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RESEARCH ARTICLE

MGIDI-based selection and stability analysis of mungbean (*Vigna radiata* L. Wilczek) mutants under acidic soils using AMMI and GGE models

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Abstract

In the present study, 84 M_3 generation mungbean mutant families along with two controls/parents were evaluated for 10 morphological and a biochemical trait(s) during *Zaid* 2024 under acidic soils of Meghalaya. Based on phenotypic selection and MGIDI selection index, ten superior mutant families, namely, B1-8, A2-8, A1-5, B1-1, A1-10, A2-9, B1-12, B1-11, B2-12 and B1-13 were identified. The selected mutant lines were evaluated for single plant yield (SYP) at four different locations of Meghalaya, having highly acidic soil conditions with pH ranging from 4.80–5.12 during *kharif* 2024. AMMI ANOVA revealed significant differences among the mutant lines, environments and mutant × environment interaction and most of the variation (65.78%) was accounted for by mutant lines, indicating the least influence of mutant × environment interaction. The mean SYP of tested genotypes involving ten mutant lines and two controls ranged from 3.12 g (Pusa 1431, control) to 10.37 g (A1-10, mutant) across the environments. The AMMI analysis also revealed that mutant line A1-10 showed higher SYP and accompanied with stable performance across the tested environments. The mutant lines, A1-10 in E1, E2 and E3; A2-8 in E1, E3 and E4 and B1-11 in E3 were found to be highly stable and gave the highest yield in their respective mega-environments. Out of four locations, E2 (NBPGR, Shillong) was the most discriminating and E3 (Farmers Field, Umeit) was the most representative to provide unbiased information about the performance of genotypes. Based on the mean vs stability graph, the mutant A1-10 stood out because of simultaneous high yield and high stability.

Keywords: Mungbean, mutants, AMMI, GGE biplots, MGIDI, selection, single plant yield

Introduction

Mungbean is an inexpensive source of high-quality protein, iron, folate, and carbohydrate (Kim et al. 2015). It is a warm-season leguminous crop with a brief life cycle of around 60 days, mostly grown on all agro-ecological conditions of India (Das et al. 2019). Mungbean is a highly valued legume crop in India because of its widespread adaptation, low water requirement and soil fertility improvement characteristics (Ali et al. 2024). This crop is gaining popularity in nontraditional farming areas due to its short growing cycle, high nutritional content, low resource requirements, soil-improvement potential, and global demand. In India, it is mainly grown in Maharashtra, Andhra Pradesh, Rajasthan, Odisha, Karnataka, and Uttar Pradesh. The temperature, crop adaptability, access to the market, and its physiographic position of the North East Hill Region (NEHR) offer an opportunity for pulse production. While the North-Eastern part of India offers favourable soil and agroclimatic conditions for the production of pulses, the region still lacks over 82% of what it actually needs in terms of pulses (Das et al. 2016). Since mungbean is a pulse crop with a short life cycle and can be easily cultivated in the North East Hill (NEH) region of India, it is critical to identify and develop genotypes that thrive in the region's acidic soils. It also gives an opportunity to include this short-duration pulse crop in the cereal-based cropping system of the NEH

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region after selection of genotypes suitable for cultivation under acidic soils.

Selecting superior parents with high heritability and genetic advancement is crucial for improving crop production. Understanding the genetic variability in yield and its related traits is crucial for enhancing the grain/seed yield. However, in self-pollinating crops like mungbean, natural variation is narrow, which limits selection opportunities (Ahir et al. 2015). The degree of progress in greengram production and productivity in India, as well as the NEH region, is quite sluggish, due to a lack of substantial genetic variation in the existing germplasms available (Sarma et al. 2022). Thus, in such instances, mutation breeding can be viewed as one of the driving forces of evolution because it results in the generation of necessary genetic variation, which leads to crop improvement. Grain yield is one of the main dependable traits and due to its complex regulatory nature, genetic improvement through direct selection is extremely slow. Therefore, in comparison to direct selection for mungbean seed yield, the selection index serves as one of the appropriate ways to increase selection efficiency.

Due to the influence of many climatic conditions across locations and seasons, high-yielding genotypes frequently fall short of their potential output. Consequently, knowing how the cultivar and test environment interact and how a variety reacts to seasonal variations would offer important information about environment-specific crop response (Sheeba and Yogameenakshi 2024). In order to select stable genotypes, a number of statistical models have been proposed, i.e., graphical presentations using additive main effects and multiplicative interaction (AMMI) analysis and genotype main effect plus genotype × environment (G × E) interaction (GGE biplot) approach for analyzing G × E interactions. Based on the aforementioned objectives and methodology, a study was conducted to assess the yield performance and stability of 10 selected M_4 mutant lines of mungbean under diverse low pH and aluminum toxic soils field environments of Meghalaya using AMMI and GGE biplot approaches.

Materials and methods

About 84 mutant families derived from two parents (Table 1) were evaluated under acidic soils with a pH of 5.0 in the institutional farm of CPGS-AS, Central Agricultural University, Imphal, at a latitude of 28.68°, longitude of 91.91° and altitude of 941.6 m above mean sea level, Umiam during *Zaid*, 2024. Initially, suitable M_3 generation mutant families that showed superior performance in acidic soils with respect to ten quantitative traits and seed protein content were selected. The experiment was conducted in randomized block design with each family replicated thrice and data was recorded for ten agro morphological traits, namely, plant height (PH), days to 50% flowering (DF), days to maturity (DM), number of clusters per plant (CP), number of primary branches per plant (PB), number of pods per plant (PP), pod length (PL), number of seeds per pod (SP), hundred seed weight (HSW) and single plant yield (SYP) choosing ten single plants from each family per replication. The total soluble protein content mg/g (SPROT) was estimated using the Lowry et al. (1951) spectrophotometric method in the seeds of $M_{3:4}$ seeds of 84 mutant families. The selection was focused on high-yielding mutants with improved seed yield attributing traits in comparison with the control parents.

Selection of superior-performing mutant families by MGIDI

The multi-trait genotype ideotype distance index (MGIDI) relies on the following principles, i.e., MGIDI estimates ideotype planning, factorial analysis of best linear unbiased prediction (BLUP) values, and variable rescaling. The following formula was used to estimate the MGIDI value.

$$MGIDI_i = \sqrt{\sum_{j=1}^{f} (F_{ij} - F_j)^2}$$

Where g and f are the number of genotypes and their factors, and F_{ij} is the i^{th} genotype score for the j^{th} factor (i = 1, 2, ..., g; j = 1, 2, ..., f). The metan package version 1.18.0 (Olivoto and Nardino, 2021) in R Studio 4.2.1 was used to analyse the MGIDI using the gamem and mgidi functions.

Ten selected mutant families along with two controls/ parents (Pusa 1031 and Pusa 1431) were evaluated under acidic soil conditions for single plant yield (g) across four locations, viz., Experimental Farm, CPGS-AS, Umiam (E1, soil pH 5.0); NBPGR Farm, Umiam (E2, soil pH 5.12); Farmers' Field, Umiet, Ribhoi, Meghalaya (E3, soil pH 5.10); and Experimental Farm, COA, Krydemkulai (E4, soil pH 4.80), simultaneously in Meghalaya state of India. The trial was conducted in a randomized block design with three replications, with each entry planted at 30 × 10 cm spacing. AMMI and GGE biplot analysis were performed based on the average data on single plant yield recorded across four locations. The AMMI and GGE biplot models were used to assess the genotype yield stability and the G x E interaction. Using the multi-trait environment analysis tool "metan" (version 1.18.0), AMMI and GGE biplot analyses were carried out in R Studio (Olivoto and Lúcio 2020). The effects of the genotype × environment interaction and genotype were partitioned as per Gauch (1988) using the AMMI model to assess stability across environments. The AMMI IPCA values for each genotype were calculated in accordance with (Purchase et al. 2000) to analyze the stability of the genotypes across environments. The relationship between genotypes and environments was further illustrated graphically using the GGE biplot, which is

Table 1. Experimental material used and their codes

S.No.	Code	Parentage/Derived from	Generation	Sl.No.	Code	Parentage/Derived from	Generation
1	PUSA 1031	Control	Parent	45	B1-2	Pusa 1431 SA (0.04 mM)	M3
2	PUSA 1431	Control	Parent	46	B1-3	Pusa 1431 SA (0.04 mM)	M3
3	A1-1	Pusa 1031 SA (0.04 mM)	M3	47	B1-4	Pusa 1431 SA (0.04 mM)	M3
4	A1-2	Pusa 1031 SA (0.04 mM)	M3	48	B1-5	Pusa 1431 SA (0.04 mM)	M3
5	A1-4	Pusa 1031 SA (0.04 mM)	M3	49	B1-6	Pusa 1431 SA (0.04 mM)	M3
6	A1-5	Pusa 1031 SA (0.04 mM)	M3	50	B1-7	Pusa 1431 SA (0.04 mM)	M3
7	A1-6	Pusa 1031 SA (0.04 mM)	M3	51	B1-8	Pusa 1431 SA (0.04 mM)	M3
8	A1-7	Pusa 1031 SA (0.04 mM)	M3	52	B1-9	Pusa 1431 SA (0.04 mM)	M3
9	A1-8	Pusa 1031 SA (0.04 mM)	M3	53	B1-10	Pusa 1431 SA (0.04 mM)	M3
10	A1-9	Pusa 1031 SA (0.04 mM)	M3	54	B1-11	Pusa 1431 SA (0.04 mM)	M3
11	A1-10	Pusa 1031 SA (0.04 mM)	M3	55	B1-12	Pusa 1431 SA (0.04 mM)	M3
12	A1-11	Pusa 1031 SA (0.04 mM)	M3	56	B1-13	Pusa 1431 SA (0.04 mM)	M3
13	A1-12	Pusa 1031 SA (0.04 mM)	M3	57	B1-14	Pusa 1431 SA (0.04 mM)	M3
14	A1-13	Pusa 1031 SA (0.04 mM)	M3	58	B1-15	Pusa 1431 SA (0.04 mM)	M3
15	A1-14	Pusa 1031 SA (0.04 mM)	M3	59	B1-16	Pusa 1431 SA (0.04 mM)	M3
16	A1-15	Pusa 1031 SA (0.04 mM)	M3	60	B1-17	Pusa 1431 SA (0.04 mM)	M3
17	A1-16	Pusa 1031 SA (0.04 mM)	M3	61	B1-19	Pusa 1431 SA (0.04 mM)	M3
18	A1-17	Pusa 1031 SA (0.04 mM)	M3	62	B1-20	Pusa 1431 SA (0.04 mM)	M3
19	A1-18	Pusa 1031 SA (0.04 mM)	M3	63	B1-21	Pusa 1431 SA (0.04 mM)	M3
20	A1-19	Pusa 1031 SA (0.04 mM)	M3	64	B1-22	Pusa 1431 SA (0.04 mM)	M3
21	A1-20	Pusa 1031 SA (0.04 mM)	M3	65	B1-23	Pusa 1431 SA (0.04 mM)	M3
22	A1-21	Pusa 1031 SA (0.04 mM)	M3	66	B2-1	Pusa 1431 EMS (33.13 mM)	M3
23	A2-1	Pusa 1031 EMS (58.81 mM)	M3	67	B2-2	Pusa 1431 EMS (33.13 mM)	M3
24	A2-2	Pusa 1031 EMS (58.81 mM)	M3	68	B2-3	Pusa 1431 EMS (33.13 mM)	M3
25	A2-3	Pusa 1031 EMS (58.81 mM)	M3	69	B2-4	Pusa 1431 EMS (33.13 mM)	M3
26	A2-4	Pusa 1031 EMS (58.81 mM)	M3	70	B2-5	Pusa 1431 EMS (33.13 mM)	M3
27	A2-5	Pusa 1031 EMS (58.81 mM)	M3	71	B2-6	Pusa 1431 EMS (33.13 mM)	M3
28	A2-6	Pusa 1031 EMS (58.81 mM)	M3	72	B2-7	Pusa 1431 EMS (33.13 mM)	M3
29	A2-7	Pusa 1031 EMS (58.81 mM)	M3	73	B2-8	Pusa 1431 EMS (33.13 mM)	M3
30	A2-8	Pusa 1031 EMS (58.81 mM)	M3	74	B2-9	Pusa 1431 EMS (33.13 mM)	M3
31	A2-9	Pusa 1031 EMS (58.81 mM)	M3	75	B2-10	Pusa 1431 EMS (33.13 mM)	M3
32	A2-10	Pusa 1031 EMS (58.81 mM)	M3	76	B2-11	Pusa 1431 EMS (33.13 mM)	M3
33	A2-11	Pusa 1031 EMS (58.81 mM)	M3	77	B2-12	Pusa 1431 EMS (33.13 mM)	M3
34	A2-12	Pusa 1031 EMS (58.81 mM)	M3	78	B2-13	Pusa 1431 EMS (33.13 mM)	M3
35	A2-13	Pusa 1031 EMS (58.81 mM)	M3	79	B2-14	Pusa 1431 EMS (33.13 mM)	M3
36	A2-14	Pusa 1031 EMS (58.81 mM)	M3	80	B2-15	Pusa 1431 EMS (33.13 mM)	M3
37	A2-15	Pusa 1031 EMS (58.81 mM)	M3	81	B2-16	Pusa 1431 EMS (33.13 mM)	M3
38	A2-16	Pusa 1031 EMS (58.81 mM)	M3	82	B2-17	Pusa 1431 EMS (33.13 mM)	M3
39	A2-17	Pusa 1031 EMS (58.81 mM)	M3	83	B2-18	Pusa 1431 EMS (33.13 mM)	M3
40	A2-18	Pusa 1031 EMS (58.81 mM)	M3	84	B2-19	Pusa 1431 EMS (33.13 mM)	M3
41	A2-19	Pusa 1031 EMS (58.81 mM)	M3	85	B2-20	Pusa 1431 EMS (33.13 mM)	M3
42	A2-20	Pusa 1031 EMS (58.81 mM)	M3	86	B2-21	Pusa 1431 EMS (33.13 mM)	M3
43	A2-21	Pusa 1031 EMS (58.81 mM)	M3				
44	B1-1	Pusa 1431 SA (0.04 mM)	M3				

based on the model as described by Yan et al. (2000).

Results and discussion

In accordance with the principal component analysis, 81.33% of the cumulative variance was explained by the first five components (Table 2). The principal objective of the mungbean breeding program is to boost yield, and which is governed by polygenes and has little heritability. Therefore, the direct selection of genotypes is inappropriate and does not provide a complete explanation for the genotypic variation. Therefore, it is more beneficial to include component variables in order to choose superior genotypes. Based on factorial analysis, the MGIDI selection process takes into account the correlation of the component variables. Thus, this factorial analysis is helpful for distinguishing between the genotypes that are particularly performed for the variables that are part of the factors (FA). The factor analysis revealed that eleven variables were grouped into three unique components. The FA1 consisted of PH, CP, PB, PP, PL, SP, SYP and HSW. FA2 included DF and DM. FA3 is comprised of seed protein content (mg/g) (SPROT). The majority of the variables showed higher heritability percentages, ranging from 90 (SP) to 99% (SYP). All of the traits had significant heritability values ($h^2 > 0.8/80\%$), indicating that traits with higher heritability have a better chance of gaining selection advantages. Every trait in the current analysis showed positive selection gain, with differences ranging from 0.11 (HSW) to 6.43% (DM).

In order to identify the best-performing mutant families among the eighty-four, a 15% selection intensity was used. Ten mutant families, i.e., B1-8, A2-8, A1-5, B1-1, A1-10, A2-9, B1-12, B1-11, B2-12 and B1-13, were chosen as higher performing genotypes based on eleven traits evaluated using the MGIDI score (Fig. 1 and Table 2). As per Palaniyappan et al. (2024), the genotype with the lowest MGIDI score performed better and was chosen as the superior genotype. In this study, B1-8 had the least amount of MGIDI score, 3.24, followed by A2-8 with 3.29 and A1-5 with 4.04 (Table 3). A narrower genetic distance between the genotype and the ideotype is illustrated by the genotype with the lowest MGIDI value. Euclidean distance is used to calculate this distance. Thus, the factors in that FA help in assessing the performance and stability of the selected genotypes. Previously, the MGIDI technique was used to select the best-performing genotypes in a variety of crops, including rice (Palaniyappan et al. 2024), barley (Pour-Aboughadareh et al. 2021), maize (Uddin et al. 2021), and soybean (Maranna et al. 2021). The reliability of MGIDI was further evaluated by testing the selected genotypes across various locations.

AMMI ANOVA

Significant variations in mutant performance, varied environment conditions, and mutant interaction with the environmental circumstances were all revealed by the AMMI ANOVA for the trait single plant yield. The mutants contributed the most to the overall variability in yield (65.78%), followed by the mutant × environment interaction (19.34%) and environment (14.88%) according to the results of the AMMI ANOVA (Table 4). In contrast to the existing practice, the results showed how the genotypes responded to the four environments and the significance of testing genotypes in diverse places rather than generations in order to preserve the high levels of genotype stability and broad adaptability. When the interaction was split among the first three interaction principal component axes (IPCA), the environment accounted for a significant amount of the variance in yield, according to the AMMI; each interaction PCA captured 56.90%, 32.60%, and 10.50% of the total variation in the GxE interaction sum of squares (Table 3). Approximately 89.5% of the variation was explained by the

Table 2. Multi-trait genotype ideotype distance index (MGIDI), PC, Eigen values, factor analysis, selection gain

S .No.	PC	Eigenvalues	Variance (%)	Cumulative Variance (%)	Variables	Factor	h2	SG (%)	Selected Mutant families	MGIDI Score
1	PC1	4.45	40.48	40.48	PH	FA1	0.98	6.1	B1-8	3.24
2	PC2	1.86	16.95	57.43	CP	FA1	0.96	0.74	A2-8	3.29
3	PC3	1.03	9.39	66.82	PB	FA1	0.96	1.93	A1-5	4.04
4	PC4	0.95	8.67	75.5	PP	FA1	0.97	3.28	B1-1	4.07
5	PC5	0.64	5.83	81.33	PL	FA1	0.98	0.21	A1-10	4.13
6	PC6	0.52	4.70	86.04	SP	FA1	0.90	0.78	A2-9	4.21
7	PC7	0.48	4.36	90.41	HSW	FA1	0.95	0.11	B1-12	4.30
8	PC8	0.41	3.72	94.13	SYP	FA1	0.99	1.52	B1-11	4.42
9	PC9	0.28	2.55	96.69	DF50	FA2	0.98	3.05	B2-12	4.46
10	PC10	0.22	2.03	98.73	DM	FA2	0.99	6.43	B1-13	4.54
11	PC11	0.14	1.27	100	SPROT	FA3	0.98	2.57		

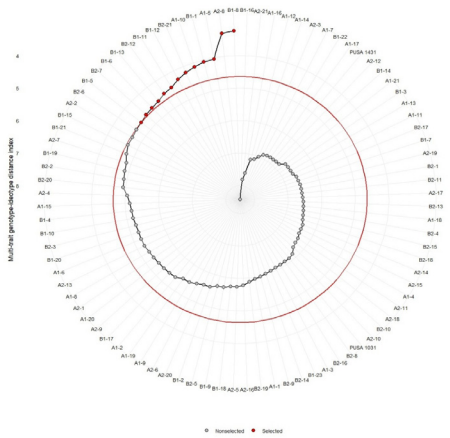

Fig. 1. MGIDI-based selection of M3 Mungbean mutant lines

Table 4. ANOVA (AMMI) for stability of single plant yield (g) in ten selected mutants along with their parents, evaluated during *Kharif* 2024

Source	Df	Sum Sq	Mean Sq	% SS Explained
Environment	3	115.60	38.53 **	14.88
Mutant	11	511.12	55.56 **	65.78
Mutant X Environment	31	150.30	1.62 **	19.34
PC1	13	30.64	2.36 **	56.90
PC2	11	17.55	1.60 **	32.60
PC3	9	5.67	0.63 **	10.50
Residuals	90	19.64	0.22	
Total	176	853.95		

two PCA axes taken together, which was highly significant. It was decided that using a GGE biplot to express the variation caused by G+E+GEI across the environments was an effective way to describe the model. According to earlier studies by Rao et al. (2023) and Sanasam et al. (2024), the initial two PCAs generated the highest GEI. Therefore, the majority of the GEI of the ten mungbean mutants analysed in four distinct environments was explained by the first two primary components of genotypes and environments. Given that mutants accounted for the majority of the variability, this suggests that they were less affected by the environment. Similar findings of the genotypes exhibiting the maximum degree of variability were noted in the research by Sheeba and Yogameenakshi (2024), Sanasam et al. (2024) in greengram.

AMMI biplot analysis

To generate the AMMI1 biplot, the IPCA1 values and average performances for the locations and genotypes were utilized. Mutant lines A1-10, A2-8 were high yielders with negative IPCA1 scores, whereas B1-1 and A2-9 had positive IPCA1 scores as well as above average yield performance (Table 4). Among the mutant lines A1-5, B2-12 had IPCA1 values near zero and were situated near the origin, indicating that they are less influenced by the environments, and had a positive IPCA1 score with average yield performance (Fig. 2a). The AMMI2 biplot solely shows the G×E interaction, as compared with the AMMI1 biplot where it shows the main effect. The genotypes present near the origin can be considered as stable, whereas the genotypes lying distant with longer spokes could be considered as heavily interacting ones. The environments E1, E2, and E4 were favorable for most genotypes. At the same time, E3 appeared to be a less interactive environment with all genotypes showing stable performance (Fig.2b). In the current study, mutant lines B2-12, B1-12, and B1-13 are situated closer to the origin, having less environmental influence. Still, mutant lines A1-5,

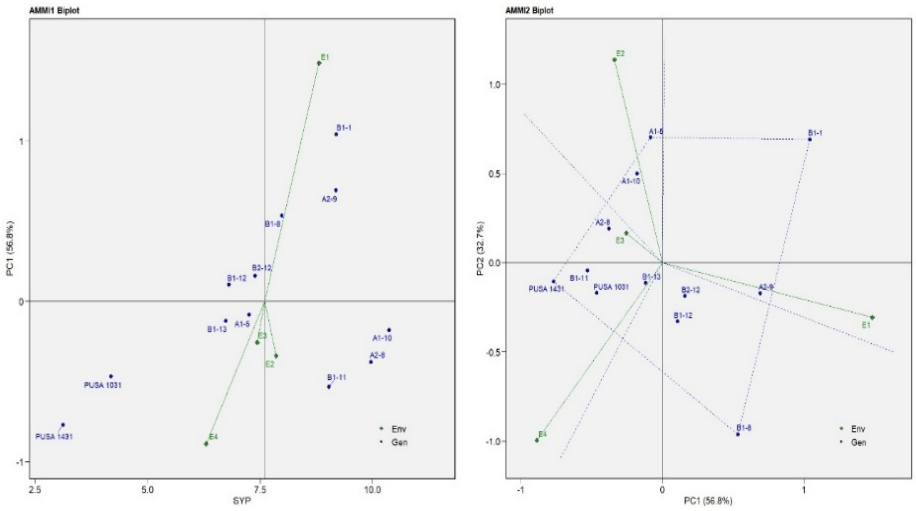

Fig. 2. (a) AMMI 1 biplot showing mean yield vs PCA1 scores (b) AMMI 2 biplot displaying PCA1 scores vs PCA2 scores of genotypes and environments.

Table 3. Mean single plant yield (g) and IPCA1 and IPCA2 scores of selected mutants along with parents

Mutant Lines	Single Plant Yield (g)	IPCA1 Score	IPCA2 Score
Pusa 1031	4.18	-0.47	-0.17
Pusa 1431	3.12	-0.77	-0.10
B1-8	7.98	0.53	-0.96
A2-8	9.96	-0.38	0.19
A1-5	7.26	-0.08	0.70
B1-1	9.19	1.04	0.69
A1-10	10.37	-0.18	0.50
A2-9	9.18	0.69	-0.17
B1-12	6.81	0.10	-0.33
B1-11	9.03	-0.53	-0.04
B2-12	7.38	0.16	-0.19
B1-13	6.73	-0.12	-0.11
E1 Experimental Farm, CPGS-AS, Umiam	8.81	1.48	-0.31
E2 (NBPGR, Shillong)	7.85	-0.34	1.14
E3 (Farmers Field Umiet, Ribhoi)	7.44	-0.26	0.17
E4 (Experimental Farm, COA, Krydemkulai)	6.30	-0.89	-1.00

B1-1, and B1-8 were influenced by the environment. On the whole, B1-13 was a stable mutant line with above-average yield.

GGE biplot analysis

GGE biplots were constructed using the mean yield of two controls and ten mutant lines across four environments. The first two principal components (PC1 = 93.54% and PC2 = 3.58%) together explained 97.12% of the total variation (Fig. 3a). The cosine of the angle between environment vectors indicated their correlation (Rao et al., 2023). Environments E2 and E4, as well as E4 and E3, were positively correlated, while an obtuse angle between E1 and E2 indicated negative correlation and strong mutant × environment interaction (Yan and Tinker, 2006). Among the test sites, E3 was the most representative environment for evaluating genotype performance, whereas E2 was the most discriminating environment for identifying widely adapted genotypes (Fig. 3a) is observed between E1 and E2 which shows high mutant × environment interaction and these environments can be considered as negatively correlated (Fig. 3a) as has been reported earlier (Yan and Tinker 2006). The Which-Won-Where graph gives the information about the genotype, which is well adapted to a particular environment and ranks the genotypes in a specific environment (Yan and Kang 2003). The environments in this study were divided into two mega environments, M1 (E2, E3, E4) and M2 (E1) (Fig. 3b). In Mega Environment 1 (M1), mutant lines A1-10, A2-8, and B1-11 are well adapted and A1-10 is

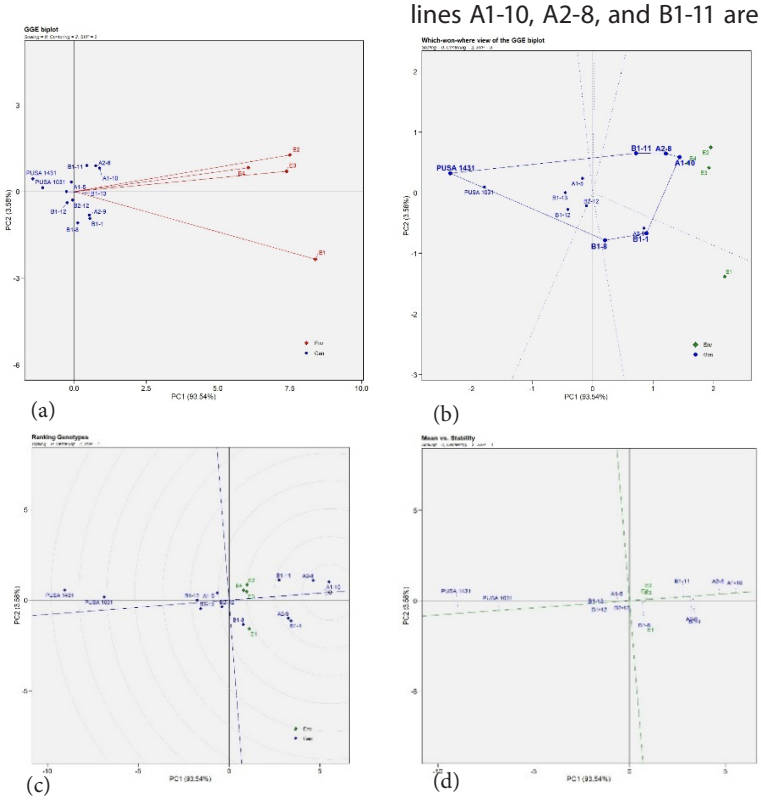

Fig. 3. (a) GGE biplot for relationship across environments (b) Which Won Where biplot for single plant yield of 10 mutant lines along with controls (c) GGE biplot representing ranking of genotypes (d) Mean Vs. Stability biplot of mutant lines and controls across environments

the winner. Mutant lines B1-1, A2-9, and B1-8 are favored in mega environment 2 (M2) and B1-1 is the winner (Fig. 3b). The mutant lines that are on the other side of the polygon, which do not fall under any environments, are considered poor performers. Hence, in the current investigation, controls, i.e., Pusa 1031 and Pusa 1431, are poor performers in comparison with the selected mutant lines. Results of this study are in agreement with Akinyosoye (2022) and Sanasam et al. (2024), who stated that genotypes performing better in a particular location may be cultivated at that site where they showed a competitive advantage.

Ranking of genotypes and biplot for mean performance and stability in different environments

If a genotype is in the middle of a concentric circle in a positive direction on the Average Environmental Axis (AEA), it is considered to be the ideal. Hence, the genotypes following the ideal genotype are considered to be the optimal performing than those situated away. In the current investigation, Fig. 3c mutant line A1-10 is near the circle and can be considered as the optimal genotype for SYP. Other mutant lines A2-8, B1-1, A2-9 and B1-11 were succeeding A1-10, indicating better SYP. Whereas, controls Pusa 1431 and Pusa 1031 were away from the ideal genotype, displaying their minimal performance in comparison with mutants at all four test locations. To identify stable genotypes, those located closer to the AEA are considered more stable. Genotypes positioned above the AEA indicate above-average yield performance, while those below the AEA represent below-average yield (Yan et al. 2007). In Fig. 3d, mutant lines A1-10, A2-8 were closer to AEA, displaying their stability and above-average SYP. Mutant lines B1-12 and B2-12 were closer to AEA with below-average single plant yield but stable.

Authors' contribution

Conceptualization of research (NSK); Designing of the experiments (NSK, SMBA); Contribution of experimental materials (NSK, SMBA); Execution of field/lab experiments and data collection (SMBA); Analysis of data and interpretation (SMBA, NSK, KSS); Preparation of the manuscript (NSK, SMBA).

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