leaf length (cm)	0.001	0.002	-0.002	-0.002	0.017	0.005	0.005	0.001	0.000	0.000	0.001	0.002	0.002	0.002	0.000	0.002	0.002	-0.001	0.000	-0.001	-0.002	-0.001
Terminal leaf width (cm)	-0.016	-0.016	0.023	0.028	0.016	0.055	0.035	-0.004	0.007	-0.003	-0.022	-0.008	-0.014	-0.001	-0.013	-0.024	-0.024	0.027	0.014	0.005	0.025	0.003
Petiole length of terminal leaf (cm)	-0.013	-0.013	0.018	0.021	0.025	0.056	0.089	0.000	0.003	0.005	-0.020	0.003	-0.002	-0.002	0.009	-0.018	-0.012	0.021	0.015	0.003	0.018	0.029
Leaf length (cm)	-0.004	-0.004	0.004	0.002	-0.001	0.001	0.000	-0.019	-0.006	-0.005	-0.003	-0.002	-0.001	-0.001	-0.002	-0.004	-0.002	0.004	0.000	0.001	0.004	0.001
Leaf width (cm)	0.009	0.009	0.000	0.001	0.000	0.006	0.002	0.014	0.043	0.025	0.007	0.006	0.003	0.003	0.003	0.005	-0.001	0.001	0.004	0.005	0.001	0.000
Petiole length of leaf (cm)	0.018	0.020	-0.006	-0.008	0.001	-0.003	0.003	0.016	0.031	0.055	0.013	0.014	0.014	0.004	0.020	0.015	0.014	-0.006	0.007	0.002	-0.009	0.001
Primary branch length (cm)	-0.012	-0.013	0.005	0.008	-0.002	0.008	0.004	-0.003	-0.003	-0.004	-0.019	-0.003	-0.005	-0.004	-0.004	-0.011	-0.010	0.010	0.002	0.003	0.010	0.002
No. of clus- ters / plant	0.009	0.010	-0.011	-0.016	0.011	-0.014	0.003	0.011	0.012	0.024	0.014	0.094	0.079	0.040	0.030	0.018	0.051	0.000	0.017	0.000	-0.008	0.001
No. of pods / plant	0.035	0.038	-0.026	-0.051	0.021	-0.050	-0.005	0.006	0.012	0.051	0.051	0.169	0.200	0.069	0.079	0.048	0.142	-0.027	0.006	-0.009	-0.037	-0.001
No. of branches	-0.002	-0.001	0.001	0.002	-0.005	0.001	0.001	-0.002	-0.003	-0.003	-0.009	-0.018	-0.015	-0.043	-0.002	-0.005	-0.014	0.003	-0.006	-0.002	0.000	0.001
Peduncle length (cm)	-0.013	-0.014	0.009	0.011	0.001	0.009	-0.004	-0.004	-0.003	-0.014	-0.008	-0.013	-0.016	-0.002	-0.040	-0.016	-0.016	0.016	0.002	0.004	0.015	0.000
No. of seeds/ pod	0.029	0.032	-0.029	-0.036	0.005	-0.022	-0.010	0.011	0.006	0.014	0.029	0.009	0.012	0.006	0.020	0.050	0.027	-0.039	-0.008	-0.010	-0.039	-0.010

(*Contd.*)

Table 4 (*Concluded*)

Character	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22
No. of seed/plant	0.294	0.329	-0.269	-0.391	0.110	-0.335	-0.107	0.096	-0.022	0.201	0.401	0.422	0.553	0.257	0.303	0.415	0.780	-0.387	-0.186	-0.115	-0.428	-0.061
100 seed weight (cm)	-0.221	-0.229	0.214	0.266	-0.027	0.186	0.091	-0.082	0.008	-0.044	-0.199	0.000	-0.052	-0.024	-0.158	-0.303	-0.192	0.386	0.187	0.098	0.319	0.073
Pod length (cm)	-0.005	-0.007	0.009	0.008	-0.001	0.011	0.007	0.000	0.004	0.005	-0.005	0.007	0.001	0.006	-0.002	-0.007	-0.010	0.020	0.041	0.006	0.020	0.009
Pod width (cm)	-0.001	-0.001	0.001	0.001	0.000	0.000	0.000	0.000	0.001	0.000	-0.001	0.000	0.000	0.000	0.000	-0.001	-0.001	0.001	0.001	0.004	0.001	0.000
Seed length (cm)	-0.134	-0.147	0.154	0.183	-0.028	0.110	0.051	-0.048	0.003	-0.038	-0.121	-0.021	-0.046	-0.003	-0.092	-0.193	-0.136	0.204	0.122	0.062	0.247	0.044
Seed width (cm)	-0.010	-0.011	0.006	0.009	-0.004	0.004	0.023	-0.004	0.000	0.001	-0.007	0.001	0.000	-0.002	0.000	-0.015	-0.006	0.014	0.015	0.005	0.013	0.072
Yield/plant (g)	-0.038	-0.012	0.156	0.082	0.136	0.051	0.198	-0.016	0.102	0.273	0.100	0.655	0.707	0.303	0.144	-0.066	0.578	0.271	0.241	0.066	0.179	0.163
Partial R²	0.001	-0.001	0.007	0.002	0.002	0.003	0.018	0.000	0.004	0.015	-0.002	0.062	0.142	-0.013	-0.006	-0.003	0.451	0.105	0.010	0.000	0.044	0.012

R^2 = 0.8529; Residual effect = 0.3835.

number of pods per plant and 100 seed weight (Table 3).

In an earlier study, Dodake and Dahat (2011) observed that number of pods per plant, number of seeds per pod, pod length, number of branches per plant and plant height at harvest have been showing highly significant positive association with seed yield per plant at genotypic level. However in this study, we found a negative correlation (although not significant) between plant height at maturity and yield per plant. Days to maturity showed non-significant negative correlation with seed yield per plant at genotypic level. The finding of the present study coincides with Sharma *et al*. (1991), Chaudhary *et al*. (2000), Sharma and Hore (1994), Baisakh (1992) and Dodake and Dahat (2011). Rice bean is a long duration crop and one of the breeding objectives is to reduce the maturity duration in this crop. No correlation between days to maturity and yield/plant suggested that selection for early maturity will not hamper yield. Significant positive association of grain yield with pod length, number of seeds/pod and 100-seed weight has also been reported earlier (Borah *et al*. 2002, Islam *et al*. 2002, Gupta *et al*. 2013). Most of the associations among other characters were significantly positive except between 100-seed weight and number of seeds/pod, which was negative.

In the present investigation, the path coefficient analysis was performed to estimate the direct and indirect contribution of various plant characters to grain yield per plant. Further compartmentalization of correlation coefficients into direct and indirect effects discerned the true nature of association between observed characters. Among direct effects towards yield (Table 4), number of seeds per plant (0.780) had the highest positive effects followed by 100 seed weight (0.386), seed length (0.247), and number of pods per plant (0.200). Whereas negative effects was recorded in number of branches (- 0.043) followed by plant height at 50% maturity (- 0.029), leaf length and primary branch length (- 0.019). High direct positive effect of seeds per plant towards yield was also observed by earlier workers (Gupta *et al*. 2013, Islam *et al*. 2002).

Genetic divergence analysis

Clustering of the 120 genotypes was carried out following Tocher method (Rao 1952). In all, 7 clusters were formed and their composition is given in Table 5. Cluster I was the largest with 94 genotypes followed by cluster II with 21 genotypes. The trait 100 seed weight was recorded as highest contribution towards genetic divergence (43.61%) followed by days to 80% maturity (11.90%), pod length (4.4%), plant height at maturity (3.75%), days to 50% flowering (3.40%), number of pods/plant (3.04%), number of cluster per plant (3.00%), number of seeds per plant (2.91), petiole length of terminal leaf (2.84%), number of branches (2.58%), plant height at 50% flowering (2.54%), seed length (2.03%), terminal leaf length (1.81%), yield per plant (1.75%), peduncle length (1.74%), petiole length of leaf (1.74%), pod width (1.33%), leaf length (1.26%), terminal leaf length (1.18%), number of seeds per pod (1.06%) while less than 1% contribution was recorded in

Table 5 Grouping of ricebean genotypes in different clusters

Cluster	Number of Genotype	Genotype List
I	94	BSKB-2, BSKB-3, BSKB-4, BSKB-5, BSKB-6, BSKB-7, BSKB-8, BSKB-9, BSKB-10, BSKB-11, BSKB-12, BSKB-13, BSKB-14, BSKB-15, BSKB-16, BSKB-17, BSKB-19, BSKB-20, BSKB-21, BSKB-22, BSKB-23, BSKB-24, BSKB-25, BSKB-26, BSKB-27, BSKB-28, BSKB-29, BSKB-30, BSKB-31, BSKB-32, BSKB-33, BSKB-34, BSKB-35, BSKB-36, BSKB-37, BSKB-40, BSKB-42, BSKB-43, BSKB-44, BSKB-45, BSKB-46, BSKB-47, LRGP-1, LRGP-2, LRGP-3, LRGP-7, LRGP-8, LRGP-10, LRGP-11, LRGP-12, LRGP-13, LRGP-14, LRGP-15, LRGP-17, LRGP-18, LRGP-19, LRGP-20, LRGP-21, LRGP-22, LRGP-24, LRGP-25, LRGP-26, LRGP-27, LRGP-29, LRGP-30, LRGP-31, LRGP-32, LRGP-34, LRGP-35, LRGP-36, LRGP-37, LRGP-38, LRGP-39, LRGP-40, LRGP-41, LRGP-43, LRGP-44, LRGP-45, LRGP-46, LRGP-48, LRGP-50, LRGP-51, LRGP-52, LRGP-54, LRGP-55, LRGP-56, LRGP-57, LRGP-59, LRGP-60, LRGP-61, LRGP-62, LRGP-63, CHAK HAWAI-7, CHAK HAWAI-24
II	21	CHAK HAWAI-11, CHAK HAWAI-13, CHAK HAWAI-14, CHAK HAWAI-15, CHAK HAWAI-16, CHAK HAWAI-17, CHAK HAWAI-18, CHAK HAWAI-19, CHAK HAWAI-20, CHAK HAWAI-22, CHAK HAWAI-26, CHAK HAWAI-27, CHAK HAWAI-28, CHAK HAWAI-29, CHAK HAWAI-30, CHAK HAWAI-31, CHAK HAWAI-34, CHAK HAWAI-36, CHAK HAWAI-1, CHAK HAWAI-5, CHAK HAWAI-8
III	1	CHAK HAWAI-21
IV	1	CHAK HAWAI-10
V	1	CHAK HAWAI-35
VI	1	CHAK HAWAI-3
VII	1	CHAK HAWAI-2

primary branch length (0.95%), leaf width (0.90%) and seed width (0.24%). High contribution of 100 seed wt. and days to maturity in genetic divergence were also reported by Misra and Swain (2010).

Intra and inter cluster distance (D) between all possible pairs of 7 clusters were computed and presented in Table 6. A study of the pooled data revealed that the inter cluster distance (D) ranged from 1444.11 to 62.53.

Cluster means of various characters

Cluster means of all the 23 characters in 120 genotypes are presented in Table 7. Among 7 clusters, cluster I had highest mean over other clusters for the trait number of seeds per plant (309.49) while lowest in seed width (0.45). Within cluster I, maximum mean was recorded in number of seed per plant (304.49) followed by plant height at maturity (116.61) and plant height at 50% flowering (101.61) while seed width (0.45 cm) showed as lowest mean. In cluster II, days to 80% maturity (132.6) showed maximum mean value followed by number of seed per plant (130.76) and plant height at maturity (67.9) while minimum in seed width (0.9 cm). In cluster III, days to 80% maturity (134.67), number of seeds per plant (101.3) and plant height at maturity (64) had highest mean whereas minimum mean was in seed width (0.73 cm).

In cluster IV, maximum mean was recorded in days to 80% maturity (122.67) followed by plant height at maturity (111.67), plant height at 50% flowering (101.33) and number of seeds per plant (81.33) while minimum in seeds length (0.56 cm). In cluster V, maximum mean was recorded in 80% maturity (137.33) followed by plant height at maturity (123.67), plant height at 50% flowering (99) and days to 50% flowering (67.67) while minimum in seed width (0.66 cm).In cluster VI, maximum mean was recorded in days to 80% maturity (124) followed by days to 50% flowering (59.33), number of seeds per plant (48.67), plant height at 50% maturity (43.13 cm) and 100 seed weight (42.01 g) while minimum in seed width (0.74

Table 6 Mahalonobis Euclidean² inter and intra cluster distance (D^2) in ricebean

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	37						
Cluster II	345.05	85.11					
Cluster III	698.51	145.24	0				
Cluster IV	106.98	138.69	374.43	0			
Cluster V	130.58	251.81	575.96	75.09	0		
Cluster VI	883.36	252.72	62.53	507.04	791.77	0	
Cluster VII	1444.11	574.09	209.77	971.19	1352.79	105.04	0

Table 7 Cluster means for different characters in ricebean

Character	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VI
Plant height at 50% flowering	101.61	58.76	48.33	101.33	99	36.67	78.67
Plant height at maturity	116.96	67.9	64	111.67	123.67	43.13	102.33
50% flowering	56.09	63.46	61	65.33	67.67	59.33	61.33
80% maturity	114.3	132.6	134.67	122.67	137.33	124	126
Terminal leaf length (cm)	4.98	4.62	4.6	4.1	4.1	4.1	4.87
Terminal leaf width (cm)	2.33	3.33	3.57	2.67	3.27	2.57	3.07
Petiole length of terminal leaf (cm)	2.95	3.96	3.8	2.73	2.17	2.03	2.93
Leaf length (cm)	10.92	9.22	7.47	9.33	8.93	9.83	11.53
Leaf width (cm)	7.1	7.02	6.47	6.63	6.53	7.57	8.07
Petiole length of leaf (cm)	17.78	16.11	15.17	11.1	10.4	19.17	18.87
Primary branch length (cm)	63.74	40.53	26.67	64	52.33	25.33	41.33
No. of clusters/plant	13.91	12.95	11.67	9	5.33	14.67	18
No. of pods/plant	41.13	35.29	23.33	19.33	11.67	22.67	47
No. of branches	2.87	2.79	3	2.67	2.67	3	2.33
Peduncle length (cm)	10.67	8.85	8.9	8.07	6.33	6.33	4.83
No. of seeds/pod	8.06	4.75	5	7.67	4	3.67	4.33
No. Of seed/plant	309.49	130.76	101.33	81.33	40.67	48.67	72.67
Yield/plant (gm)	27.68	35.56	45.38	11.82	7.17	19.54	39.38
100 Seed Weight (gm)	9.35	26.34	38.47	16.66	11.39	42.01	52.43
Pod length (cm)	9.81	10.67	10.37	11.72	7.3	12.52	12.94
Pod width (cm)	0.65	0.9	1.04	0.79	0.7	1.01	1.27
Seed length (cm)	0.74	1.11	1.1	1.09	1.05	1.18	1.03
Seed width (cm)	0.45	1.77	0.73	0.56	0.66	0.74	0.6

cm). In cluster VII, maximum mean was recorded in days to 80% maturity (126) followed by plant height at maturity (102.33), plant height at 50% flowering (78.67) and number of seeds per plant (72.67) while minimum in seed width (0.6 cm).

Wide variations for various agronomic traits were recorded among different germplasm. Genotype in cluster VII (Chak Hawai-2) may be used as parent for developing long pod with bold seed cultivar. Genotype in cluster II i.e. Chak Hawai-31 (80.50 g) may be used as parent for developing high yielding genotypes. For creating wide spectrum of variability and improving the grain yield, the genotypes in cluster III would be crossed with genotypes in cluster V. Another option of crossing genotype of cluster VII with genotypes of cluster IV may be explored for creating wide spectrum of variability. BKSB-23 of cluster I have less bold seed, but high yield (67.9 g) may be used as parents for developing small seed and high yielding variety.

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