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Genetic Parameters, Genetic Association and Principal Component Analysis of Yield and Yield Contributing Traits in Ricebean (*Vigna umbellata*)

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ABSTRACT

Background: Ricebean (*Vigna umbellata*) is a minor pulse crop mainly cultivated for food, fodder and green manure. The assessment of variability is essential pre requisite for formulating an effective breeding programme, as the existing variability can be used to enhance the yield level of cultivars.

Methods: The present experiment was carried out during *rabi* season 2022-23. The experiment was carried out using Augmented design II at Department of Pulses, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore.

Result: Morphological characterization of ricebean genotypes revealed the presence of low variability for the qualitative traits except for growth habit, twining tendency, terminal leaflet shape and stem pubescence. High heritability coupled with high genetic advance as per cent of mean was noticed for the following traits *viz*., number of pods per plant (95.56, 63.92), number of clusters per plant (87.58, 52.88), number of primary branches per plant (70.29,32.77), hundred seed weight (97.32, 26.29) and single plant yield (90.76, 43.36). The traits *viz*., number of pods per plant (0.881), number of clusters per plant (0.720), pod length (0.326), number of seeds per pod (0.311), plant height (0.257), number of primary branches per plant (0.196) and hundred seed weight (0.192) exhibited significant positive association with single plant yield. PCA analysis revealed that the following traits *viz*., number of pods per plant, single plant yield, number of clusters per plant, number of seeds per pod and pod length contributed maximum to the genetic variability. In addition, it also earmarked the best performing genotypes for each biometrical trait. Hence, the above findings could be effectively utilized for the development of ricebean cultivars with desirable plant type.

Key words: Cluster analysis, Genetic association, Genetic variability, PCA, Ricebean.

INTRODUCTION

Legumes are the second most important crop group after cereals, serving as a key element in human nutrition. For the majority of the global population, they represent the primary source of protein (Gnanasekaran *et al*., 2025). Despite the availability of number of edible legumes, their consumption far exceeds their production. In this scenario, underutilized legume species offer potential solutions to bridge this gap (Anandhinatchiar *et al*., 2023). Ricebean (*Vigna umbellata*) is one such underutilized legume species. It belongs to the genus *Vigna* and subgenus *Ceratotropis*. It is a multipurpose grain legume crop primarily cultivated for food, fodder and green manure, especially by poor farmers in marginal areas (Shitri *et al*., 2019). Typically, it is grown in rotation or intercropped with cereals. In India, ricebean cultivation is mainly confined to the tribal regions of Northern and Northeastern India (Arora *et al*., 1980), with a few varieties released for both grain and fodder purposes. The grain yield of ricebean is generally higher than that of greengram and blackgram (Bhardwaj *et al*., 2021). Additionally, it is relatively less susceptible to pests and diseases and exhibits wide adaptability along with tolerance to abiotic stresses. However, its widespread cultivation is limited due to certain disadvantages, such as photosensitivity, pod shattering and a semi-determinate to indeterminate growth habit (Pattanayak *et al*., 2018).

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To overcome these challenges, genetic improvement of plant type is necessary for developing high-yielding varieties by enhancing yield components. The first step in any breeding program is to identify and utilize the genetic variability present in the germplasm to maintain, evaluate and exploit it effectively. Key genetic parameters *viz*., Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) help to measure the extent of genetic and environmental influences on traits. Heritability indicates the proportion of variation that is genetically inherited, guiding the efficiency of selection. Genetic

advance predicts the potential improvement through selection, while genetic associations reveal correlations among traits, which is essential for indirect selection, especially for complex traits like yield. The PCA determines the genetic relatedness of genotypes, the interdependence of different traits and the significance of traits in relation to total variance (Sivabharathi *et al*., 2023). Effective selection of superior genotypes requires a comprehensive understanding of genetic variability and the exploitation of genetic diversity (Upadhyay *et al*., 2025).

Together, these parameters are critical for designing efficient breeding strategies and enhancing crop performance. Therefore, the main objective of the present investigation was to characterize a set of ricebean genotypes based on morphological traits and to estimate genetic variability, genetic diversity and genetic associations among yield and yield-contributing traits.

MATERIALS AND METHODS

Experimental site

The experiment was conducted during *Rabi*, 2022-23 at Department of Pulses, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore. The area comes under humid tropical climate with an average annual rainfall of 674.2 mm and a year-round mean of minimum and maximum temperature of 21.7°C and 31.8°C respectively (ACRC-TNAU).

Plant material

A set of 109 ricebean germplasm with seven checks were evaluated. The seed materials of the above genotypes and checks were initially obtained from National Bureau of Plant Genetic Resources, New Delhi.

Experimental design and cultural practices

The genotypes were evaluated in Augmented design II. The whole experimental area was divided in to three blocks. Each block encompassed a portion of the test entries and all the seven checks. Thus, the checks were replicated three times. The first, second and third block was allotted with 40, 40 and 29 test entries, respectively. The genotypes were planted in a single row of four-meter length with a spacing of 45 × 15 cm. In order to establish a good crop, all the recommended package of practices was carried out at appropriate time.

Data observation

A total of 29 qualitative traits were observed. The scaling adopted was as per the descriptor of ricebean available in genesys portal. In addition, nine quantitative traits were recorded on five potential competitive plants selected from each genotype except days to 50 per cent flowering which was recorded on row basis.

Statistical analysis

The mean values were used for statistical analysis. Analysis of variance for Augmented design II and genetic variability parameters were derived using augmented RCBD package (Arvind *et al*., 2021). Genetic association analysis and principal component analysis (Pearson, 1901) were carried out using R software with the packages, psych (Revelle, 2013) and factoextra (Kassambara and Mundt, 2020), respectively. Agglomerative hierarchical clustering using Euclidean distance measure and average linkage method was used for cluster analysis in STAR software version 2.0.1 of IRRI, Philippines.

RESULTS AND DISCUSSION

Morphological characterization

The details of the score, phenotype and per cent frequency of occurrence of the morphological traits are presented in Annexure 1. Out of 116 genotypes, most of the genotypes were indeterminate climbers (65.52%), whereas less (27.59%) and very less (6.89%) number of genotypes were indeterminate semi climbers and determinate types, respectively. Genotypes with determinate growth habit are desirable since they have synchronous maturity, dwarf and compact stature. Similar kind of variation for plant growth habit was reported by Pattanayak *et al*. (2018) and Tad-awan and Palaes (2022) in ricebean. More than half of the genotypes (61.21%) were noticed with pronounced twining tendency, 31.90% of the genotypes were identified with slight twining nature, while 6.89 per cent of the genotypes were observed with the absence of twinning tendency. Therefore, the genotypes without any twining nature could be used to develop varieties for the inter- cropping system as they do not require much space. Among the ricebean genotypes, lanceolate shape was the most prevalent type (67.24%) followed by ovate type (31.03%) and lobed type (1.72%). Likewise, Tad-awan and Palaes (2022) also reported variation for terminal leaflet shape in ricebean. Stem pubescence was sparse in most of the genotypes (70.69%), whereas it was moderate in rest of the genotypes (29.31%). Morphological characterization of ricebean genotypes revealed the presence of low variability for the qualitative traits except growth habit, twining tendency, terminal leaflet shape and stem pubescence. Similar findings of low variation for qualitative traits except for growth habit, twining tendency, terminal leaflet and seed coat colour was documented by Tad-awan and Palaes (2022) in ricebean.

Genetic variability

Analysis of variance revealed significant differences for all the quantitative traits studied among 116 ricebean genotypes (Table 1). An assessment of variability parameters revealed the presence of sufficient variation among the genotypes (Table 2). In the present study, PCV was larger than GCV for all the nine biometrical traits. However, the difference between PCV and GCV was meagre for all the traits signifying that these traits are less influenced by the environment. This implies the possibility of employing phenotypic selection for these traits. High estimates of PCV and GCV (>20%) were recorded for number of pods per plant, number of clusters per plant and single plant yield. High PCV and GCV implies the

presence of wide range of variability for the above traits indicating the possibility for improvement of the above traits through selection. Similar to the present study, high PCV and GCV were recorded for number of pods per plant (Devi *et al*., 2018 in ricebean; Shitiri *et al*., 2019 in ricebean), number of clusters per plant (Devi *et al*., 2018 [high PCV alone]) and single plant yield (Devi *et al*., 2018; Sawant *et al*., 2019; Shitiri *et al*., 2019 in ricebean). Number of primary branches per plant was observed with high PCV and moderate GCV. Devi *et al*. (2018) also reported

Annexure 1: Frequency distribution of morphological traits in ricebean genotypes.

Character	Score	Phenotype	Frequency per cent
Type of emergence	3	Hypogeal	100.00
Hypocotyl colour	5	Purple	100.00
Growth pattern	123	Determinate In determinate semi climber In determinate climber	6.8927.5965.52
Twining tendency	038	None Slight Pronounced	6.8931.9061.21
Terminal leaflet shape	2411	Ovate Lanceolate Lobed	31.0367.241.72
Leaf pubescence	5	Pubescent	100.00
Leaf colour	4	Light green	100.00
Petiole colour	11	Green purple	100.00
Colour of leaf blade joint	3	Green	100.00
Colour of leaf axil	1	Green	100.00
Stem colour	2	Green	100.00
Stem pubescence	35	Sparsely pubescent Moderately pubescent	70.6929.31
Branching pattern	4	All over	100.00
Calyx colour	4	Purple	100.00
Corolla colour	1	Yellow	100.00
Colour of flower keel petal	10	Translucent yellow	100.00
Colour of flower standard petal	9	Yellow	100.00
Raceme position	3	Upright	100.00
Peduncle colour	1	Green	100.00
Peduncle pubescence	3	Puberulent (Sparsely pubescent)	100.00
Pod colour at immature stage	4	Dark green	100.00
Colour of ventral suture of immature pod	3	Green	100.00
Pod beak shape	1	Short	100.00
Pod curvature	2	Slightly curved	100.00
Pod pubescence	0	Glabrous	100.00
Constriction of pod between seeds	0	Absent	100.00
Pod colour at maturity	2	Straw	100.00
Lusture on seed surface	1	Present	100.00
Hilum	1	Concave (deeply furrowed aril prominent)	100.00

Table 1: Analysis of variance for biometrical traits in ricebean genotypes.

Characters	Total genotypes (df = 115)	Checks (df = 6)	Test genotypes (df = 108)	Test genotypes Vs Checks (df =1)	Error (df = 12)
Days to 50% flowering	19.10**	8.43**	16.27**	389.37**	1.26
Plant height	27.83**	151.79**	19.19*	217.54**	7.63
Number of branches per plant	0.41**	1.44**	0.23*	14.61**	0.07
Number of clusters per plant	20.44**	48.84**	18.16**	95.66**	2.26
Number of pods per plant	255.73**	354.33**	251.14**	160.42**	11.15
Pod length	0.30**	0.69**	0.26**	2.68**	0.01
Number of seeds per pod	0.35**	0.95**	0.31**	1.17**	0.04
Hundred seed weight	0.36**	0.19**	0.37**	0.001	0.01
Single plant yield	7.92**	6.90**	7.51**	59.16**	0.69

* - p≤0.05 and ** - p≤0.01.

moderate GCV for number of primary branches per plant in ricebean. Moderate PCV and GCV (10-20%) were registered for plant height and hundred seed weight. Similarly, moderate PCV and GCV were observed by Bhardwaj and Thakur (2017) in ricebean for plant height; Singh *et al*. (2019) and Shitiri *et al*. (2019) for hundred seed weight in ricebean. Low PCV and GCV (<10%) estimates were observed for days to 50 per cent flowering, number of seeds per pod and pod length.

In the present investigation, high heritability (>60%) coupled with high genetic advance as per cent of mean (GAM) (>20%) was noticed for the following traits *viz*., number of pods per plant, number of clusters per plant, number of primary branches per plant, hundred seed weight and single plant yield. Similar results of high heritability along with high GAM were reported in ricebean by Shitiri *et al*. (2019), Singh *et al*. (2019) for number of pods per plant; Devi *et al*. (2018) for number of clusters per plant in ricebean; Sawant *et al*. (2019) for number of primary branches per plant in ricebean; Devi *et al*. (2018), Shitiri *et al*. (2019) and Singh *et al*. (2019) for hundred seed weight in ricebean; Devi *et al*. (2018); Sawant *et al*. (2019), Shitiri *et al*. (2019) and Singh *et al*. (2019) for single plant yield in ricebean. Presence of high heritability coupled with high GAM for the above traits indicates that the traits were controlled by additive gene action. This, in turn, implies that simple selection is effective for the above traits, resulting in high genetic gain during the selection process.

On the other hand, high heritability (>60%) coupled with moderate GAM (11-20%) was recorded for the traits *viz*., pod length, days to 50 per cent flowering, number of seeds per pod and plant height. The above results were in accordance with the findings of Devi *et al*. (2018) and Sawant *et al*. (2019) for pod length in ricebean; Bhardwaj and Thakur (2017) and Devi *et al*. (2018) for days to 50 per cent flowering in ricebean; Shitiri *et al*. (2019) for number of seeds per pod in ricebean; Singh *et al*. (2019) for plant height in ricebean. Presence of high heritability and moderate GAM for the above traits indicates that high heritability might be due to desirable environmental effect and moderate GAM might be due to additive gene action. Therefore, through rigorous selection, the above traits could be improved in successive breeding cycles.

Genetic association

In order to investigate the presence of any potential association among the yield attributing traits, Pearson correlation analysis was carried out (Table 3). In the present investigation, single plant yield exhibited significant positive correlation with the following traits *viz*., number of pods per plant (0.881), number of clusters per plant (0.720), pod length (0.326), number of seeds per pod (0.311), plant height (0.257), number of primary branches per plant (0.196) and hundred seed weight (0.192). Likewise, in ricebean, significant positive association of single plant yield with number of pods per plant was reported by Singh and Kumar (2018); number of clusters per plant by Raiger *et al*. 2019; pod length by Singh and Kumar (2018) and Raiger *et al*. 2019; number of seeds per pod by Singh and Kumar (2018); both plant height and number of branches per plant by Singh and Kumar (2018) and Raiger *et al*. (2019). Plant height showed significant positive association with number of primary branches per plant (0.337), number of pods per plant (0.282), single plant yield (0.257), number of seeds per pod (0.244) and pod length (0.187). Pod length (0.256), number of seeds per pod (0.235), number of pods per plant (0.205) and single plant yield (0.196) exhibited significant positive association with number of primary branches per plant. Number of clusters per plant exhibited significant positive association with number of pods per plant (0.803), single plant yield (0.720), pod length (0.259), number of seeds per pod (0.241) and hundred seed weight (0.199). Number of pods per plant displayed significant positive association with single plant yield (0.881), number of seeds per pod (0.316), pod length (0.279) and hundred seed weight (0.188). Similar to the present investigation, number of pods per plant exhibited positive association with single plant yield by Singh and Kumar (2018); number of seeds per pod by Singh and Kumar (2018) and pod length by Raiger *et al*. (2019). Pod length exhibited significant positive association with number of seeds per pod (0.639) and single plant yield (0.326). Number of seeds per pod showed significant positive association with single plant yield (0.311). Hundred seed weight exhibited positive association with single plant yield (0.192).

Principal component analysis

Principal component analysis for nine biometrical traits was carried out in order to figure out the traits that accounted

Table 2: Genetic variability parameters for biometrical traits in ricebean genotypes.

Traits	PCV %	GCV %	h^2 %	GAM
Days to 50% flowering	8.03	7.71	92.24	15.28
Plant height	13.22	10.26	60.21	16.42
Number of primary branches per plant	22.59	18.94	70.29	32.77
Number of clusters per plant	29.27	27.39	87.58	52.88
Number of pods per plant	32.43	31.70	95.56	63.92
Pod length	6.32	6.17	95.19	12.41
Number of seeds per pod	7.04	6.55	86.52	12.57
Hundred seed weight	13.09	12.92	97.32	26.29
Single plant yield	23.16	22.06	90.76	43.36

Table 3: Genetic relationship among biometrical traits in ricebean.

Characters	Days to 50 per cent flowering	Plant height	Number of primary branches per plant	Number of clusters per plant	Number of pods per plant	Pod length	Number of seeds per pod	Hundred seed weight	Single plant yield
Days to 50% flowering	1.000	0.115	0.169	-0.030	-0.078	0.125	0.168	-0.113	-0.159
Plant height		1.000	0.337**	0.114	0.282**	0.187*	0.244**	0.022	0.257**
Number of primary branches per plant			1.000	0.122	0.205*	0.256**	0.235*	-0.011	0.196*
Number of clusters per plant				1.000	0.803**	0.259**	0.241**	0.199*	0.720**
Number of pods per plant					1.000	0.279**	0.316**	0.188*	0.881**
Pod length						1.000	0.639**	0.051	0.326**
Number of seeds per pod							1.000	0.073	0.311**
Hundred seed weight								1.000	0.192**

* - p≤0.05 and ** - p≤0.01.

more genetic variability among the ricebean genotypes. Out of nine principal components, first three principal components were found to have Eigen value more than one (Table 4). Eigen values of the first three principal components were 3.2504, 1.6525 and 1.0248, respectively. The first three principal components explained 36.12, 18.36 and 11.39 per cent of variance, respectively to the total variance and the three components collectively contributed 65.86 per cent of the variance to the total variance. The results were in line with the findings of Meena *et al*. (2017) in ricebean, Kumar *et al*. (2022) in blackgram and Azam *et al*. (2023) in greengram who reported 61.65, 71.19 and 64.60 per cent of the total variation through first two, four and two principal components, respectively.

All the nine biometrical traits contributed positively to the variation in the first principal component (36.12%) (Table 5). Number of pods per plant contributed maximum to the variability by high positive loading of 0.885. It was followed by single plant yield (0.867), number of clusters per plant (0.789), number of seeds per pod (0.593) and pod length (0.584). Similar results were obtained by Meena *et al*. (2017) with the study of 64 ricebean genotypes who reported that variation in the first principal component was positively contributed by number of pods per plant, single plant yield, number of clusters per plant, number of seeds per pod and pod length. The variability of 18.36 per cent in the second principal component was attributed due to the

Table 4: Eigen value, proportion of variance and cumulative proportion of the principal components for biometrical traits.

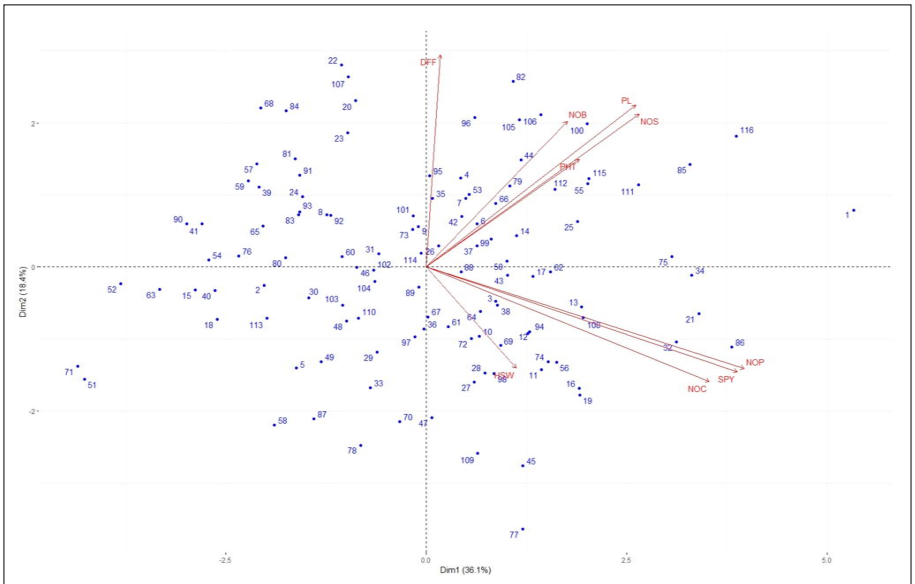
Components	Eigen values	Proportion of variance (%)	Total variance (%)
PC1	3.2504	36.12	36.12
PC2	1.6525	18.36	54.48
PC3	1.0248	11.39	65.86
PC4	0.9131	10.15	76.01
PC5	0.7921	8.80	84.81
PC6	0.6628	7.36	92.17
PC7	0.3561	3.96	96.13
PC8	0.2511	2.79	98.92
PC9	0.0971	1.08	100.00

Table 5: Component matrix representing Eigen vectors and scores of first three principal components of biometrical traits.

Traits	PC1	PC2	PC3
Days to 50% flowering	0.039	0.657	0.082
Plant height	0.426	0.333	-0.577
Number of primary branches per plant	0.393	0.452	-0.484
Number of clusters per plant	0.789	-0.355	0.036
Number of pods per plant	0.885	-0.315	-0.105
Pod length	0.584	0.501	0.434
Number of seeds per pod	0.593	0.474	0.396
Hundred seed weight	0.251	-0.313	0.296
Single plant yield	0.867	-0.325	-0.074

positive loading of days to 50 per cent flowering (0.657) and the negative loading of hundred seed weight (-0.313). The negative loadings of plant height (-0.577) and number of primary branches per plant (-0.484) were related more to the variations in the third principal component. Positive and negative loading indicates the positive and negative association between the components and the variables. Therefore, the aforementioned traits with high (either positive or negative) loadings contributed majority of the genetic variability (65.86%) through the corresponding principal components among the ricebean genotypes. Hence, the above traits could be given due importance in the crop improvement programmes.

A loading plot's vector, which is traced from the origin to each trait, makes it easier to appreciate how the various traits are associated. In the present study, the angle between the trait vectors *viz*., number of pods per plant and single plant yield; pod length and number of seeds per pod; plant height and number of primary branches per plant; plant height and number of seeds per pod; number of primary branches per plant and pod length; number of pods per plant and number of clusters per plant; number



DFF- Days to 50 per cent flowering; PL- Pod length; PHT- Plant heigh; NOS- Number of seeds per pod; NOB- Number of primary branches per plant; HSW- Hundred seed weight; NOC- Number of clusters per plant; SPY- Single plant yield; NOP- Number of pods per plant.

Fig 1: Genotype by trait biplot demonstrating the association between PC1 and PC2 for biometrical traits.

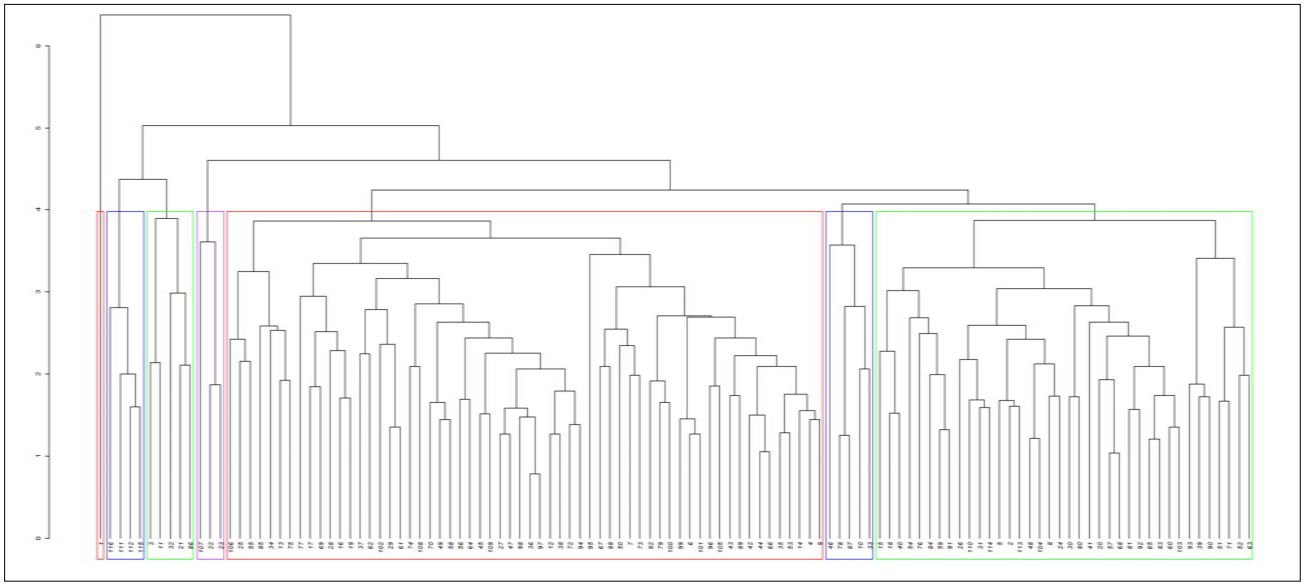


Fig 2: Agglograph depicting clustering of 116 ricebean genotypes for biometrical traits.

Table 6: Cluster composition of ricebean genotypes based on biometrical traits using agglomerative hierarchical clustering.

Clusters	Number of genotypes	Genotypes
1	1	IC 520980
2	38	IC 520905, IC 102832, IC 520958, IC 520901, IC 361365, IC 342238, IC 520929, IC 469171, IC 520956, IC 360608, IC 521012, IC 520925, IC 520898, IC 417831, IC 421938, IC 423291, IC 520891, IC 520893, IC 520887, IC 419602, IC 342378, IC 520594, IC 469200, IC 520945, IC 419493, IC 521000, IC 444184, IC 469193, IC 341966, IC 520903, IC 520953, IC 469190, IC 389691, IC 444138, IC 360621, LRB 556, LRB 583 and RBL 35
3	5	IC 444185, IC 469202, IC 469191, IC 969187 and IC 342374
4	60	IC 10283, IC 520961, IC 520960, IC 520996, IC 360617, IC 520945, IC 361364, IC 520971, IC 521171, IC 342375, IC 520943, IC 417830, IC 520942, 520900, IC 341969, IC 520964, IC 52068, IC 521034, IC 520972, IC 989196, IC 520994, IC 342226, IC 369282, IC 520983, IC 469178, IC 521037, IC 419590, IC 521031, IC 444191, IC 520947, IC 520997, IC 520931, IC 520941, IC 520909, IC 521350, IC 520895, IC 469192, IC 521010, IC 520951, IC 600615, IC 49182, IC 521005, IC 469197, IC 469193, IC 469181, IC 520967, IC 520963, IC 521004, IC 341951, IC 520957, IC 341967, IC 520976, IC 520897, IC 444157, IC 520949, IC 520750, IC 341974, IC 469165, IC RBL 1 and LRB 324
5	5	IC 520932, IC 520916, IC 360363, IC 395028 and IC 520978
6	3	IC 521174, IC 342376 and IC 520846
7	4	LRB 559, LRB 576, RRB 15 and RRB 18

of pods per plant and hundred seed weight were observed as less than 90° implying positive association between the traits (Fig 1). Further, no association was detected for the following trait pairs *viz*., number of primary branches per plant and number of clusters per plant; days to 50 per cent flowering and hundred seed weight. No significant association of hundred seed weight with number of primary branches per plant, plant height, number of seeds per pod and pod length was detected from the biplot.

Within a biplot, position of a genotype with reference to the orientation of the trait vector arrow indicates the performance of that genotype for that particular trait (Aslam, 2014). Genotypes situated close to the trait vector demonstrate enhanced performance for that specific trait, whereas the genotypes positioned opposite to the trait vector indicates the below par performance for that trait (Fig 2). The following genotypes *viz*., RBL 35 and IC 520951 (days to 50 per cent flowering); LRB 559 and RRB 18 (plant height); IC 444157 (number of primary branches per plant); IC 341969 (number of clusters per plant); IC 969187 (number of pods per plant); IC 469181 and RRB 18 (pod length); IC 469181 and RRB 18 (number of seeds per pod); IC 521004 (hundred seed weight); IC 342374 and IC 469191 (single plant yield) were identified as desirable genotypes for the corresponding traits from the biplot. Therefore, the above-mentioned genotypes for the respective traits could be utilized in the future ricebean breeding programmes.

In order to formulate an effective hybridization plan, it is foremost to assess the genetic diversity. Cluster analysis is one of the methods to assess the genetic diversity in a given population. It determines the genetic relationship among the genotypes and find out the suitable genotypes for future breeding programme. The genetic diversity within the ricebean genotypes under study was assessed using agglomerative hierarchical clustering through average linkage method for nine biometrical traits. The genotypes were grouped into seven clusters (Table 6). Cluster IV was the largest cluster with 60 genotypes. It was followed by cluster II which comprised 38 genotypes. Cluster I, III, V, VI and VII consisted of one, five, five, three and four genotypes, respectively. Grouping of genotypes into different clusters confirmed the presence of sufficient diversity among genotypes.

CONCLUSION

The best performing genotypes *viz*., IC 342375 and IC 469191 (for single plant yield) identified in the present study could be further tested in multi-location trials for their utilization in commercial cultivation. Genetic variability and principal component analysis (PCA) indicated that the traits number of pods per plant, number of clusters per plant and single plant yield contributed substantially to the overall genetic variation. These traits also demonstrated high heritability and high genetic advance as a percentage of the mean. Furthermore, the number of pods per plant and number of clusters per plant exhibited a positive association with single plant yield. In order to develop a ricebean cultivar with desirable plant type, hybridization could be carried out between diverse genotypes and selection could be made among the progenies using the associated traits established in the present study.

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Disclaimers

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Conflict of interest

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