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RESEARCH ARTICLE

Stability analysis of yield and yield related traits in ricebean [*Vigna umbellata* (Thunb.) Ohwi and Ohashi]

W. S. Philanim*, Amit Kumar, Nivedita Shittegar, S. Mukesh Sankar[1], C. Bharadwaj[1], Umakanta Ngangkham[2] and Bijoya Bhattacharjee

Abstract

A study on stability analysis was carried out in 30 diverse genotypes of ricebean (*Vigna umbellata* Thunb.) in eastern hill region of India. Significant differences among the genotypes over the years were observed for all the three traits studied. The first two principal components axis (IPCA1, 90.4% and IPCA2, 9.6%) could explain 100% of the total of the interaction variation. Correlation study showed that the stability parameters are highly associated with each other ($p < 0.01$). Multi trait stability index and genotype selection along with strength and weakness view of the genotypes to the traits inferred higher productivity of BSKB 28 (G29) for number of pods/plant and seed yield/plant and Ukhrul 15 (G17) for number of seeds/pod. Different stability measures selected seven genotypes, namely, Bete 6 (G22), IC002567 (G8), Ukhrul 6 (G13), Ukhrul 14 (G16), Ukhrul 15 (G17), Bete 4 (G21) and BSKB 3 (G28) as the most desirable and stable performing with good yield over the years.

Keywords: AMMI, MGIDI, ricebean, stability analysis, yield related traits

Introduction

Ricebean [(*Vigna umbellata* (Thunb.) Ohwi and Ohashi)], earlier known as *Phaseolus calcaratus*, an underutilized diploid (2n=22) grain legume, is grown mostly in the North-Eastern Himalayan regions of India which is considered as one of the biological hotspots and is integral to the region (Barthakur et al. 2001). It has various synonyms viz., *Azukia umbellata* (Thunb.) Ohwi, *Phaseolus calcaratus* Roxb. and *Phaseolus pubescens* (Duke 1981). It is commonly known as red bean, Japanese rice bean, climbing mountain bean, Mambi bean and oriental bean in English (Duke 1981; Mejia 1984). It is a self-pollinating, warm *kharif* season perennial legume that can also be grown annually. Indo-China border is the most probable origin of ricebean. It is considered to be evolved from its wild form, *Vigna umbellata* var. *gracilis*, a typically small-leaved, fine stemmed, freely branching, sporadic and asynchronous flowering, photoperiod sensitive with indeterminate growth habit and strongly dehiscent pods with small and hard seeds. The crop duration of ricebean ranges between 120-150 days with a deep root system of 100-150 cm long and the plant type is erect to semi-erect vine, which can grow up to a height of 100 cm. Ricebean is rich in protein content (25%) consumed whole as it cannot be processed into dal, and also used as fodder and green manure to enrich soil. Ricebean is known to tolerate harsh conditions of acidic soil, drought and water logging alongside its innate nitrogen-fixing capacity that adds to soil fertility makes it ideal for the north-eastern region of India. The twinning habit of rice bean makes them suitable to intercrop with maize, sorghum and millets or pearl millet. Despite its high nutritional value and excellent seed productivity, it has failed to emerge as a major leguminous crop. Ricebean is one of the most important minor pulse crop which is cultivated in marginal lands with humid sub-tropical to warm to cool climate under range of soil types that contribute hugely towards pulse production,

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Division of Crop Sciences, ICAR-RC-NEH Region, Umiam, Meghalaya 793 103, India; [1]Division of Genetics, ICAR-IARI, New Delhi 110 012; [2]Division of Biotechnology, ICAR-RC-NEH Region, Manipur Centre 795 004, India

***Corresponding Author:** W. S. Philanim, Division of Crop Sciences, ICAR-RC-NEH Region, Umiam, Meghalaya 793 103, India, E-Mail: philanim09@gmail.com

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although its production and productivity remains very low (Viswanatha et al. 2016). No modern plant breeding methods have been applied to improve the crop and only landraces having low yield are cultivated by the farmer. A major initiative has been taken up under INCO programme of the European Commission's Sixth Framework Programme (FP6) and FOSRIN (Food Security through ricebean Research in India and Nepal) (Anderson 2012), which targets to promote rice bean on a wider scale, assess production chain and nutritional aspects of the crop, and to evaluate the range of germplasm and indigenous information available. Ricebean is a household pulse in the north-eastern region of India. However, its consumption is limited due to its non-availability in sufficient quantity. The contribution of northeast India to the total pulse production is negligible and ricebean production is meagre as the crop is confined to kitchen gardens and unproductive marginal lands. A major portion of the region's ricebean consumption is met through imports from neighboring countries like Myanmar and Bangladesh. Different environmental factors such as temperature, day length, fertility, sowing time and soil moisture influence plant growth strongly during its various developmental stages (Bull et al. 1992). As little information is available on ricebean, it is pertinent to understand the genotype response to environmental changes based on which variety recommendation can be made. Ricebean performance assessed at different environments will be useful to identify location-specific genotypes and stable genotypes across locations or environments to enhance the yield of ricebean and propel its popularity and adoption. When the performance of cultivars is compared across sites, several cultivar attributes are considered, of which grain yield is the most important (Sabaghpour et al. 2012). Average global yield of rice bean has been very low, about 225 kg/ha (Duke 1981). Production of as high as 1979 kg/ha (Zaman and Malik 1999) and 3000 kg/ha seed and 8000 Kg/ha dry herbage has been reported by Mukherjee et al. (1980). Systematic improvement work has not been pursued to develop high-yielding varieties. Grain yield, being a quantitative trait, is highly influenced by the environment, so a breeder should identify a variety that is less influenced by environments, i.e., a stable one. For consistent performance of a genotype over locations, any deviation in the performance is termed as genotype-environment interaction. Due to specific adaptation, some genotypes may perform poorly in one environment but better in a different environment (Dwivedi et al. 2020) and, therefore, some may be the case of ricebean.

The AMMI method is a popular statistic used in stability analysis as it is well-suited for data with many environmental influences, deciphers better knowledge of the G×E interaction establishes patterns of relationships between genotypes and environments, and provide accurate trait estimates (Gauch 1988; Zobel et al. 1988; Crossa et al. 1990). The AMMI (Additive Main Effects and Multiplicative Interaction) analysis uses analysis of variance (ANOVA) followed by principal component analysis (PCA) applied to the sums of squares allocated by the ANOVA to the G×E interaction to identify suitable genotypes with both high stability and high mean performance across environments (Sabaghpour et al. 2012). Ricebean improvement for yield can be achieved by utilizing good performing stable genotypes in crossing programmes. Therefore, the present study was conducted to identify stable and high yielding ricebean genotypes across the environments for north east hill region of India.

Materials and methods

A total of 30 ricebean germplasm lines collected from Manipur, Mizoram, Meghalaya and ICAR-NBPGR, Shimla were included in the study (Table 1).

Experimental design and trial

The materials were grown at Upland Plant Breeding farm, ICAR-Research Complex for North Eastern Hill Region, Umiam, Meghalaya. The field experiments were conducted in three growing seasons viz., 2018, 2019 and 2020 in Randomised Complete Block Design (RCBD) using three checks, namely, PRR1 (G9), PRR2 (G10) and RBL6 (G27) in three replications with 45 cm row to row spacing and 15 cm between plant to plant in all the years, respectively. Geographically, the experimental site is located at 25°.41' N latitude and 91°.54' E longitude at the altitude of 963m amsl. The average maximum temperature was 25.8°C and the average minimum temperature was 14.2°C with Relative Humidity (RH) of 63.2-65.9 and total rainfall of 2245 mm during the cropping seasons. Data were recorded on yield and yield attributing traits from each plot on five randomly selected plants. Standard agronomic practices for ricebean were followed during all the years.

Measures of stability used in the study

The AMMI based stability parameters (ASTABs) such as AMMI stability value (ASV) as per Purchase (2020), sums of the absolute value of the IPC Scores (SIPC) and averages of the squared eigen value (EV) as proposed by Sneller et al. (1997), absolute value of the relative contribution of IPCs to the interaction (ZA) as per the procedure of Zali et al. (2012) and Weighted Average of Absolute Scores (WAAS) according to Olivoto et al. (2019) were calculated.

Multi-trait genotype-ideotype distance index (MGIDI)

The multi-trait genotype-ideotype distance index (MGIDI) was used to rank the genotypes based on information of multiple traits as proposed by Olivoto and Nardino (2020). Initially, the rescaling of data was carried out within a range between 0

Table 1. Mean performance of yield and yield related traits in 30 ricebean genotypes evaluated for three years

S.No.	Genotype	Pods per plant	Seeds per Pod	Seed yield per plant
G1	EC000843	61.09	9.11	37.21
G2	EC012436	31.28	9.00	16.30
G3	EC014075	76.56	8.33	38.44
G4	EC016136	62.74	8.44	31.20
G5	EC018171	47.51	8.22	24.81
G6	EC018181	78.23	8.56	56.90
G7	IC002074	86.90	8.78	51.30
G8	IC002567	91.42	8.56	60.67
G9	PRR1	111.48	8.67	72.76
G10	PRR2	65.24	8.33	30.66
G11	IC469203	56.66	8.89	30.41
G12	IC469204	56.94	7.78	33.76
G13	Ukhrul-6	111.72	8.11	127.83
G14	Ukhrul-12	102.70	8.11	72.03
G15	Ukhrul-13	50.70	8.89	51.64
G16	Ukhrul-14	137.03	6.78	141.93
G17	Ukhrul-15	125.07	8.78	84.20
G18	Ukhrul-16	78.33	7.33	67.74
G19	Ukhrul-17	124.92	8.00	76.97
G20	Ukhrul-19	76.51	9.22	62.08
G21	Bete-4	116.69	8.44	68.03
G22	Bete-6	113.98	8.89	85.08
G23	Bete-9	30.54	8.56	26.49
G24	LRGP-3	111.88	8.33	68.68
G25	LRGP-4	65.31	7.78	37.53
G26	LRGP-5	68.48	8.78	56.29
G27	RBL6	84.44	8.11	44.27
G28	BSKB-13	144.60	9.22	120.98
G29	BSKB-28	148.81	9.33	122.40
G30	BSKB-29	64.74	9.67	61.14

and 100, followed by factor analysis to generate an ideotype matrix as given by Olivoto and Nardino (2020). Later, MGIDI index was computed as the Euclidean distance between the scores of accessions and the ideal genotype. The genotype with the lowest MGIDI is closer to the ideal genotype and thus indicates desired values for all the measured traits. The selection differential for all traits was performed considering approximately 10% selection intensity.

The proportion of MGIDI index of the ith treatment explained by the jth factor (ω_{ij}) was used to show the strengths and weaknesses of the treatments and was computed as:

$$\omega_{ij} = \frac{\sqrt{D_{ij}^2}}{\sum_{j=1}^{f}\sqrt{D_{ij}^2}}$$

where D_{ij} is the distance between the ith treatment and ideal treatment for the jth factor. Low contributions of a factor indicating that the traits within such a factor are close to the ideal treatment.

Statistical analysis for all the stability-related parameters was performed by functions available in the 'metan' package (v. 1.16.0) (Olivoto and Lucio 2020) in R version 3.6.1 (http://www.r-project.org/).

Results and discussion

AMMI analysis of variance

The performances with respect to yield and yield-related traits *viz.*, number of seeds per pod, number of pods per plant and seed yield per plant is presented in Table 1. Combined ANOVA for number of seeds per pod (SPP), number of pods per plant (PPP) and seed yield per plant **(**SYPP**)** across the years was analyzed, taking the years as random effects and genotypes as fixed effects. The results show that the genotypes (G), environmental (E) and interaction (GEI) effects being highly significant ($p<0.01$) for all the traits studied, indicating the prominence of all the three types of effects which is merely not random or due to chance.

The AMMI analysis of variance for seed yield per plant (g) of 30 genotypes tested across three environments showed significant variances for ($p<0.01$) due to environments, genotypes and G×E interactions. A higher value of sum of squares for genotypes designated that the genotypes were diverse, causing variation in seed yield due to large differences among the genotypic means. The analysis revealed that the main effects viz., genotype and environment accounted for 70.5% and 5.9% of the total variation. The G×E interaction component was partitioned into first two interaction principal components (IPCA), which was found non-significant. The IPCA1 explained 90.4% and IPCA2 explained 9.6% of the G x E interaction, thus the first two principal components could explain 100% of the G×E variation (Table 2). This is in concurrent with the findings of Gauch and Zobel (1988), Tilahun et al. (2015) and Devi et al. (2021) who reported the first two IPCAs as a measure to predict the most accurate model for AMMI. However, this contradicted the findings of Akter et al. (2014), Darai et al. (2017), Simeon et al. (2018), Manivannan et al. (2020) and Anuradha et al. (2022) where the genotype and environment interaction (GEI) was partitioned into more than two IPCAs by the AMMI model. These results suggest the number of terms to be included in AMMI model cannot be specified prior and factors like germplasm diversity, crop type and scale of environmental conditions will influence the degree of complexity of the best predictive model (Crossa et al. 1990; Kaya et al. 2002). The mean sum of squares due to environment is the largest, indicating the greater control of environmental conditions on seed yield, which supports

Table 2. Additive Main effects and Multiplicative interaction (AMMI) analysis of variance for seed yield per plant (g) across three years

Source	Df	Sum Sq.	Mean Sq.	Proportion	Accumulated	Explained SS (%)
ENV	2	22803.2	11401.6**			5.9
REP(ENV)	6	1547.557	257.9261**			
GEN	29	272288.2	9389.248**			70.5
GEN:ENV	58	41923.99	722.8274**			10.9
IPCA1	30	37887.09	1262.903**	90.4	90.4	
IPCA2	28	4036.902	144.1751**	9.6	100	
Residuals	174	5745.39	33.01948			
Total	327	386232.3	1181.139			

*significance at $p \le 0.05$ **significance at $p \le 0.01$

the fact that yield is a complex trait and, therefore, strongly relies on the environment to express the trait.

Stability analysis by AMMI model

Genotype environment signal (GEs) was calculated (Gauch 2013) to ascertain the appropriateness of the data to AMMI analysis. GEs were calculated by subtracting GE_N (GE noise) from GEI. For calculating GE_N, error mean sum of square and degrees of freedom (df) for GE is required. Thus the first step included the calculation of GE_N by multiplying the error mean sum of square with the degrees of freedom for GE (33.01 x 58 = 1915.1 for seed yield; 59.91 x 58= 3474.78 for number of pods per plant and 0.25 x 58 =14.5 for number of seeds per pod. Further, GEs was computed (41923.9-1915.1 = 40008.8 for seed yield; 117704.1-3474.78 = 114229.32 for pods per plant; 73.8-14.5 = 59.3 for seeds per pod). The reference here is that when SS due to GE_N is almost equal to SS due to GEI obtained in ANOVA, then GEI is said to be buried in the noise and thus considered signal poor. However, in this study, SS due to GE_N for seed yield, pods per plant and number of seeds per pod was found far lesser than GEI sum of squares. Thus, the interaction was almost signal rich and not buried in the noise. This pronounced the usefulness of AMMI analysis in the study.

AMMI1 biplot analysis

AMMI biplots are a powerful interpretative tool to understand the role of main effects and interaction effects on yield and yield associated traits. In AMMI1 biplot, the main effects (genotype mean and environment mean) are plotted against IPCA1 scores for both genotypes and environments. The inference from the analysis is that the genotypes displacement along the abscissa indicates differences in the main (additive) effects, and displacement along the ordinate indicates differences in interaction effects. Genotypes that group together have similar adaptation, while environments that group together influences the genotypes in the same way (Kempton 1984). Genotypes and environments on the right side of the midpoint of this axis has higher yields than those on left hand side and a genotype or environment on the same parallel line, relative, or ordinate have similar yields (Akter et al. 2014). The analysis showed that genotypes viz., G8, G9, G13, G22, G28 and G29 lying on the right side of the perpendicular are less influenced by the G×E interaction for seed yield. Genotypes viz., G8, G9 and G22 were found stable across the years for seed yield as they lie more close to the centre point in the biplot. G7, G8, G9, G13, G28 and G29 for pods per plant and G8, G23, G26, G20, G28, G29 were found to perform well across all the years and uneffected by the environment. Closer to the origin of the biplot is G7 and G8 for pods per plant and G8 and G10 for seeds per pod indicating their stable performance over environments (Figs. 1, 2 and 3). Combined analysis of variance carried out by several workers earlier (Gajghate et al. 2021; Lal et a. 2021) suggested the genotypic effect as a predominant source of

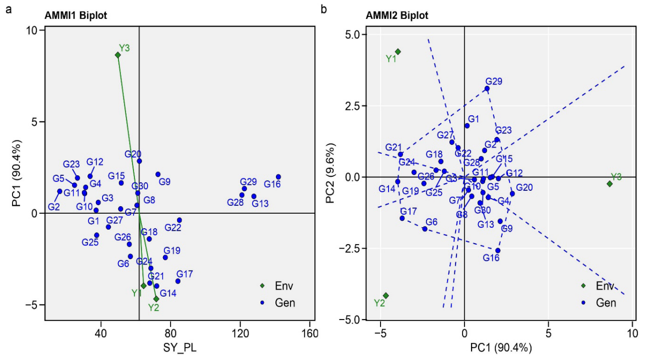

Fig. 1. AMMI1 and AMMI2 biplot of 30 ricebean genotypes for seed yield per plant across three years

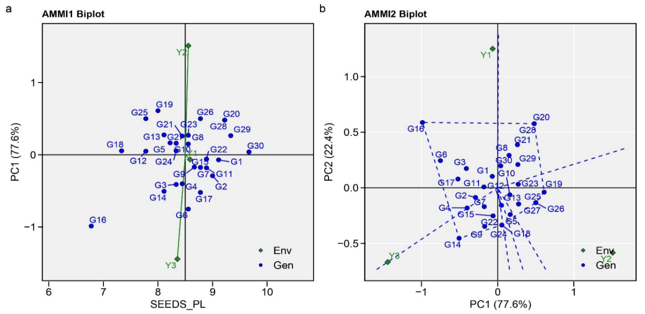

Fig. 2. AMMI1 and AMMI2 biplot of 30 ricebean genotypes for number of seeds per pod across three years

variation followed by GEI and environment effect. AMMI and biplot analysis were used to analyze the effects of GEI on grain yield and compute the AMMI stability value and yield stability index, which identified the above listed genotypes that are highly adapted, stable, and high yielding.

AMMI2 biplot analysis

This is based on a plot of IPCA1 vs IPCA2 and elucidates the magnitude of interaction of each genotype with the environment. Genotypes clustering in close proximity on the plot will have similar yields across all the years and genotypes that are drifted apart have variation in yields or shows a different pattern of response to environments. Genotypes and environments that fall into the same sector interact positively and negatively if they fall into opposite sectors (Osiru et al. 2009). Genotypes viz., G10, G11, G12, G7, G8, G30 occurring close together on the biplot have similar yields across the three years and G16, G17 and G29 showed difference in mean yield across the years. Genotypes near the origin are indicative of the stable performance in all the years. G8, G7, G28 and G13 were found stable and showed less interaction with the environmental-interactive forces. Genotypes G29 and G16 were away from the origin, indicating their responsiveness to different environmental factors for seed yield. G1, G12 and G13 that are knitted together and closer to the origin indicate stability for seeds per pod. G14, G16 and G20 were scattered far away from the centre thus rendering less stable. For pods per plant, stable genotypes were identified as G1, G15, G11, G7 and G30, which also had similar yields across the years. G16, G17, G21 and G29 were identified as the most unstable genotypes with high response to the environment for pods per plant (Figs. 1, 2 and 3).

The AMMI stability value (ASV)

To ascertain stable genotypes, AMMI stability value (ASV), the most appropriate single method of describing the stability of genotypes, was calculated for each genotype according to the relative contributions of the principal component axis scores (IPCA1 and IPCA2) to the interaction sum of squares as per Purchase et al. (2000). The yield stability index (YSI) was also calculated using the sum of the ranking based on yield and ranking based on the AMMI stability value. YSI incorporates both mean yield and stability in a single criterion. As per the ASV ranking, the most stable genotypes were G7, G1, G22 and G8 for seed yield as determined by the lowest ASV value. All three genotypes except G22 had low mean yield while G14, G21 and G17 were noted as the most unstable genotypes with high mean yield. For pods per plant, the most stable genotypes were G7, G22 and G8 with a relatively high mean number of pods per plant across the years, whereas the most unstable genotypes were identified as G17, G21 and G14. ASV ranking selected G12, G30 and G1 as the most stable genotypes, although G12 has a number of seeds per pod lower than the overall mean. G16, G6 and G19 were conferred as the most unstable genotypes based on the stability score (Table 3, Supplementary Tables S1 and S2). ASV uses two IPC scores to produce a balanced measurement between them and is therefore useful in our study where the first two IPCs accounted for a considerable amount of GEI, explaining major proportion of the total variation.

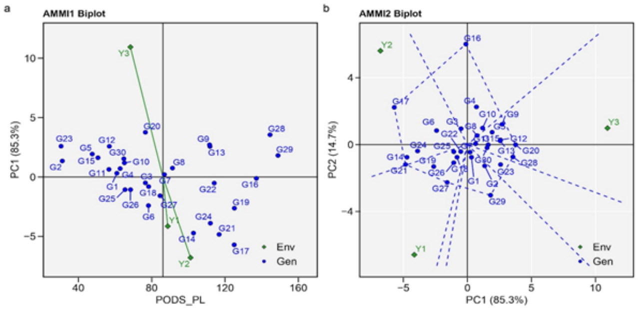

Fig. 3. AMMI1 and AMMI2 biplot of 30 ricebean genotypes for number of pods per plant across three years

Sums of the absolute value of the IPC Scores (SIPC)

The SIPC scores for the i^th^ genotype and N was the number of IPC that were retained in the AMMI model via F tests (Sneller et al. 1997). The absolute value of first IPCA scores represented the simplest measure of yield stability. The closer the SIPC scores are to zero, the more stable the genotypes are across test environments. Lowest SIPC scores for seed yield were seen in G3, G7, G8 and G11, indicating good stability across environments, but their seed yield was lower than the mean yield except G11. Genotypes G22, G28 and G30 had good stability and high mean yield. High-yielding genotypes like G16, G17, G22 and G29 were found unstable and, therefore, irrelevant for selecting stable genotypes in different environmental conditions. Genotypes G22, G7 and G8 were found to perform uniformly across the years with high number of pods per plant. The most unstable genotypes were G17, G16 and G21. For number of seeds per pod, the least environment responsive genotypes were G1 and G11 and the least stable genotypes were identified as G16 and G20 (Table 3, Supplementary Tables S1 and S2).

Averages of the squared eigen value (EV)

The next AMMI stability statistic (EV) was suggested by Sneller et al. (1994), and is averages of the squared eigenvector values, for the j^th^ cultivar and N were the number of IPC which were significant. Genotypes with lowest EV score represent the most desired and stable genotype. EV scoring identified G8 and G30 as uniform performing lines across environments with good mean yield. G1 was ranked first in stability but was a poor yielder. So was G7, G10, G11 and G25 that ranked among the top four in EV stability index but their individual yield was lesser than the

Table 3. Ranking of 30 ricebean genotypes as per stability measures for seed yield per plant

Sp. No.	GEN	Genotype	Y	Y_R	ASV	ASV_R	ASV_SSI	SIPC	SIPC_R	SIPC_SSI	EV	EV_R	EV_SSI	ZA	ZA_R	ZA_SSI	WAAS	WAAS_R	WAAS_SSI
1	G1	EC000843	37.21	23	2.34	2	25	1.96	15	38	0.04	23	46	0.04	2	25	0.32	2	25
2	G10	EC012436	30.66	26	10.14	9	35	1.23	5	31	0.01	3	29	0.09	8	34	0.99	9	35
3	G11	EC014075	30.41	27	10.57	11	38	1.19	4	31	0.01	4	31	0.10	10	37	1.02	10	37
4	G12	EC016136	33.76	24	18.96	22	46	2.07	17	41	0.02	16	40	0.17	20	44	1.83	20	44
5	G13	EC018171	127.83	2	8.71	7	9	1.83	12	14	0.01	13	15	0.09	7	9	0.92	7	9
6	G14	EC018181	72.03	9	37.31	30	39	4.14	25	34	0.07	26	35	0.34	30	39	3.61	30	39
7	G15	IC002074	51.64	18	15.55	18	36	1.67	11	29	0.01	10	28	0.14	17	35	1.50	17	35
8	G16	IC002567	141.93	1	18.84	21	22	4.57	28	29	0.11	29	30	0.21	24	25	2.04	22	23
9	G17	IC007537-6	84.20	6	34.85	28	34	5.15	30	36	0.09	28	34	0.34	29	35	3.49	28	34
10	G18	IC469202	67.74	12	13.20	15	27	1.95	14	26	0.01	11	23	0.13	14	26	1.32	14	26
11	G19	IC469203	76.97	7	22.68	25	32	2.64	20	27	0.03	19	26	0.21	23	30	2.21	24	31
12	G2	IC469204	16.30	30	11.28	13	43	2.13	19	49	0.02	17	47	0.12	13	43	1.17	13	43
13	G20	Ukhrul-6	62.08	13	26.76	26	39	3.43	23	36	0.04	22	35	0.25	26	39	2.63	26	39
14	G21	Ukhrul-12	68.03	11	35.81	29	40	4.61	29	40	0.07	27	38	0.34	28	39	3.52	29	40
15	G22	Ukhrul-13	85.08	5	3.69	3	8	1.40	6	11	0.01	14	19	0.05	4	9	0.44	3	8
16	G23	Ukhrul-14	26.49	28	18.13	20	48	3.24	22	50	0.04	20	48	0.19	21	49	1.87	21	49
17	G24	Ukhrul-15	68.68	10	28.19	27	37	3.17	21	31	0.04	21	31	0.26	27	37	2.73	27	37
18	G25	Ukhrul-16	37.53	22	11.28	12	34	1.40	7	29	0.01	5	27	0.11	12	34	1.11	12	34
19	G26	Ukhrul-17	56.29	17	15.89	19	36	1.93	13	30	0.01	12	29	0.15	18	35	1.55	19	36
20	G27	Ukhrul-19	44.27	20	7.14	6	26	1.97	16	36	0.02	18	38	0.08	6	26	0.79	6	26
21	G28	Bete-4	120.98	4	9.36	8	12	1.64	9	13	0.01	8	12	0.10	9	13	0.96	8	12
22	G29	Bete-6	122.40	3	13.01	14	17	4.45	27	30	0.14	30	33	0.16	19	22	1.51	18	21
23	G3	Bete-9	38.44	21	5.54	5	26	0.68	1	22	0.00	1	22	0.05	5	26	0.54	5	26
24	G30	LRGP-3	61.14	14	10.35	10	24	1.65	10	24	0.01	7	21	0.10	11	25	1.05	11	25
25	G4	LRGP-4	31.20	25	13.30	16	41	2.13	18	43	0.02	15	40	0.13	16	41	1.35	15	40
26	G5	LRGP-5	24.81	29	14.38	17	46	1.55	8	37	0.01	9	38	0.13	15	44	1.39	16	45
27	G6	LRGP-7	56.90	16	22.22	24	40	4.18	26	42	0.07	25	41	0.23	25	41	2.31	25	41
28	G7	BSKB-13	51.30	19	2.28	1	20	0.69	2	21	0.00	2	21	0.03	1	20	0.26	1	20
29	G8	BSKB-28	60.67	15	4.11	4	19	1.11	3	18	0.01	6	21	0.05	3	18	0.46	4	19
30	G9	BSKB-29	72.76	8	20.01	23	31	3.67	24	32	0.05	24	32	0.21	22	30	2.07	23	31

mean yield. Genotypes with highest mean yield *viz.*, G16, G17 and G29 were rendered unsuitable for wide adaption, which is indicative from the low EV ranking. The most stable genotypes were G11, G8, G7 and G22, although genotype G11 has a low number of pods per plant. Genotypes G16, G17 and G21 were highly responsive to environmental conditions and ranked lowest in the stability measures. For number of seeds per pod, the most stable genotypes were considered to be G1 and G11, and the least stable genotypes were G16, G20 and G28 (Table 3, Supplementary Tables S1 and S2).

Absolute value of the relative contribution of IPCs to the interaction (ZA)

Zali et al. (2012) also proposed the absolute value of relative contribution IPCA as another statistic to measure stability of genotypic performance under multi-location testing. Lower values of Za show the highest stability. ZA parameters showed genotypes G4, G7, G9 and G11 as most stable with relatively high mean yield. Genotypes, G7, G1 and G8 were ranked highest as the most stable genotypes but are poor yielders and yields lower than the mean yield. The most unstable genotypes were identified as G17 and G14 with high mean performance. Genotypes G16 and G29 with the highest mean yield were rendered unstable as indicated by their ZA score and ranking. For the number of pods per plant, G7, G22 and G8 were the most favourable genotypes and G17, G21 and G14 were the most unstable genotypes. Genotypes G1, G12 and G30 with the lowest value of ZA parameter for number of seeds per pod were identified as stable genotypes, while the most unstable genotypes were G16 and G6 (Table 3, Supplementary Tables S1 and S2). In a study carried out by Lal et al. (2021) it was reported that values for the three IPCAs were also highly significant and accounted jointly for 100% of the GEI effect. The IPCA 1 IPCA 2 and IPCA 3 accounted for a total variation caused by interaction in peanut. AMMI-1 biplot of certain genotypes can be used to explain the stability of a genotype and few of them were very stable and experienced very low environmental effect.

Weighted Average of Absolute Scores (WAAS)

Olivoto et al. (2019) developed WAAS model, an integrated stability statistic combining the AMMI and BLUP models based on the singular value decomposition of the matrix of the best linear unbiased predictions for the genotype × environment interaction effects generated by a linear mixed-effect model. The genotypes with the lowest WAAS score is considered as best stable genotype. WAAS measure selected G22, G8, G13 and G28 for their stable behaviour with high mean yield, whereas G21, G17 and G14 were considered the least stable. G29 and G16 have high mean yield but were highly unstable across environments. Uniform and good performing genotypes for pods per plant were selected to be G7, G22 and G8, while the least performing highly environment interactive genotypes were selected to be G17, G2 and G14. For the number of seeds per pod, G12, G30 and G1 were scored as the most stable genotypes, whereas the least stable genotypes were identified as G16, G6 and G20 (Table 3, Supplementary Tables S1 and S2).

Association analysis, multi-trait stability index and genotype selection

All the stability measures showed a positive correlation with each other. ASV index showed positive and highly significant association with SIPC, ZA and WAAS. Similar relation of highly significant positive was seen for SIPC index with EV, ZA and WAAS. EV index revealed positive association with ZA and WAAS (Table 4). The multi-trait stability index (Olivoto et al. 2021) has been proven useful for selecting genotypes for multiple traits based on mean performance and stability. Stable genotypes of soybean were also identified for stress conditions by Zuffo et al. (2020). Benakanahalli et al. (2021) made a suitable genotypic selection to identify stable guar genotypes with productive traits under differential environmental conditions through Multi-Trait Stability Index (MTSI) and Multi-Trait Genotype-Ideotype Distance Index (MGIDI). In the present study, the genotypes selected by the MGIDI index were G13, G17, G29 and G28 as indicated by the red line that suggests the number of genotypes selected based on the selection pressure. G22 was very close to the cut point (point closes to the red line) suggesting the presence of interesting features in this genotype (Fig. 4)**.**

The strengths and weaknesses view

Fig. 5 shows the strengths and weaknesses view of the selected genotypes by MGIDI index. The contribution of each factor to the MGIDI index is ranked from the most contributing factor (close to plot center) to the less contributing factor (close to the plot edge). The selected genotypes have strengths related to FA1, which indicates that G29 presents higher productivity in terms of higher values for pods per plant and seed yield per plant. Comparing G29 regarding FA1, we can conclude that G29 performed well for the traits within FA2, which is inferred by the lower contribution of FA2 for G29 (Fig. 5). The G29 had comparatively poor performance with respect to no. of seeds per plant and can be considered the weakness for the genotype. In contrast, G17 had a better contribution from traits from FA2 such as seeds per plant.

Table 4. Correlation study among the stability indexes for ricebean genotypes

	ASV	SIPC	EV	ZA	WAAS
ASV	1	0.804**	0.55**	0.992**	0.998**
SIPC		1	0.903**	0.872**	0.843**
EV			1	0.638**	0.601**
ZA				1	0.998**
WAAS					1

Table 5. Factors linked to correlated traits, selection differential, heritability, and indicators for ricebean traits

Trait	Factor	indicator	Xo	Xs	SDperc	Heritability
PPP	FA 1	Increase	86.1	129	49.7	0.796
SYPP	FA 1	Increase	62	112	81	0.91
SPP	FA 2	Increase	8.5	8.81	3.6	0.648

Xo = The mean value for the trait in base population; Xs = The mean value for the trait in a population with selected genotypes and SDperc: The selection differential expressed in percentage.

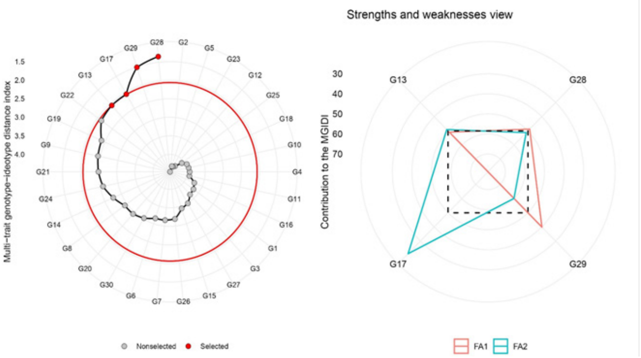

Fig. 4 **Fig. 5**

Figs. 4 and 5. Multitrait Genotype Ideotype Distance Index for genotype ranking and selection of genotypes considering 10% selection intensity; Strength and weakness view of the ricebean genotypes

In general, the parameters (SIPC4, EV4 and Za4) that use the number of IPC retained in the AMMI model via F tests are considered better than those parameters (ASV) that use the first of IPC or the first two of IPC. However, in situations where the first two IPCs account for most of the GEI and the portion of total variation explained is high, the ASV parameters can be effectively used as it uses two IPC scores to produce a balanced measurement between them. Also, using SIPC, EV, Za and ASV parameters is a way to consider all of significant IPC simultaneously (Zali et al. 2012). ASV, ZA and WAAS parameters commonly selected G22, G8, G13 and G28 as the most stable genotypes with relatively high mean yield and G14 as the most unstable genotype. Stability measures SIPC and EV selected G28 as the most stable genotype with high mean yield and G17, G16 and G21 as the most unstable genotypes. Genotype G28 could be introduced as the most favourable genotype with high mean yield and stability as inferred by all the five stability indexes. In any breeding work, the aim is to select genotypes that would perform in a number of given environments with acceptable yield performance. Selecting such genotypes would provide steady yields across locations or years. Lines with high yield and low stability score can be considered for location-specific adaptation.

Authors' contribution

The conceptualisation of research (PWS, AK, SMS, CB); Designing of the experiments (PWS, UN, NS); Contribution of experimental materials (PWS, AK, UN); Execution of field/lab experiments and data collection (PWS, AK, NS, BB); Analysis of data and interpretation (AK, SMS, CB); Preparation of manuscript (PWS, AK, SMS, BB).

Supplementary materials

Supplementary Tables S1 to S2 are provided.

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. Ranking of 30 ricebean genotypes as per stability measures for seeds per pod

Sl. No	GEN	Y	Y_R	ASV	ASV_R	ASV_SSI	SIPC	SIPC_R	SIPC_SSI	EV	EV_R	EV_SSI	ZA	ZA_R	ZA_SSI	WAAS	WAAS_R	WAAS_ SSI
1	G1	9.111111	5	0.265339	3	8	0.17355	1	6	0.002826	1	6	0.041269	1	6	0.077868	3	8
2	G10	8.333333	19.5	0.556712	8	27.5	0.222416	4	23.5	0.003757	3	22.5	0.068475	7	26.5	0.138016	8	27.5
3	G11	8.888889	8	0.626011	11	19	0.188999	2	10	0.003755	2	10	0.068321	6	14	0.142135	9	17
4	G12	7.777778	27.5	0.232959	1	28.5	0.206967	3	30.5	0.005554	4	31.5	0.041423	2	29.5	0.073749	1	28.5
5	G13	8.111111	24	0.963091	16	40	0.420399	14	38	0.013157	9	33	0.123347	16	40	0.245958	16	40
6	G14	8.111111	24	1.810338	27	51	0.959619	26	50	0.073105	26	50	0.254218	26	50	0.494385	26	50
7	G15	8.888889	8	0.32782	4	12	0.312597	7	15	0.013949	11	19	0.059323	4	12	0.103439	4	12
8	G16	6.777778	30	3.468212	30	60	1.574881	30	60	0.18508	30	60	0.452426	30	60	0.897729	30	60
9	G17	8.777778	10	1.806822	26	36	0.600414	21	31	0.032439	21	31	0.205117	22	32	0.422286	24	34
10	G18	7.333333	29	0.384627	7	36	0.389502	12	41	0.024217	17	46	0.069243	9	38	0.117425	7	36
11	G19	8	26	2.114055	28	54	0.64928	25	51	0.042975	25	51	0.232322	25	51	0.482434	25	51
12	G2	9	6	1.011054	19	25	0.377456	10	16	0.011282	8	14	0.120664	15	21	0.245155	15	21
13	G20	9.222222	3.5	1.759486	25	28.5	1.056594	29	32.5	0.097147	29	32.5	0.262526	28	31.5	0.501716	28	31.5
14	G21	8.444444	17.5	0.979323	18	35.5	0.646866	24	41.5	0.039626	24	41.5	0.153043	19	36.5	0.288324	19	36.5
15	G22	8.888889	8	0.32782	5	13	0.312597	8	16	0.013949	12	20	0.059323	5	13	0.103439	5	13
16	G23	8.555556	15	0.935115	14	29	0.301996	6	21	0.008558	6	21	0.104901	13	28	0.216649	14	29
17	G24	8.333333	19.5	0.384627	6	25.5	0.389502	11	30.5	0.024217	16	35.5	0.069243	8	27.5	0.117425	6	25.5
18	G25	7.777778	27.5	1.737446	23	50.5	0.633831	22.5	50	0.032445	23	50.5	0.205271	24	51.5	0.418167	23	50.5
19	G26	8.777778	11.5	1.737446	22	33.5	0.633831	22.5	34	0.032445	22	33.5	0.205271	23	34.5	0.418167	22	33.5
20	G27	8.111111	24	0.963091	17	41	0.420399	15	39	0.013157	10	34	0.123347	17	41	0.245958	17	41
21	G28	9.222222	3.5	1.759486	24	27.5	1.056594	28	31.5	0.097147	28	31.5	0.262526	27	30.5	0.501716	27	30.5
22	G29	9.333333	2	0.940718	15	17	0.474431	17	19	0.017381	14	16	0.128972	18	20	0.252486	18	20
23	G3	8.333333	21	1.434267	21	42	0.584965	20	41	0.025781	19	40	0.178065	21	42	0.358019	21	42
24	G30	9.666667	1	0.240361	2	3	0.237137	5	6	0.008495	5	6	0.04356	3	4	0.074933	2	3
25	G4	8.444444	17.5	1.400508	20	37.5	0.58232	19	36.5	0.025406	18	35.5	0.175405	20	37.5	0.351851	20	37.5
26	G5	8.222222	22	0.619123	10	32	0.404951	13	35	0.015388	13	35	0.096295	11	33	0.181692	12	34
27	G6	8.555556	15	2.614305	29	44	0.99638	27	42	0.077422	27	42	0.314861	29	44	0.63817	29	44
28	G7	8.777778	11.5	0.631583	12	23.5	0.345026	9	20.5	0.009637	7	18.5	0.089993	10	21.5	0.174297	10	21.5
29	G8	8.555556	15	0.594976	9	24	0.442001	16	31	0.020762	15	30	0.098302	12	27	0.181628	11	26
30	G9	8.666667	13	0.685212	13	26	0.517461	18	31	0.028941	20	33	0.114064	14	27	0.210135	13	26

Supplementary Table S2. Ranking of 30 ricebean genotypes as per stability measures for number of pods per plant

Sl.No.	GEN	Y	Y_R	ASV		ASV_ SSI	SIPC	SIPC_R	SIPC_ SSI	EV	EV_R	EV_ SSI	ZA	ZA_R	ZA_SSI	WAAS	WAAS_R	WAAS_ SSI
1	G1	61	24	2.000722	2	26	1.076981	4	28	0.004077	5	29	0.032856	2	26	0.382677	2	26
2	G10	65.11111	21	6.982332	12	33	2.173921	12	33	0.010275	11	32	0.091495	11	32	1.157356	12	33
3	G11	56.66667	26	3.735633	5	31	0.690227	2	28	0.001139	1	27	0.041263	4	30	0.554201	4	30
4	G12	56.88889	25	15.03659	21	46	2.85955	16	41	0.018714	16	41	0.167453	21	46	2.242548	21	46
5	G13	111.7778	9	14.94765	20	29	2.786504	15	24	0.01831	15	24	0.165523	19	28	2.221145	20	29
6	G14	102.7778	11	27.50548	28	39	5.479432	27	38	0.064681	26	37	0.310463	28	39	4.138002	28	39
7	G15	50.66667	27	9.446909	15	42	1.633416	9	36	0.007188	10	37	0.102463	13	40	1.385122	15	42
8	G16	137.1111	3	6.045599	9	12	6.124341	29	32	0.237956	30	33	0.108831	15	18	0.983462	10	13
9	G17	125	5	33.33228	30	35	7.933641	30	35	0.121693	29	34	0.39758	30	35	5.197274	30	35
10	G18	78.33333	15	4.77746	8	23	1.567681	8	23	0.00558	7	22	0.063858	7	22	0.802168	7	22
11	G19	125.1111	4	15.36734	23	27	3.945058	23	27	0.030308	20	24	0.187973	23	27	2.435671	23	27
12	G2	31.22222	29	7.961863	13	42	2.622603	13	42	0.015666	14	43	0.106578	14	43	1.338118	13	42
13	G20	76.55556	17.5	21.9306	26	43.5	3.776181	19	36.5	0.038733	23	40.5	0.237599	26	43.5	3.213192	26	43.5
14	G21	116.7778	6	28.1802	29	35	6.027281	28	34	0.073234	28	34	0.324943	29	35	4.298519	29	35
15	G22	114.1111	7	3.029636	3	10	0.935701	3	10	0.001892	3	10	0.039581	3	10	0.501198	3	10
16	G23	30.55556	30	15.14298	22	52	3.786678	20	50	0.02777	18	48	0.183594	22	52	2.386319	22	52
17	G24	112	8	22.66377	27	35	4.278026	24	32	0.042344	25	33	0.251857	27	35	3.375425	27	35
18	G25	65.44444	20	6.205176	10	30	1.492854	7	27	0.004306	6	26	0.074274	8	28	0.969737	9	29
19	G26	68.44444	19	6.295956	11	30	2.151162	11	30	0.010882	12	31	0.085477	10	29	1.067872	11	30
20	G27	84.55556	14	9.468609	16	30	3.842316	21	35	0.040606	24	38	0.137749	17	31	1.679175	16	30
21	G28	144.5556	2	20.72789	25	27	4.296022	25	27	0.038165	22	24	0.236736	25	27	3.142235	25	27
22	G29	148.8889	1	10.98177	17	18	4.843523	26	27	0.069573	27	28	0.165441	18	19	1.991324	18	19
23	G3	76.55556	17.5	3.041986	4	21.5	1.446198	6	23.5	0.006625	8	25.5	0.047323	5	22.5	0.56285	5	22.5
24	G30	64.77778	22	8.952911	14	36	1.730718	10	32	0.0067	9	31	0.100173	12	34	1.339296	14	36
25	G4	62.77778	23	4.695157	7	30	2.957338	17	40	0.034748	21	44	0.082594	9	32	0.934214	8	31
26	G5	47.55556	28	11.26738	18	46	2.668817	14	42	0.013778	13	41	0.134182	16	44	1.755038	17	45
27	G6	78.22222	16	14.03748	19	35	3.242024	18	34	0.020426	17	33	0.165813	20	36	2.174964	19	35
28	G7	86.88889	13	1.300457	1	14	0.663945	1	14	0.001483	2	15	0.020867	1	14	0.245269	1	14
29	G8	91.33333	12	4.400044	6	18	1.286872	5	17	0.003438	4	16	0.056344	6	18	0.718488	6	18
30	G9	111.5556	10	15.83559	24	34	3.919317	22	32	0.02971	19	29	0.191332	24	34	2.48989	24	34