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Principal Component Analysis and Genetic Association of Seed Related Traits in an Underutilized Pulse Crop, Ricebean (*Vigna umbellata*)

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ABSTRACT

Background: Seed related traits are important since they directly draw consumer preference. But there are only limited numbers of studies with reference to seed related traits. Hence, the present study was undertaken to study the genetic diversity and genetic relationship among seed traits in ricebean.

Methods: During *Rabi*, 2022-23, a set of 109 ricebean germplasm with seven checks were evaluated in Augmented design II at Department of Pulses, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore.

Result: Morphological characterization of 109 genotypes revealed that green yellow was the predominant seed coat colour. Seed coat pattern was absent in most of the genotypes and in rest of the genotypes, speckled type was predominant. The traits *viz*., bulk density, seed volume and hundred seed weight exhibited high heritability with high genetic advance as per cent of mean. Seed volume, seed thickness, bulk density, seed length and seed breadth evidenced highly significant and positive association with hundred seed weight. PCA analysis revealed that the traits *viz*., length breadth ratio, bulk density, hundred seed weight, seed volume, seed length and seed thickness contributed to the maximum genetic variability. In addition, it also earmarked the best performing genotypes for each seed related trait. Hence, the above findings could be effectively utilized for the development of ricebean cultivars with ideal seed characteristics.

Key words: Genetic association, Genetic variability, PCA, Ricebean, Seed related traits.

INTRODUCTION

Legumes are the second most significant crop group after cereals which form the core component of human nutrition. For vast majority of the people, they are the chief source of protein. Despite the availability of a number of edible legumes, their rate of consumption is significantly higher than their rate of production. In this context, underutilized legumes have scope to address this challenge. Hence, efforts need to be undertaken to integrate the underutilized crops in to the mainstream cultivation. This could be effective in resolving the protein malnutrition. In India, ricebean [*Vigna umbellata* (Thunb.) Ohwi and Ohashi] remains as an underutilized legume species, despite having a good nutritional profile and many desirable traits such as high harvest index, resistance to bruchids, yellow mosaic virus, cercospora leaf spot, bacterial leaf spot, drought tolerance *etc*.

Among the biometrical traits, seed related traits *viz*., seed coat colour, seed size and hundred seed weight are important since the later two are directly related with single plant yield. These traits also draw consumer preference, thereby fetching high market value. But there are limited numbers of studies with reference to seed related traits. Hence, the present study was undertaken to study the genetic diversity and relationship among seed traits present among the set of ricebean germplasm.

MATERIALS AND METHODS

A set of 109 ricebean germplasm with seven checks were evaluated in Augmented design II during *Rabi*, 2022-23 at Department of Pulses, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore.

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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.

All the hundred and nine ricebean germplasm accessions were characterized for 10 seed related traits (three qualitative and seven quantitative traits). For qualitative traits, *viz*., seed coat colour, seed coat pattern and type of seed coat pattern, the scaling adopted was as per the descriptor of ricebean available in genesys portal. For quantitative traits, five plants of each genotype were randomly selected; seeds were collected and used to record data on seed thickness, seed length, seed breadth, length breadth ratio, bulk density, seed volume and hundred seed weight.

A total of 25 seeds were selected randomly from five plants (5 random seeds /plant), of each genotype and used for measuring seed thickness, seed length and seed width. Seed thickness was measured using digital vernier calliper, whereas graphical method was adopted to measure seed length and seed breadth. Length breadth ratio was calculated by dividing the values of seed length with the corresponding seed breadth values.

Bulk density refers to the ratio of mass of seed sample to the total volume occupied by the seed sample. It was determined by recording the mass of known number of seeds (100 seeds) and dividing it by the total volume of the seeds. Seed volume refers to the rise in volume of water (Mohsenin, 1986). To determine seed volume, an initial quantity of 10 ml of water was taken in a graduated measuring cylinder. Then, known quantity of seeds (100 seeds) was added to the water. The rise in volume of water gives the seed volume.

The mean data was used for testing the statistical significance. Analysis of variance, genetic variability parameters, genetic association analysis and principal component analysis were done using the R software version 4.2.3. Analysis of variance for Augmented design II and genetic variability parameters were derived using augmented RCBD package (Aravind *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. Genetic variability parameters *viz*., genotypic coefficient of variation, phenotypic coefficient of variation, genetic advance as per cent of mean were determined as per the formula given by Jhonson *et al.* (1955). Heritability (broad sense) was calculated according to the formula given by Lush (1940).The estimates of genotypic and phenotypic correlation coefficients were worked as per the formula given by Jhonson *et al*. (1955).

RESULTS AND DISCUSSION

Morphological characterization of 109 ricebean germplasm accessions revealed that green yellow seed coat colour was predominant and was present in 50.00% of the genotypes, followed by yellow (25.86%), cream yellow (15.52%), dark green (5.17%), maroon (1.72%) and brown (1.72%) (Table 1). Seed coat pattern was absent in majority of the genotypes (83.62%), whereas the pattern was medium in 16.38% of the genotypes in which speckled type of seed coat pattern (100.00%) was present as the exclusive pattern type.

The mean performance of the genotypes for the seven seed traits is given in Table 2. Analysis of variance indicated that all the 109 ricebean germplasm accessions exhibited significant differences for the seven quantitative traits studied, signifying the prevalence of sufficient amount of variability in the experimental material (Table 3).

For all the seven traits studied, the phenotypic coefficient of variation (PCV) was marginally higher than the genotypic coefficient of variation (GCV) (Table 4). This revealed the lower influence of environment and preponderance of genetic factors in demonstrating variability on these traits. Bulk density, seed volume and hundred seed weight recorded moderate PCV and GCV (11-20%) which signifies a relatively better potential for further improvement through selection. Similar findings of moderate PCV and GCV were recorded for hundred seed weight (Adewale *et al*., 2012 in African yam bean; Latha *et al*., 2013 in horsegram; Devi *et al*., 2021 in pre-breeding lines of blackgram) and seed volume (Adewale *et al*., 2012). In the present study,

Table 1: Frequency distribution of seed traits of in ricebean germplasm accessions.

Character	Score	Phenotype	Frequency per cent
Seed coat colour	1	White	-
	2	Light green	-
	3	Dark green	5.17
	4	Green yellow	50.00
	5	Cream yellow	15.52
	6	Yellow	25.86
	7	Red	-
	8	Maroon	1.72
	9	Purple	-
	10	Brown	1.72
	11	Chocolate	-
	12	Grey	-
	13	Ashgrey	-
	14	Black	-
	15	Others	-
Seed coat pattern	0	Absent	83.62
	1	Light	-
	2	Medium	16.38
	3	Heavy	-
Type of seed coat pattern	1	Flecked	-
	2	Striped	-
	3	Intensively striped	-
	4	Almost continuous	-
	5	Speckled	100.00

Table 2: Mean performance of ricebean genotypes for seed related traits.

Genotypes	Seed thickness (mm)	Seed length (mm)	Seed breadth (mm)	Length breadth ratio	Bulk density (g/cm^3)	Seed volume (ml)	Hundred seed weight (g)
IC 520980	2.81	6.94	3.24	2.14	0.79	4.75	5.87
IC 520905	2.71	6.64	3.11	2.14	0.56	3.55	4.13
IC 444185	2.65	7.07	3.19	2.21	0.72	4.75	5.14
IC 10283	2.58	6.26	3.09	2.02	0.69	4.35	5.05
IC 102832	2.77	7.25	3.19	2.28	0.54	3.43	4.28
IC 520961	2.64	6.73	3.28	2.05	0.62	3.45	4.06
IC 520960	2.42	6.33	2.87	2.21	0.61	2.95	3.50
IC 520958	2.62	6.18	2.73	2.26	0.63	2.88	3.69
IC 520996	2.59	6.31	2.78	2.27	0.77	3.30	4.97
IC 520932	2.75	6.75	3.31	2.04	0.59	3.58	4.18
IC 469202	2.62	5.95	2.67	2.23	0.62	4.25	5.85
IC 360617	2.65	6.70	3.10	2.16	0.73	4.15	5.46
IC 520945	2.68	6.43	3.26	1.97	0.62	3.35	4.07
IC 361364	2.95	6.92	3.42	2.03	0.68	4.80	5.18
IC 520901	2.36	6.46	3.09	2.09	0.57	3.73	5.05
IC 520971	2.73	6.51	3.26	2.00	0.68	3.90	4.65
IC 521171	2.63	6.13	2.93	2.10	0.83	2.40	3.96
IC 361365	2.80	7.09	3.24	2.19	0.51	4.28	5.28
IC 342375	2.75	7.01	3.35	2.10	0.64	4.20	5.05
IC 342238	2.65	5.67	2.95	1.92	0.62	3.13	4.07
IC 469191	3.18	7.21	3.40	2.12	0.50	4.13	4.95
IC 521174	2.52	6.20	2.87	2.16	0.67	3.25	4.28
IC 342376	2.73	6.80	3.07	2.22	0.75	3.25	4.43
IC 520929	2.46	6.18	2.89	2.14	0.70	3.05	4.12
IC 520943	2.86	6.47	3.04	2.13	0.57	3.65	4.17
IC 469171	2.87	6.56	2.94	2.23	0.75	4.25	5.18
IC 417830	2.87	6.75	3.28	2.06	0.70	4.08	5.10
IC 520942	2.78	6.54	3.21	2.04	0.58	3.48	4.26
IC 520900	2.84	6.89	3.23	2.14	0.76	4.45	5.28
IC 520956	2.75	5.95	2.48	2.40	0.62	3.75	4.24
IC 360608	2.68	6.33	3.09	2.05	0.72	3.63	4.32
IC 969187	2.58	6.42	3.10	2.07	0.74	3.53	4.10
IC 520916	2.51	6.21	3.09	2.02	0.63	3.50	4.19
IC 341969	2.63	6.43	2.90	2.22	0.67	4.08	4.70
IC 520964	2.80	6.68	3.17	2.11	0.50	4.00	4.45
IC 52068	2.68	6.77	3.09	2.19	0.74	3.80	4.80
IC 521034	2.48	6.33	2.79	2.27	0.78	4.78	5.25
IC 520972	2.82	6.87	3.13	2.20	0.57	3.93	4.53
IC 521012	2.78	7.09	3.28	2.16	0.74	4.10	5.51
IC 520925	2.93	6.64	3.15	2.11	0.55	3.15	4.67
IC 520898	2.40	6.75	3.02	2.24	0.48	2.94	3.77
IC 989196	2.60	6.54	2.86	2.29	0.65	3.43	4.15
IC 520994	2.52	6.20	2.89	2.15	0.71	4.15	4.84
IC 342226	2.95	6.40	3.33	1.93	0.62	3.88	4.27
IC 369282	3.11	7.24	3.32	2.18	0.73	5.13	5.77
IC 360363	2.65	5.98	3.05	1.96	0.70	3.38	4.07
IC 520983	2.85	6.48	3.03	2.14	0.88	3.78	5.22
IC 417831	2.68	6.36	2.91	2.19	0.78	3.40	4.15
IC 469178	2.48	6.49	2.84	2.29	0.72	4.40	5.09

Table 2: Continue...

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IC 521037	2.75	6.32	3.09	2.05	0.61	3.10	4.21
IC 421938	2.58	5.74	2.94	1.95	0.66	4.17	4.18
IC 423291	2.51	6.20	2.72	2.28	0.63	3.08	3.71
IC 419590	2.63	6.57	2.97	2.21	0.71	4.03	4.68
IC 520891	2.75	6.54	3.17	2.07	0.82	3.65	5.18
IC 521031	2.57	6.73	2.96	2.27	0.79	3.10	4.86
IC 444191	2.68	6.69	3.20	2.09	0.57	4.10	5.05
IC 520893	2.58	6.42	2.86	2.25	0.71	3.50	4.47
IC 520947	2.97	6.74	3.03	2.22	0.68	4.38	5.48
IC 520887	2.76	6.28	2.90	2.17	0.87	3.53	4.84
IC 419602	2.75	6.85	3.05	2.25	0.53	3.28	4.17
IC 520997	2.97	6.73	3.25	2.07	0.72	4.13	5.24
IC 520931	2.79	7.20	3.33	2.17	0.72	4.53	5.89
IC 342378	2.68	6.88	3.19	2.16	0.68	3.93	4.53
IC 520941	2.69	7.11	2.96	2.40	0.85	3.63	5.27
IC 520594	2.73	6.36	2.95	2.16	0.70	3.30	3.83
IC 520909	2.76	6.73	2.83	2.38	0.61	3.35	4.22
IC 521350	2.79	6.36	3.04	2.09	0.63	2.73	3.76
IC 469200	2.63	6.25	2.86	2.18	0.68	3.05	4.48
IC 520895	2.61	6.80	2.90	2.35	0.62	3.10	4.13
IC 469192	2.65	6.44	2.98	2.17	0.85	4.50	5.42
IC 520945	2.81	6.85	3.17	2.17	0.64	3.75	4.12
IC 521010	2.88	6.49	3.16	2.05	0.82	5.03	5.72
IC 520931	2.71	5.79	2.77	2.09	0.72	3.20	3.83
IC 600615	2.79	6.46	3.08	2.10	0.53	4.03	4.82
IC 49182	2.59	6.85	3.15	2.17	0.63	3.83	4.20
IC 419493	3.12	6.69	3.25	2.06	0.81	4.83	5.63
IC 521005	2.72	6.18	3.08	2.01	0.77	3.60	4.88
IC 395028	2.73	6.34	3.06	2.07	0.56	3.50	4.10
IC 469197	2.78	6.65	2.93	2.27	0.62	3.13	4.23
IC 521000	2.77	6.84	3.25	2.11	0.61	4.03	4.24
IC 444184	2.51	6.51	3.11	2.09	0.67	3.82	4.21
IC 469193	2.80	6.17	3.03	2.03	0.65	4.13	4.68
IC 469185	2.62	5.96	2.61	2.29	0.61	3.10	3.49
IC 341966	2.83	6.50	3.08	2.11	0.69	4.81	5.43
IC 469181	2.70	6.39	2.94	2.17	0.71	3.50	4.52
IC 342374	3.19	6.31	3.43	1.84	0.83	3.63	5.29
IC 520978	2.72	6.38	2.87	2.22	0.59	3.50	4.11
IC 520967	2.49	6.33	2.84	2.23	0.71	3.95	4.32
IC 520963	2.68	6.72	3.03	2.22	0.57	4.03	4.67
IC 520903	2.71	6.52	3.08	2.12	0.70	4.46	4.56
IC 520953	2.66	6.61	3.07	2.15	0.67	4.40	4.63
IC 469190	2.75	6.41	3.07	2.09	0.67	4.11	4.62
IC 389691	2.69	6.60	3.08	2.15	0.70	4.29	4.71
IC 521004	3.03	7.05	3.24	2.18	0.74	5.38	5.86
IC 341951	2.70	6.08	2.90	2.10	0.54	3.90	4.38
IC 520957	2.81	6.61	3.34	1.98	0.75	4.10	4.88
IC 341967	2.77	6.50	3.04	2.14	0.80	4.13	5.05
IC 520976	2.74	6.45	2.89	2.23	0.75	3.88	4.84
IC 520897	2.83	7.01	3.12	2.25	0.69	3.78	4.51
IC 444157	2.76	6.37	2.77	2.30	0.81	3.45	4.54

Table 2: Continue...

Table 2: Continue...

IC 520949	2.82	6.03	2.79	2.17	0.59	3.55	4.12
IC 520750	2.91	6.79	3.43	1.98	0.72	5.13	5.65
IC 444138	2.69	6.13	2.86	2.14	0.65	2.88	4.22
IC 360621	2.74	6.29	3.19	1.97	0.56	3.08	4.08
IC 341974	2.81	6.88	3.18	2.16	0.74	4.33	4.78
IC 469165	3.17	6.85	3.43	2.00	0.56	3.18	4.01
IC 520846	2.28	6.71	2.99	2.24	0.86	2.43	3.08
RBL 1	2.80	6.88	2.98	2.31	0.73	3.75	5.03
LRB 324	3.01	6.87	3.17	2.17	0.84	5.13	5.93
LRB 556 (Check)	2.63	6.71	2.88	2.32	0.77	3.40	4.72
LRB 559(Check)	2.62	6.77	2.92	2.27	0.71	3.81	4.37
LRB 576 (Check)	2.69	6.67	2.90	2.30	0.78	4.13	4.91
LRB 583 (Check)	2.40	6.47	2.64	2.43	0.67	3.14	4.23
RBL 35 (Check)	2.69	6.57	3.21	2.04	0.66	4.05	4.74
RRB 15 (Check)	2.69	6.67	3.01	2.17	0.79	3.44	4.85
RRB 18 (Check)	2.60	6.25	2.70	2.27	0.84	3.70	4.60
Mean	2.72	6.54	3.04	2.15	0.68	3.79	4.63
Minimum	2.28	5.67	2.48	1.84	0.48	2.40	3.08
Maximum	3.19	7.25	3.43	2.43	0.88	5.38	5.93
SE	0.01	0.03	0.02	0.01	0.01	0.06	0.05
CD	0.19	0.19	0.14	0.16	0.08	0.26	0.27

Table 3: Analysis of variance for seed related traits in ricebean genotypes.

Characters	Mean sum of squares				
	Total genotypes	Checks	Test genotypes	Checks Vs Test genotypes	Error
Seed thickness	0.030**	0.030**	0.030**	0.200**	0.001
Seed length	0.110**	0.090**	0.110**	0.040*	0.003
Seed breadth	0.040**	0.110**	0.040**	0.450**	0.010
Length breadth ratio	0.010**	0.040**	0.010*	0.210**	0.004
Bulk density	0.010**	0.010**	0.010**	0.080**	0.005
Seed volume	0.370**	0.390**	0.360**	0.310**	0.010
Hundred seed weight	0.360**	0.190**	0.370**	0.001	0.010

* - $p \leq 0.05$ and ** - $p \leq 0.01$.

Table 4: Estimates of genetic variability parameters for seed related traits in ricebean germplasm.

Traits	GCV (%)	PCV (%)	h^2 (%)	GAM
Seed thickness	5.43	6.05	80.64	10.07
Seed length	5.01	5.12	95.68	10.10
Seed breadth	5.96	6.19	92.47	11.82
Length breadth ratio	4.10	4.94	68.67	7.02
Bulk density	12.69	13.48	88.53	24.62
Seed volume	15.71	15.91	97.43	31.99
Hundred seed weight	12.92	13.09	97.32	26.29

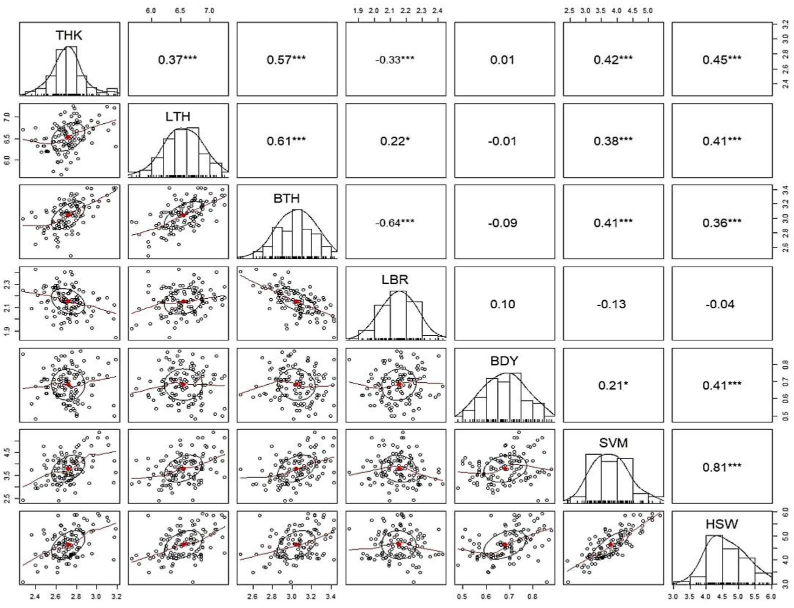
GCV- Genotypic coefficient of variation, PCV- Phenotypic coefficient of variation.

h^2- Heritability (broad sense), GAM- Genetic advance as per cent of mean.

the traits *viz*., seed thickness, seed length, seed breadth and length breadth ratio recorded low PCV and GCV (<10%) which implies a limited scope for further improvement of these traits. Similar results of low PCV and GCV were reported for seed thickness (Latha *et al*., 2013 and Devi *et al*., 2021), seed length (Adewale *et al*., 2012; Latha *et al*., 2013 and Devi *et al*., 2021), seed breadth (Adewale *et al*., 2012 and Devi *et al*., 2021) and length breadth ratio (Sulistyo *et al*., 2021 [low GCV alone] and Devi *et al*., 2021).

High heritability along with high genetic advance as per cent of mean (GAM) were recorded for the traits *viz*., bulk density, seed volume and hundred seed weight. In earlier investigations also, high heritability was noted for hundred seed weight in soybean by Sulistyo *et al*. (2021), whereas high heritability combined with high GAM was reported for seed volume in horsegram by Latha *et al*. (2013) and for hundred seed weight in horsegram and blackgram pre-breeding lines by Latha *et al*. (2013) and Devi *et al*. (2021), respectively. This indicates that the above traits are controlled by additive gene action and simple directional selection would be effective. High heritability along with moderate GAM were recorded for seed thickness, seed length and seed breadth. Similarly, high heritability was observed by Sulistyo *et al.* (2021) for seed breadth and seed thickness in soybean. This implies that the high heritability might be due to favourable environmental influence and moderate GAM might be due to additive gene action. Hence, through stringent selection, these traits could be improved in the successive breeding cycles. High heritability along with low GAM was recorded for length breadth ratio. This highlight there is no scope for improvement of these traits through direct selection.

In order to investigate the presence of any potential association between the seven seed related traits, Pearson correlation analysis was carried out. In the present investigation, seed volume (0.81), seed thickness (0.45), bulk density (0.41), seed length (0.41) and seed breadth (0.36) exhibited highly significant and positive correlation with hundred seed weight (Fig 1). Similarly, significant positive association of hundred seed weight with seed thickness, seed length and seed volume was reported by Latha *et al*. (2013) in horsegram; with seed length and seed breadth was recorded by Khamassi *et al.* (2021) in faba bean. Hence, these traits could be considered during indirect selection in order to improve the hundred seed weight. In addition, seed thickness evidenced highly significant and positive correlation with seed breadth (0.57) followed by seed volume (0.42) and seed length (0.37). Akin to the present study, Latha *et al*. (2013) also reported that the trait seed thickness exhibited positive association with seed breadth. However, seed thickness also exhibited highly significant and negative correlation with length breadth ratio (-0.33). From the results, it could be ascertained that, in ricebean, the traits *viz*., seed breadth, seed volume and seed length have a positive influence on seed thickness, whereas length breadth ratio has a negative influence on seed thickness. Hence, seed thickness could be increased by selecting genotypes with increased seed length, but only up to a certain limit. Therefore, in order to increase seed thickness, selection of genotypes with high seed breadth value and moderate seed length value might be rewarding. Further, the trait seed length expressed highly significant and positive correlation with seed breadth (0.61), seed volume (0.38) and length breadth ratio (0.22). In line with the present finding, significant positive correlation of seed length with seed breadth and seed volume was reported by Latha *et al*. (2013); with seed breadth by Khamassi *et al*. (2021). This indicates that increase in seed length increases seed breadth, length breadth ratio and ultimately, volume of the seeds. Besides, seed breadth showed highly significant and positive correlation with seed volume (0.41), whereas highly significant and negative correlation with length breadth ratio



THK- Seed thickness, LTH- Seed length, BTH- Seed breadth, LBR- Length breadth Ratio, BDY- Bulk density, SVM- Seed volume and HSW- Hundred seed weight. * - p≤0.05, ** - p≤0.01 and *** - p≤0.001.

Fig 1: Genetic relationships among seed related traits in ricebean germplasm.

(-0.64). Latha *et al*. (2013) also reported significant positive association between seed breadth and seed volume in horsegram accessions. Moreover, significant and positive correlation (0.21) was also observed between seed volume and bulk density.

Table 5: Eigen value, proportion of variance and cumulative proportion of the principal components.

Components	Eigen values	Proportion of variance (%)	Total variance (%)
PC1	3.0319	43.31	43.31
PC2	1.5742	22.49	65.80
PC3	1.1062	15.80	81.60
PC4	0.6145	8.78	90.38
PC5	0.5150	7.36	97.74
PC6	0.1557	2.22	99.96
PC7	0.0025	0.04	100.00

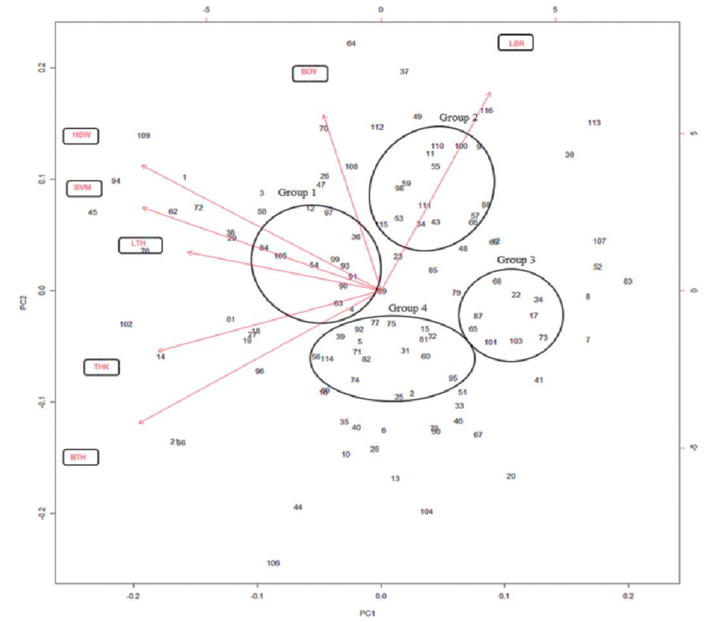
Table 6: Component matrix representing Eigen vectors and scores of first three principal components.

Variables	PC1	PC2	PC3
Seed thickness	-0.4254	-0.1785	-0.0138
Seed length	-0.3694	0.1130	-0.6560
Seed breadth	-0.4615	-0.3907	-0.0914
Length breadth ratio	0.2078	0.5832	-0.5267
Bulk density	-0.1097	0.5167	0.4940
Seed volume	-0.4544	0.2440	0.1178
Hundred seed weight	-0.4560	0.3688	0.1606

Principal component analysis revealed that the first three principal components were found with Eigen value greater than one (Table 5). Eigen values of the first three principal components were 3.0319, 1.5742 and 1.1062, respectively. The first principal component accounted for 43.31% of the variance to the total variance, whereas the second and third principal components attributed 22.49% and 15.80% of the variance, respectively and the above three components cumulatively accounted 81.60% to the total variance.

The variation in the first principal component was ascribed due to positive loading of length breadth ratio (0.2078), whereas the variation in the second principal component was due to positive loading of the following traits *viz*., length breadth ratio (0.5832), bulk density (0.5167), hundred seed weight (0.3688), seed volume (0.2440) and seed length (0.1130) (Table 6). The traits *viz*., bulk density (0.4940), hundred seed weight (0.1606) and seed volume (0.1178) contributed variation to the third principal component.

In the present study, the angle between the trait vectors, hundred seed weight and seed volume; seed volume and seed length; seed length and seed thickness; seed thickness and seed breadth were found to be less than 90° (Fig 2) indicating a strong positive correlation between the traits pairs. Besides, a strong negative correlation was observed between seed breadth and length breadth ratio as well as between seed thickness and length breadth ratio since the angle between the trait pairs were greater than 90°.



THK- Seed thickness, LTH- Seed length, BTH- Seed breadth, LBR- Length breadth ratio, BDY- Bulk density, SVM- Seed volume and HSW- Hundred seed weight.

Fig 2: Genotype by trait biplot demonstrating the association between PC1 and PC2 for seed related traits.

Table 7: Groupings of the ricebean genotypes from the trait by genotype biplot.

Groups	Number of genotypes (excluding the outliers)	Genotypes
1	12	IC520941, IC341974, IC520891, IC520897, IC389691,IC520953, IC520903, IC342378, IC10283, IC360617, IC341967 and IC52068
2	15	RRB15, IC419590, IC341969, IC520994, IC520909, IC520893, IC520967, LRB559, IC520976, IC520887, IC521031, IC469202, LRB556, IC444157 and IC520996
3	9	IC520978, IC520594, IC520949, IC444138, IC520931, IC521171, IC520929, IC521174 and IC469200
4	18	IC444191, RBL35, IC60015, IC520943, IC520905, IC341951, IC520972, IC520948, IC469193, IC102832, IC469190, IC521005, IC49182, IC360608, IC419602, IC444184, IC969187 and IC520996

The genotypes in the biplot were dispersed among all the four quadrants indicating the presence of significant amount of genetic diversity among the accessions. However, the genotypes (excluding the outliers) could be grouped in to four groups in which group 1, 2, 3 and 4 comprised of 12,15,9 and 18 genotypes, respectively (Table 7). The genotypes within each group, as compared to other groups, exhibited relatively similar range of values for the seed related traits.

The interrelationships among the accessions and seed related traits based on PC1 and PC2 were delineated in the trait by genotype biplot (Fig 2). In a biplot, the location of a genotype with reference to the direction of arrow reveals the performance of that genotype for a specific trait. The biplot revealed that seed thickness was maximal in the genotype IC361364 and IC520750, while the seed length was greater in the genotype IC369282. The values of seed breadth were determined to be higher in the genotypes IC469191 and IC342374. The genotype IC444157was detected with higher length breadth ratio. Bulk density was high in the genotypes *viz*., IC469192 and IC520941, whereas seed volume was observed to be high in the genotypes IC369282 and IC521004. Hundred seed weight was maximum in the genotypes IC521004 and LRB324.

CONCLUSION

The best performing genotypes identified in the present study for the seed traits, could be further tested for yield. In order to develop a ricebean cultivar with one or more desired seed characteristics, hybridization could be effected across the corresponding groups and selection could be made among the progenies using the associated traits established in the present study.

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