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Evaluation of 17 sweet potato (Ipomoea batatas L.) genotypes across five environments for high yield and stability

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Abstract: The study was carried out in five regions of Bangladesh—Gazipur, Bogura, Jamalpur, Jashore, and Chattogram—utilizing a randomized complete block design and involving 17 genotypes of sweet potatoes. The objective was to evaluate their performance, environmental adaptability, and stability in terms of root yield. The analysis was carried out using fixed and random effects models. The results revealed that BARI Mistialu-12 had the highest storage root yield (45.35 t/ha). Among the locations, Bogura (sandy loam soil) achieved the highest yield, at 37.05 t/ha, followed by Jamalpur (36.15 t/ha). ANOVA showed significant variation in root yield across genotype, environment, and their interaction (GEI). Both the additive main effects and multiplicative interaction (AMMI) effect models and a linear mixed model (LMM) confirmed substantial GEI variance. Considering LMM, 53.58% of the total variation was due to genotypes, with a selection accuracy of 94%, leading to the use of a best linear unbiased prediction (BLUP) index for genotype selection. BARI Mistialu-12, BARI Mistialu-16, BARI Mistialu-11, BARI Mistialu-8, BARI Mistialu-2, and BARI Mistialu-13 were identified as high-performing genotypes in the BLUP index. Based on the AMMI stability value (ASV), the first two principal components explained 74.60% of the total GEI variance (20.16%), with BARI Mistialu-14 being the most stable genotype. Additionally, the interaction principal components axis analysis identified Bogura, Jashore, and Chattogram as key testing sites for root yield. The weighted average of absolute scores biplot highlighted BARI Mistialu-16 as the most stable variety. In the megaenvironment analysis, BARI Mistialu-11 and BARI Mistialu-2 excelled in Jamalpur, while BARI Mistialu-12 and BARI Mistialu-16 led in Gazipur, Bogura, and Jashore. Bogura was the best location for production. These findings are crucial for future breeding efforts to expand the sweet potato industry, demonstrating consistent high-yield potential across various agroecological conditions.

Key words: Genotype–environment interaction, storage root yield, AMMI stability, WAAS, BLUP, GGE

1. Introduction

Sweet potato (*Ipomoea batatas* L.) is considered a "superfood" because it is rich in antioxidants, vitamins, minerals, and healthy fibers (Alam et al., 2020). Gupta and Mishra (2021) highlight that sweet potatoes are an ideal food in terms of calories. According to the NIH, baking a sweet potato with the skin delivers 1.5 times the recommended daily value of nutrients, making it an excellent source of vitamins. The antioxidants in sweet potatoes may help prevent diseases such as diabetes and cancer (Rumbaoa et al., 2009). In Bangladesh, 2% of children aged 1–6 years suffer from night blindness due to vitamin A deficiency, resulting in about 88 children losing their vision each day.[1] Implementing nutritional interventions and educational programs to promote sweet potato consumption could help mitigate this problem.

Sweet potato production in Bangladesh has steadily increased over the past decade. From 2018–19 to 2020–21, the overall sweet potato yield in the country rose by a significant 16% (BBS, 2022). This growth is attributed to the introduction and widespread adoption of improved genotypes, which are notable for their high vitamin A content and ability to yield over 40 t/ha (Alam et al., 2023a, 2023b, 2024a, 2024b, 2024c, 2024d). However, local farmers still cultivate sweet potatoes with an average root yield of about 10.50 t/ha, indicating a lack of consistent production (BARI, 2023).

[1]Banglapedia (2021). Night Blindness [Online]. Website https://en.banglapedia.org/index.php?title=Night_Blindness [accessed 16 November 23].

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A major issue is that sweet potato genotypes developed by the Tuber Crops Research Center (TCRC) of the Bangladesh Agricultural Research Institute (BARI) have exhibited reduced storage root yields in different areas of Bangladesh (Sultana et al., 2019; Mahmud et al., 2021; Alam et al., 2023a, 2023b).

Evaluating sweet potato genotypes in diverse agroecological settings is crucial for boosting production, offering a cost-effective and sustainable solution to food and nutrition issues. This evaluation must consider genotype–environment interactions (GEIs) to identify the most stable and reliable genotypes (Alam et al., 2024b; Habib et al., 2024). Studies indicate that sweet potato genotypes react differently to GEIs in various countries (Liu et al., 2024; Gurmu et al., 2024; Torres-Ordoñez et al., 2024). Global breeding initiatives have primarily aimed at enhancing productivity and improving fresh root consumption to guide breeding programs (Ebem et al., 2021; Alam et al., 2024d). To achieve consistent performance and uniform phenotypes, researchers need to select genotypes that exhibit stability or adaptability to specific environments with minimal GEIs (Hasan et al., 2022). The scarcity of research on GEIs among sweet potato genotypes in Bangladesh drives researchers to identify high-yielding genotypes for multienvironment trials (METs).

Researchers have employed two-way ANOVA in a fixed-effect model to select high-yielding genotypes (Yan and Frégeau-Reid, 2018). Using random effects in a linear mixed model (LMM) enhances selection efficiency by determining predicted genotypic values for key breeding objective traits (Pimentel et al., 2014; Santos et al., 2015; Messele et al., 2023). They use restricted maximum likelihood (REML) to estimate variance components and best linear unbiased prediction (BLUP) to predict genotypic values. These methods serve as efficient selection models in this context (de Oliveira Silva et al., 2022; Grüneberg et al., 2022; Norman et al., 2022; Ahsan et al., 2024; Khan et al., 2024).

In the pursuit of stable genotypes, researchers utilize the additive main effects and multiplicative interaction (AMMI) model. They also integrate a new index called weighted average absolute scores (WAAS), based on the AMMI model, into indices for MET analysis. In addition to AMMI, the genotype-genotype environment (GGE) biplot graphical model is widely used to identify suitable environments and top-performing genotypes within specific environments (Gauch and Zobel, 1997; Yan et al., 2007; Kulsum et al., 2012; Hossain et al., 2023). Researchers employ the GGE biplot method to identify stable genotypes and assess their interactions with yield and environments. To introduce new crop varieties while minimizing the impact of GEIs, they consider both yield and stability. Consequently, they have introduced an index named WAASBY, which combines WAASB (WAAS + BLUP) and yield (Y) (Olivoto et al., 2019).

Introducing and adopting stable and high-yielding sweet potato genotypes in Bangladesh that are adaptable to a range of agricultural conditions is aimed. It is proposed that employing REML, BLUP, AMMI, WAAS, and WAASBY to choose genotypes with minimal GEI will help identify stable, high-yielding sweet potato genotype aiding sustainable cultivation and informed breeding in Bangladesh. The aim of the present study was to identify high-yielding sweet potato genotypes and assess their stability and adaptability in terms of storage root yield. This study presents an innovative method for sweet potato breeding by integrating AMMI, WAAS, REML, and BLUP models to identify high-yielding and stable genotypes. The WAASBY index improves selection efficiency for sustainable farming by integrating yield and stability factors.

2. Materials and methods

2.1. Descriptions of study areas

During the 2022–23 growing season, we conducted the study at five locations in Bangladesh: Gazipur, Bogura, Jamalpur, Jashore, and Chattogram. These locations were selected to represent the diverse environmental contexts across Bangladesh. Table 1 provides an overview of the GPS coordinates and climate and soil data for these areas, and Figure 1 contains a map showing the locations of the study sites.

2.2. Plant materials

We utilized 17 sweet potato genotypes sourced from the TCRC, BARI, Bangladesh. Table 2 provides a detailed description of the genotypes studied.

2.3. Experimental design

We utilized a randomized complete block (RCB) design in the study. Sweet potato vines were planted in each location on October 31, 2022, following the procedure described by Alam et al. (2023a). Each plot comprised ten rows, with ten vines of each genotype planted in a row, making a total of 50 plants per plot across five rows. These plots were replicated three times at each location.

2.4. Crop husbandry and data collection

The research sites were prepared by plowing with oxen to create a fine tilth, followed by manual ridge construction using traditional hoes, consistent with local farming methods. The field was divided into three blocks, each with five plots, totaling 15 plots. Each plot measured 3 m × 3 m and was arranged in five rows, each containing ten plants, with a spacing of 30 cm between plants and 60 cm between rows. Treatments were randomly assigned within each block, with 1 m and 1.5 m gaps between plots and

Table 1. Description of GPS coordinates and soil and environmental conditions in the study areas (Alam et al., 2023a).

Locations (codes)	GPS coordinates	Soil				Weather (October, 2022 to March, 2023)		
		Agro-ecological representation	Range of altitude	Soil texture	pH (H_2O)	Total rainfall (mm)	Avg. night temperature (°C)	Avg. day temperature (°C)
Gazipur (E1)	23.9905° N, 90.3877° E	AEZ28	34	SCL	5.73	283.08	17.25	28
Bogura (E2)	24.8526° N, 89.3730° E	AEZ25	20	SL	6.23	163.71	17	27.75
Jamalpur (E3)	24.9270° N, 89.9480° E	AEZ9	24	SL	6.48	182.87	17.75	28.5
Jashore (E4)	23.1641° N, 89.2065° E	AEZ18	6	SL	6.61	272.75	17.25	28.25
Chattogram (E5)	22.3752° N, 91.8349° E	AEZ11	29	STL	4.58	218.67	18.75	27

[GPS] Global Positioning System, [AEZ28] Madupur Tract, [AEZ25] Level Barind Tract, [AEZ9] Old Brahmaputra Floodplain, [AEZ18] Young Meghna Estuarine Floodplain, [AEZ11] High Ganges River Floodplain, [SCL] silty clay loam, [SL] sandy loam, [STL] silty loam.

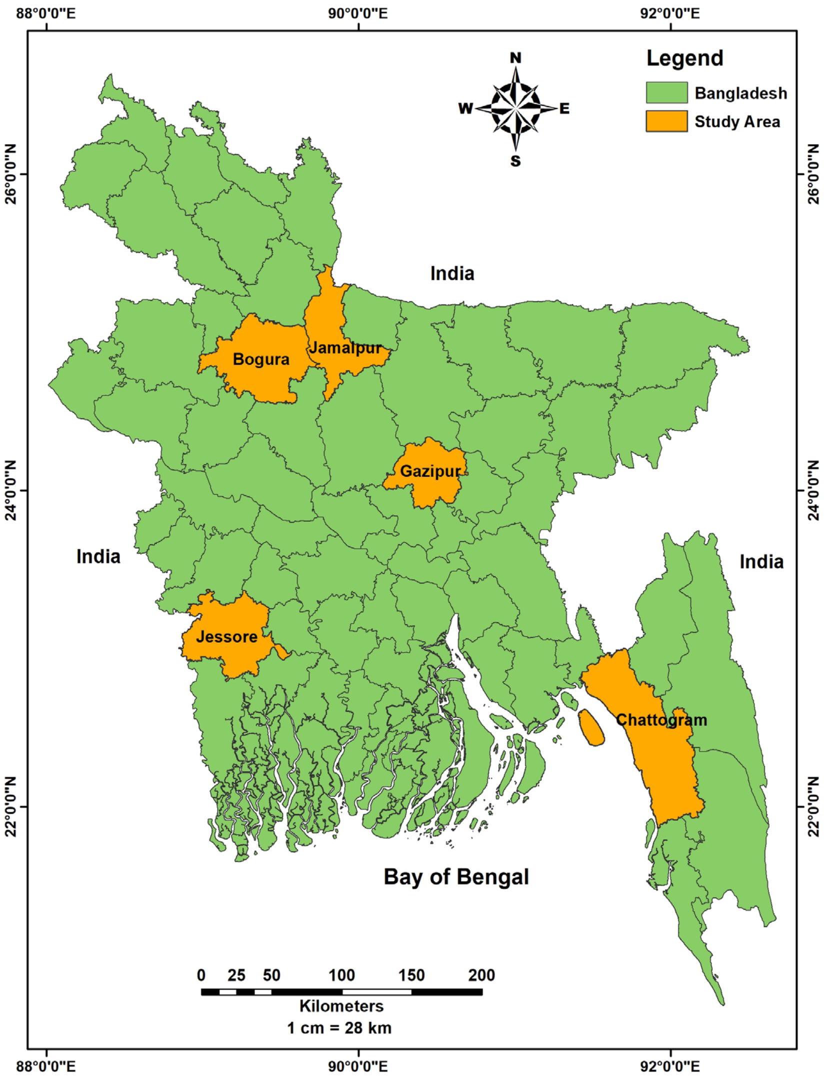

Figure 1. Map of the study areas.

Table 2. A detailed description of the 17 BARI released sweet potato genotypes used in this study (BARI, 2023; Sultana et al., 2019).

Variety	Code	Origin	AL (m)	YR	Pedigree	BM	PH (cm)	RDM (%)	BC (mg/100g)	RS	RSC	RFC	FSC
BARI Mistialu-1	G1	Taiwan	1150	1985	NA	Introduction	114.00	29.82	0.99	Elliptic	Cream	Pale yellow	Pink
BARI Mistialu-2	G2	Philippines	442	1985	NA	Introduction	138.00	21.67	13.59	Elliptic	Red	Dark yellow	
BARI Mistialu-3	G3	Bangladesh	105	1988	NA	Selection	123.47	28.56	0.03	Long elliptic	White	Pink	
BARI Mistialu-4	G4	Bangladesh	105	1994	NA	Full diallel	117.87	27.97	7.23	Ovate	Pale orange	Dark orange	Green
BARI Mistialu-5	G5	Bangladesh	105	1994	NA	Full diallel	119.73	22.79	4.41	Oblong	Red	Pale orange	
BARI Mistialu-6	G6	Peru	1555	1998	NA	Introduction	127.07	24.15	1.04	Oblong	Pale orange	Pale orange	
BARI Mistialu-7	G7	Peru	1555	1998	NA	Introduction	121.60	28.99	0.69	Oblong	White	Pale yellow	
BARI Mistialu-8	G8	Peru	1555	2008	CIP- 440025	Introduction	120.13	35.82	1.76	Long irregular	Pink	Pale yellow	
BARI Mistialu-9	G9	Peru	1555	2008	CIP-440074.2	Introduction	96.76	20.04	4.41	Long irregular	Red	Light orange	
BARI Mistialu-10	G10	Bangladesh	105	2013	♀H_8	Half diallel	103.40	27.14	0.12	Oblong	White	Dark orange	
BARI Mistialu-11	G11	Bangladesh	105	2013	SP-613	Selection	113.33	35.70	0.04	Long elliptic	Pink	Cream	
BARI Mistialu-12	G12	Peru	1555	2013	CIP- 440001	Introduction	124.13	35.93	5.46	Long oblong	Cream	Pale orange	Pink
BARI Mistialu-13	G13	Peru	1555	2013	CIP- 440014	Introduction	130.93	29.35	6.12	Long oblong	Yellow	Light orange	
BARI Mistialu-14	G14	Bangladesh	105	2017	CIP- 441132	Introduction	149.33	25.06	14.67	Long irregular	Pink	Dark orange	
BARI Mistialu-15	G15	Peru	1555	2017	CIP-440267.2	Introduction	102.25	21.94	12.35	Long irregular	Pink	Dark orange	
BARI Mistialu-16	G16	Bangladesh	105	2018	♀H_2/08	Half diallel	122.12	23.42	16.20	Long irregular	White	Dark orange	
BARI Mistialu-17	G17	Indonesia	367	2021	Antho SP-01	Introduction	98.22	35.45	NA	Long irregular	Pink	Pink	

^{AL} altitude of origin, ^{YR} year of release, ^{NA} information not available, ^{BM} methods of breeding, ^{PH} matured plant height, ^{RDM} storage root dry matter, ^{BC} beta carotene content of fresh storage root, ^{RS} storage root shape, ^{RSC} storage root skin color, ^{RFC} storage root flesh color, ^{FSC} fresh stem color blocks, respectively. Vine cuttings, each 30 cm long, were planted with two-thirds of their length buried in the soil, with one cutting per ridge hole. Dead vines were replaced 1 week after planting. Throughout the growing season, the plots were kept free of weeds by hand hoeing. Soil earthing-up was done three times at monthly intervals starting from the second month after planting to prevent root exposure. The fertilization regime included 260 kg/ha urea, 150 kg/ha triple superphosphate (TSP), 250 kg/ha muriate of potash (MOP), 75 kg/ha gypsum, 12 kg/ha zinc sulfate, 10 kg/ha boric acid, and 10 t/ha cow dung. The TSP, gypsum, zinc sulfate, boric acid, and cow dung were applied in full doses during the final land preparation, along with half of the urea and MOP doses. The remaining urea and MOP were top-dressed 40 days after planting, followed by watering and additional earthing-up (Alam et al., 2023a). Disease and insect infestations were managed through regular inspections and pesticide applications. Harvesting occurred when the leaves turned yellow, with the roots carefully dug out using hoes, hand-picked, and with vines and leaves removed. After 130 days from planting, sweet potato storage roots from one row in each plot were harvested. The average weight of storage roots from ten plants was used to calculate the yield per hectare, reported as storage root yield (YLD) in tons per hectare (t/ha).

2.5. Statistical analysis

The replication mean was calculated by averaging the row data from each replication (Sarker et al., 2022a, 2022b). Statistical and biometrical analysis of the average data for various traits was conducted (Prodhan et al., 2022; Azad et al., 2022; Hassan et al., 2022; Hossain et al., 2022; Rahman et al., 2022; Akter et al., 2024). ANOVA and mean separation were employed to assess genotypes, environments, and their interaction (GEI). The least significant difference (LSD) test was utilized to distinguish mean values at a significance level of $p < 0.05$. Furthermore, AMMI ANOVA, calculation of interactive principal component axis (IPCA) values for tested genotypes and environments, and determination of the AMMI stability value (ASV) were performed. The WAAS biplot, BLUP index, WAASBY index, and GGE biplot were generated using the metan package in R software, version 4.2.0 (R studio, 2020).

3. Results

3.1. Estimation of variance and mean performance

Significant differences ($p \leq 0.001$) in sweet potato storage root yield (YLD) were observed among the various genotypes (G), environments (E), and their interactions (GEI) (Table 3). The greatest variation was attributed to G (54.17%), followed by the GEI (25.25%), residuals (10.99%), and E (8.65%). The coefficient of variation (CV) was 8.14%. Table 4 presents the mean YLD of 17 sweet potato genotypes across five distinct locations. Bogura exhibited the highest yield (GY), at 37.05 t/ha, followed by Jamalpur (36.15 t/ha) and Gazipur (34.70 t/ha). Among the genotypes, BARI Mistialu-12 recorded the highest YLD, at 45.35 t/ha, followed closely by BARI Mistialu-16, at 44.64 t/ha. In terms of GEI, the highest mean yield was observed in Gazipur with genotype BARI Mistialu-12 (55.08 t/ha), followed by Jamalpur with genotype BARI Mistialu-11 (49.74 t/ha).

Table 3. ANOVA of root yield for 17 sweet potato genotypes studied in five locations.

SV	DF	SS	MSS	PV (%)	CV (%)
E	4	1049	262.4***	8.65	
R	2	113	56.6***	0.93	
G	16	6567	410.4***	54.17	8.14
GEI	64	3061	47.8***	25.25	
Residuals	168	1332	7.9	10.99	

^{SV} source of variation, ^{E} environment, ^{G} genotype, ^{R} replication, ^{DF} degrees of freedom, ^{SS} sum of squares, ^{MSS} mean sum of squares, ^{PV} proportional variation of total variation, *** significant at $p \leq 0.001$, ^{CV} coefficient of variation.

Table 4. Interactional mean performance of genotype and environment studied in five locations.

Genotypes	YLD (t/ha)					Mean^{R}
	Gazipur	Bogura	Jamalpur	Jashore	Chattogram	
BARI Mistialu-12	51.85	47.64	48.19	42.18	36.9	45.35^{1}
BARI Mistialu-16	42.15	46.86	45.31	47.78	41.09	44.64^{2}
BARI Mistialu-11	34	45.16	49.74	32	37.67	39.71^{3}
BARI Mistialu-8	41.15	44.85	35.84	37.3	35.88	39.00^{4}
BARI Mistialu-2	42.82	32.78	44.86	30.74	29.59	36.16^{5}
BARI Mistialu-13	33.7	38.4	47.14	32.96	28.55	36.15^{6}

Table 4. (Continued.)

BARI Mistialu-15	42.59	34.58	29.71	29.89	32.74	33.90[7]
BARI Mistialu-7	32	35.88	36.88	32.33	29.77	33.37[8]
BARI Mistialu-6	31.37	39.44	31.34	33.07	31.18	33.28[9]
BARI Mistialu-5	31.67	32.21	37.05	35.26	29.16	33.07[10]
BARI Mistialu-10	31.56	37.6	34.86	32.41	27.18	32.72[11]
BARI Mistialu-9	31.44	37.98	29.25	34.07	28.78	32.31[12]
BARI Mistialu-14	33.3	35.36	32.68	28.34	29.63	31.86[13]
BARI Mistialu-3	26.67	37.78	29.79	31.22	30.21	31.14[14]
BARI Mistialu-4	30.57	31.67	30.68	33.93	28.59	31.09[15]
BARI Mistialu-17	27.02	24.99	26.85	32.22	26.46	27.51[16]
BARI Mistialu-1	26	26.74	24.33	24.63	28.25	25.99[17]
Mean[R]	34.70[3]	37.05[1]	36.15[2]	33.55[4]	31.27[5]	

[YLD] storage root yield, [R] ranking of mean value (high to low).

3.2. Genetic parameters and mean performance estimation using a linear mixed model (LMM)

The likelihood ratio test (LRT) revealed a significant effect ($p < 0.001$) of both G and GEI on YLD (Table 5). G contributed the highest percentage of variance (53.58%), followed by E (29.78%), with the residual variance accounting for 16.64%. The broad-sense heritability of YLD was calculated to be 54%. The GEI correlation coefficient was 0.30, and the selection accuracy was 94% (Table 5). Figure 2 presents the BLUP values used to evaluate the average performance of sweet potato genotypes. Blue circles denote instances of significantly superior mean performances, while red circles indicate below-average performances. Genotypes located at the lower end of the scale exhibited the least favorable performances (Figure 2). The horizontal error bars in Figure 2 represent 95% confidence intervals for the predicted YLD values. Among the genotypes tested, BARI Mistialu-12 showed the highest predicted mean YLD, followed by BARI Mistialu-16, BARI Mistialu-11, BARI Mistialu-8, BARI Mistialu-2, and BARI Mistialu-13—all of which exceeded the mean. In contrast, the lowest predicted mean YLD was observed in BARI Mistialu-1, followed by BARI Mistialu-17, BARI Mistialu-4, BARI Mistialu-3, and BARI Mistialu-14.

3.3. AMMI ANOVA and AMMI stability

Table 6 presents the results of the AMMI ANOVA conducted on the YLD of 17 sweet potato genotypes. Significant effects ($p \leq 0.001$) were observed for E, G, and GEI. The total variance was partitioned as follows: 6.91% attributed to E, 43.25% to G, and 47.82% to GEI. The GEI variance was further decomposed into two significant ($p \leq 0.001$) principal components (PCs): PC1 accounted for 44.00% of the variance and PC2 accounted for 30.50%. The remaining 25.4% of the variance was attributed to residual noise components. Table 7 details the IPCA1 and IPCA2 values across different environments—Gazipur, Bogura, Jamalpur, Jashore, and Chattogram—which ranged from –0.03 to 1.48 for IPCA1 and from –3.68 to 0.50 for IPCA2. Smaller IPCA1 and IPCA2 values were observed in Bogura, Jashore, and Chattogram. The AMMI analysis results for the genotypes BARI Mistialu-5, BARI Mistialu-7, BARI Mistialu-10, and BARI Mistialu-14 indicated relatively low values for both positive and negative IPCA1 and IPCA2. The ASV parameter rankings identified five genotypes with values below 1 as the highest ranked, namely BARI Mistialu-14, BARI Mistialu-5, BARI Mistialu-10, BARI Mistialu-7, and BARI Mistialu-16. In contrast, the lowest-ranked genotypes were BARI Mistialu-2, followed by BARI Mistialu-13 and BARI Mistialu-11.

3.4. WAAS biplot stability analysis

Figure 3 illustrates the average YLD across all environments on the vertical axis, with genotypes positioned further to the right indicating higher YLD and those to the left indicating lower YLD. The horizontal axis represents the mean WAAS, dividing the biplot into four quadrants. Genotypes in different quadrants are categorized based on their stability and yield performance. Quadrant I typically contain genotypes with low stability and low yield, such as BARI Mistialu-15. Genotypes located in quadrant II exhibit elevated WAAS values, suggesting a significant impact of GEI and high YLD. This quadrant includes genotypes like BARI Mistialu-12, BARI Mistialu-13, BARI Mistialu-2, and BARI Mistialu-11. Quadrants III and IV display lower WAAS values, indicating higher stability. However, genotypes within quadrant III demonstrate YLD below the average. Genotypes in quadrant IV, such as BARI Mistialu-8 and BARI Mistialu-16, exhibit both high YLD and stability across diverse environments.

Table 5. Estimation of variance and variance components using LMM for sweet potato storage root yield.

Components	Value
Genotype variance (%)	53.58
GEI variance (%)	29.78
Residual variance (%)	16.64
Heritability	0.54
r^2(GEI)	0.30
Selection accuracy	0.94
Mean yield (t/ha)	34.54
LRT (GEN)	39.44***
LRT (GEI)	89.82***

$^{r2(GEI)}$ GEI correlation of coefficient, ***Significant at 0.1% probability level by chi-square (X^2) test in likelihood ratio test (LRT).

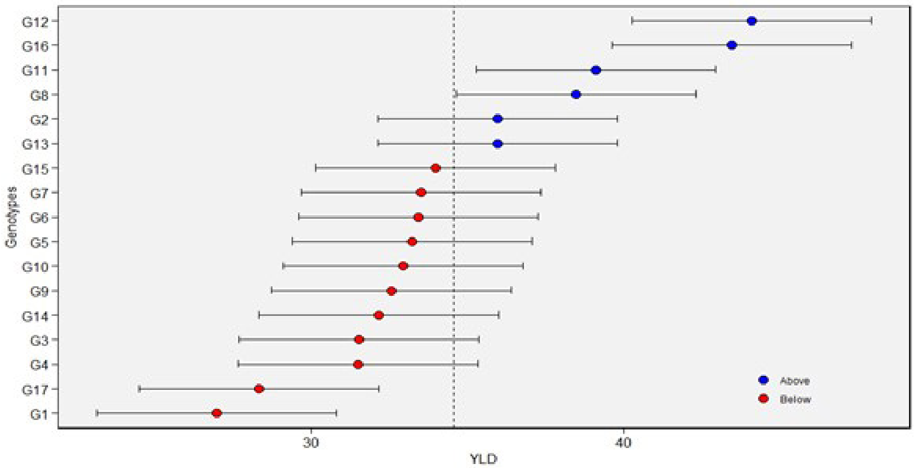

Figure 2. BLUP values for the average storage root yield (YLD) of 17 sweet potato genotypes. ^{G1} BARI Mistialu-1, ^{G2} BARI Mistialu-2, ^{G3} BARI Mistialu-3, ^{G4} BARI Mistialu-4, ^{G5} BARI Mistialu-5, ^{G6} BARI Mistialu-6, ^{G7} BARI Mistialu-7, ^{G8} BARI Mistialu-8, ^{G9} BARI Mistialu-9, ^{G10} BARI Mistialu-10, ^{G11} BARI Mistialu-11, ^{G12} BARI Mistialu-12, ^{G13} BARI Mistialu-13, ^{G14} BARI Mistialu-14, ^{G15} BARI Mistialu-15, ^{G16} BARI Mistialu-16, ^{G17} BARI Mistialu-17.

Table 6. AMMI ANOVA of storage root yield for sweet potato genotypes studied in five locations.

SV	DF	SS	MSS	VT (%)	VP (%)	CP (%)
E	4	1049.41	262.35***	6.91	-	-
R(E)	10	244.65	24.47***	1.61	-	-
G	16	6567.11	410.44***	43.25	-	-
GEI	64	3060.52	47.82***	20.16	-	-
PC1	19	1347.95	70.94***	8.88	44	44
PC2	17	934.44	54.97***	6.15	30.5	74.6
Noise	28	778.12	27.79	5.12	25.4	-
Error	160	1200.90	7.51	7.91	-	-
Total	318	15183.10	47.75	-	-	-

^{SV} source of variation, ^{E} environment, ^{R} replication, ^{G} genotype, ^{GEI} genotype-environment interaction, ^{PC} principal component, ^{DF} degrees of freedom, ^{SS} sum of squares, ^{MSS} mean sum of squares, ^{VT} variation percentage of total, ^{VP} variation percentage of total GEI, ^{CP} cumulative variation of PCs, *** significant at $p \leq 0.001$.

Table 7. Mean yield and IPCA 1 and IPCA 2 values of 17 sweet potato genotypes and five tested environments and AMMI stability value (ASV) along with ranks of the studied genotypes.

Genotypes	Average root yield (t/ha)	IPCA1	IPCA2	ASV	Rank
BARI Mistialu-1	25.99	0.90	–0.14	1.31	7
BARI Mistialu-2	36.16	–2.10	–1.85	3.55	17
BARI Mistialu-3	31.14	0.92	1.32	1.87	12
BARI Mistialu-4	31.09	0.71	0.05	1.02	6
BARI Mistialu-5	33.07	–0.29	0.24	0.49	2
BARI Mistialu-6	33.28	0.91	0.67	1.47	10
BARI Mistialu-7	33.37	–0.38	0.40	0.67	4
BARI Mistialu-8	39.00	0.91	–0.35	1.37	9
BARI Mistialu-9	32.31	1.17	0.40	1.74	11
BARI Mistialu-10	32.72	–0.13	0.48	0.52	3
BARI Mistialu-11	39.71	–1.96	1.64	3.27	15
BARI Mistialu-12	45.35	–0.80	–1.52	1.91	13
BARI Mistialu-13	36.15	–2.22	0.74	3.29	16
BARI Mistialu-14	31.86	0.02	–0.29	0.29	1
BARI Mistialu-15	33.90	0.88	–2.28	2.62	14
BARI Mistialu-16	44.64	0.51	0.65	0.98	5
BARI Mistialu-17	27.51	0.93	–0.13	1.35	8
Environments					
Gazipur	34.70	–0.03	–3.68	-	-
Bogura	37.05	0.59	1.63	-	-
Jamalpur	36.15	–3.90	0.82	-	-
Jashore	33.55	1.86	0.74	-	-
Chattogram	31.27	1.48	0.50	-	-

ASV AMMI stability value.

3.5. Mean plus stability using WAASBY

Figure 4 ranks and selects genotypes based on their storage root yield and stability, represented by the WAASBY index. Genotypes with higher WAASBY values are indicated by blue circles, while those with lower WAASBY values are marked by red circles. The genotypes BARI Mistialu-16, BARI Mistialu-12, BARI Mistialu-7, BARI Mistialu-8, BARI Mistialu-10, BARI Mistialu-14, BARI Mistialu-5, and BARI Mistialu-4 all exceeded the mean WAASBY index (Figure 4).

3.6. Identification of winner genotypes using megaenvironment analysis

The polygonal biplot in Figure 5 illustrates a polygon formed by connecting the vertices of key genotypes, including BARI Mistialu-12, BARI Mistialu-16, BARI Mistialu-8, BARI Mistialu-15, BARI Mistialu-1, BARI Mistialu-13, and BARI Mistialu-11. This polygon is divided into seven distinct sectors by rays extending from the plot's origin, perpendicular to the sides of the polygon. The sectors where environments are located and genotypes are positioned above them indicate the superior performance of those specific genotypes in those environments. Conversely, genotypes located in sectors without any environments are considered unsuitable for cultivation in the tested environments and are classified as weak performers in most settings. For example, genotypes BARI Mistialu-11 and BARI Mistialu-2 demonstrated superior yield performance in Jamalpur, while genotypes BARI Mistialu-12 and BARI Mistialu-16 exhibited desirable yield in Gazipur, Bogura, Jashore, and Chattogram. The remaining five sectors comprise genotypes that are not specifically associated with any particular environment.

3.7. Discriminativeness vs. representativeness of tested environments and their relationship

In Figure 6a, the line extending from the origin of the biplot and marked with an arrow is referred to as the average environment axis (AEA). The AEA forms the smallest angle with the Bogura environment, followed by Gazipur, Chattogram, Jashore, and Jamalpur. In Figure 6b, the longest environmental vector is associated with Jamalpur, followed by Gazipur, Bogura, Jashore, and Chattogram. The angles between the Jamalpur vector and those of Gazipur, Bogura, Chattogram, and Jashore are larger compared to the angles between the vectors of Gazipur, Bogura, Jashore, and Chattogram.

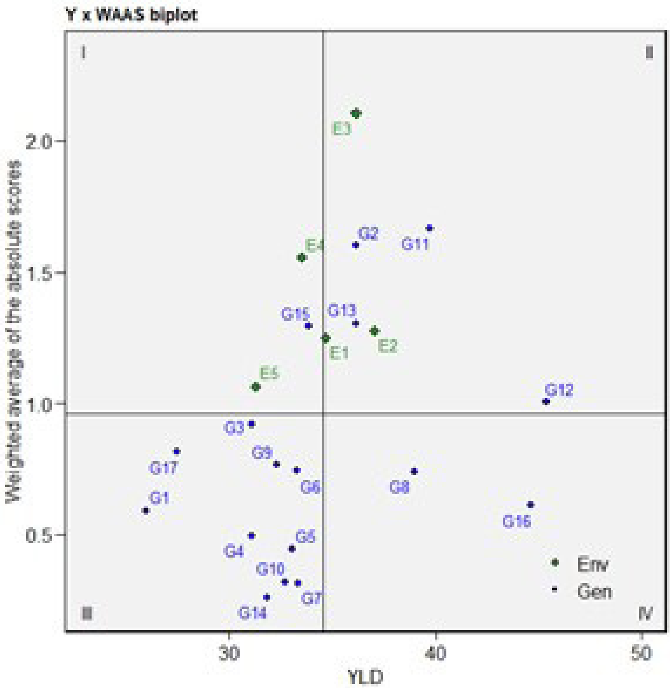

Figure 3. The WAAS biplot with the average performances of the storage root yield (YLD). G1 BARI Mistialu-1, G2 BARI Mistialu-2, G3 BARI Mistialu-3, G4 BARI Mistialu-4, G5 BARI Mistialu-5, G6 BARI Mistialu-6, G7 BARI Mistialu-7, G8 BARI Mistialu-8, G9 BARI Mistialu-9, G10 BARI Mistialu-10, G11 BARI Mistialu-11, G12 BARI Mistialu-12, G13 BARI Mistialu-13, G14 BARI Mistialu-14, G15 BARI Mistialu-15, G16 BARI Mistialu-16, G17 BARI Mistialu-17, E1 Gazipur, E2 Bogura, E3 Jamalpur, E4 Jashore, E5 Chattogram.

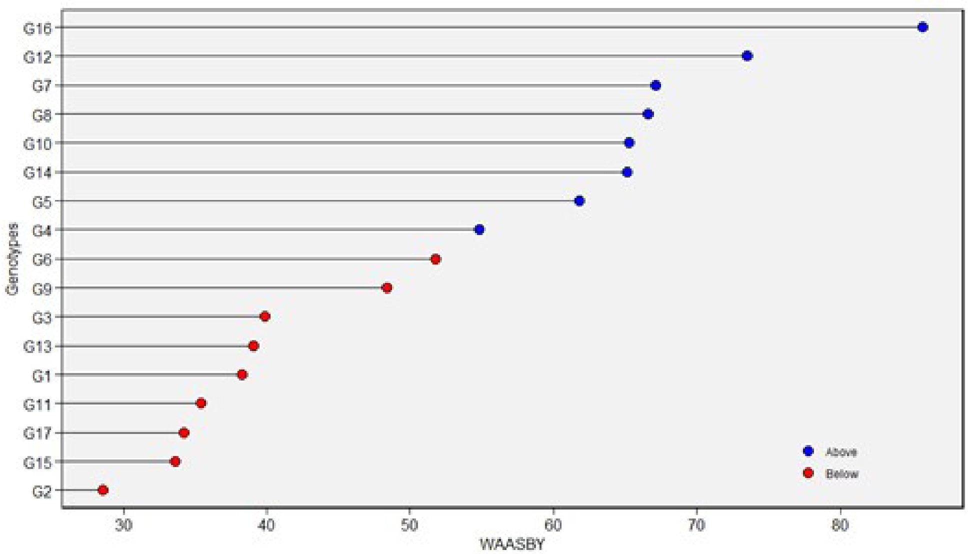

Figure 4. The WAASBY index for the root yield of 17 sweet potato genotypes. G1 BARI Mistialu-1, G2 BARI Mistialu-2, G3 BARI Mistialu-3, G4 BARI Mistialu-4, G5 BARI Mistialu-5, G6 BARI Mistialu-6, G7 BARI Mistialu-7, G8 BARI Mistialu-8, G9 BARI Mistialu-9, G10 BARI Mistialu-10, G11 BARI Mistialu-11, G12 BARI Mistialu-12, G13 BARI Mistialu-13, G14 BARI Mistialu-14, G15 BARI Mistialu-15, G16 BARI Mistialu-16, G17 BARI Mistialu-17.

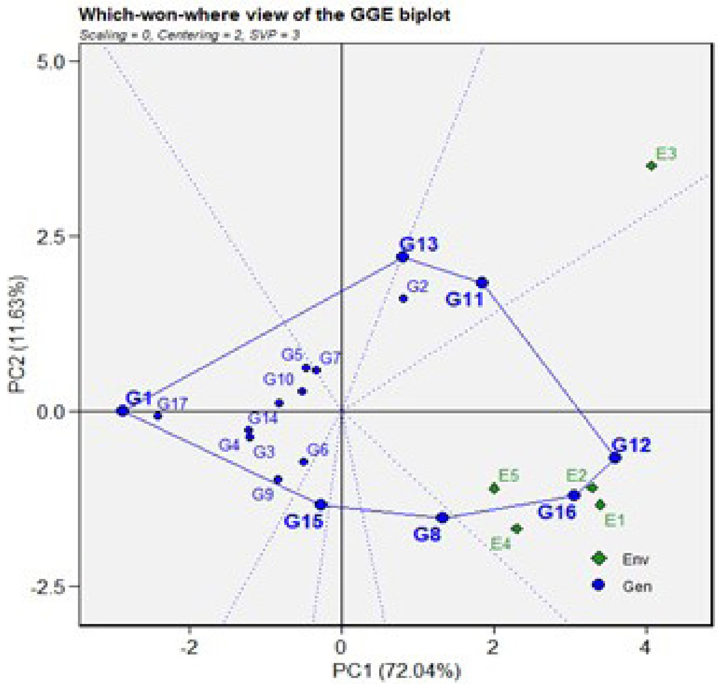

Figure 5. GGE biplot of winner in respective megaenvironments for storage root yield. [G1] BARI Mistialu-1, [G2] BARI Mistialu-2, [G3] BARI Mistialu-3, [G4] BARI Mistialu-4, [G5] BARI Mistialu-5, [G6] BARI Mistialu-6, [G7] BARI Mistialu-7, [G8] BARI Mistialu-8, [G9] BARI Mistialu-9, [G10] BARI Mistialu-10, [G11] BARI Mistialu-11, [G12] BARI Mistialu-12, [G13] BARI Mistialu-13, [G14] BARI Mistialu-14, [G15] BARI Mistialu-15, [G16] BARI Mistialu-16, [G17] BARI Mistialu-17, [E1] Gazipur, [E2] Bogura, [E3] Jamalpur, [E4] Jashore, [E5] Chattogram.

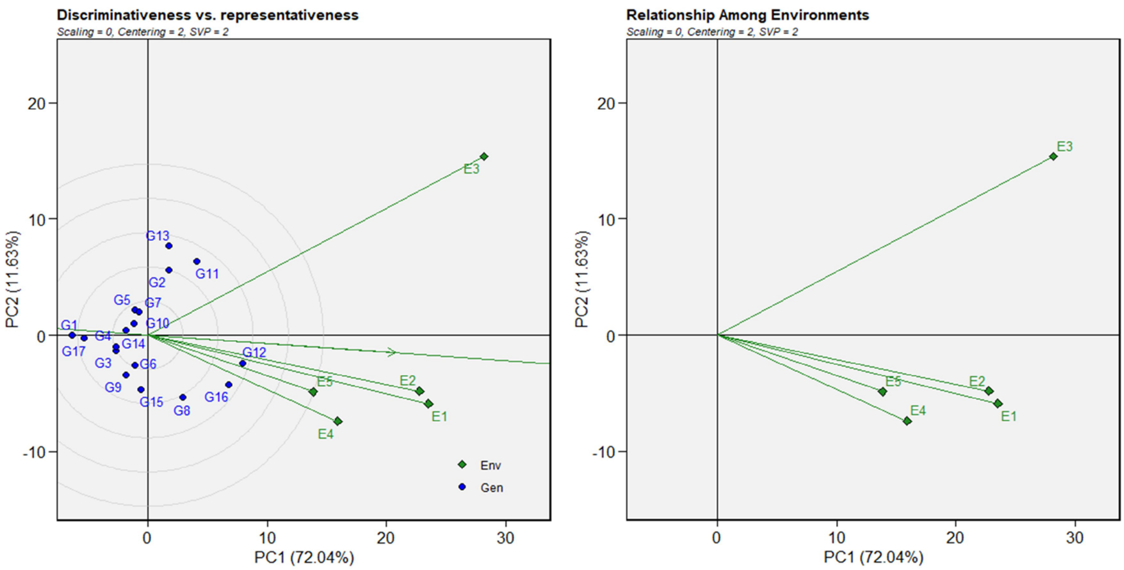

Figure 6. Discrimination ability vs. representativeness for five testing environments (a) and relationship between the environments (b) through biplot examination for the root yield performance. [G1] BARI Mistialu-1, [G2] BARI Mistialu-2, [G3] BARI Mistialu-3, [G4] BARI Mistialu-4, [G5] BARI Mistialu-5, [G6] BARI Mistialu-6, [G7] BARI Mistialu-7, [G8] BARI Mistialu-8, [G9] BARI Mistialu-9, [G10] BARI Mistialu-10, [G11] BARI Mistialu-11, [G12] BARI Mistialu-12, [G13] BARI Mistialu-13, [G14] BARI Mistialu-14, [G15] BARI Mistialu-15, [G16] BARI Mistialu-16, [G17] BARI Mistialu-17, [E1] Gazipur, [E2] Bogura, [E3] Jamalpur, [E4] Jashore, [E5] Chattogram.

4. Discussion

4.1. Genetic and environmental regulation on sweet potato root yield

In Bangladesh, there is an ongoing need to identify sweet potato genotypes with high yield potential and stability across various environments (Mahmud et al., 2021). The present study confirms that the yields of genotypes differ depending on the genotype, environmental conditions, and genotype–environment interactions (Table 3). These results align with previous studies on sweet potato (Sultana et al., 2019; Alam et al., 2023a) and research on rice genotypes (Hasan-Ud-Daula and Sarker, 2020; Hasan et al., 2020, 2022; Faysal et al., 2022; Kulsum et al., 2022), *Zea mays* (Azam et al., 2014, 2022a), mung beans (Azam et al., 2022b; 2023), field pea (Azam et al., 2024), and various *Amaranthus* species (Rashad and Sarker, 2020; Sarker et al., 2022c, 2022d, 2022e, 2022f; Jahan et al., 2023; Sarker et al., 2023, 2024). The observed yield variations are influenced by factors such as meteorological conditions, drought, soil texture, soil nutrient composition, genetic traits, and pest pressures (Mao et al., 2001; Fan et al., 2023; Daemo and Ashango, 2024; Halpin-McCormick et al., 2024; Qiu et al., 2024).

Sweet potato genotypes showed the highest mean root yield in Bogura and Jamalpur, likely due to favorable environmental conditions (Table 1). Conversely, lower yields in Gazipur, Jashore, and Chattogram were linked to high rainfall during the growing season, ranging from 218.67 to 283.07 mm (Table 1). Flooding stress can severely diminish sweet potato root yield, with Roberts and Russo (1991) reporting reductions of up to 57%, as noted by Lin et al. (2006). Adubasim et al. (2017) recommended optimizing resource use in well-drained sandy loam soils for maximizing tuber yield in the humid tropics. Burbano-Erazo et al. (2020) found significant ecophysiological variability among sweet potato genotypes from various altitudes, with some adapting well to low-altitude conditions, consistent with our observations of genotypes at lower elevations. These findings highlight the vulnerability of sweet potatoes to adverse environmental conditions and emphasize the importance of identifying resilient genotypes. Developing genotypes with high yield potential and stability across different environments is crucial for producing resilient cultivars that can withstand challenging weather and soil conditions.

The nutrient absorption and utilization abilities of different sweet potato cultivars play a crucial role in determining root yield, which directly affects overall crop productivity (Alam et al., 2024b). In our research, BARI Mistialu-12 exhibited the highest storage root yield, highlighting the differences in nutrient absorption and utilization across cultivars. These variations stress the importance of developing agronomic practices that are specifically tailored to each genotype's unique needs. By optimizing fertilizer use and other inputs accordingly, crop productivity and sustainability can be significantly improved.

4.2. Assessment of variability and genotypic prediction

The analysis of the CV (8.14%) indicated its distribution, with the lowest values associated with GEI, followed by the environment and genotype (Table 3). This finding was corroborated by the LMM examining random effects detailed in Table 5. Similarly, Gemechu et al. (2022) reported that environmental variance significantly influenced sweet potato root yield (83.35%), while GEI (8.83%) and genotype (3.49%) had smaller effects.

The incorporation of previously released genotypes is anticipated to minimize environmental variation due to their broad adaptability across diverse agroecologies in Bangladesh. This makes the selection of high-performing genotypes, which exhibit high genetic variance, heritability, selection accuracy, and a weak correlation with GEI (Table 5), particularly effective in Bangladeshi conditions. Saremirad et al. (2021) emphasized that greater genetic variability and heritability enhance the feasibility of identifying high-performing genotypes. The BLUP method is optimal for predicting random effects on genotype performance when an LMM effect is present (Smith et al., 2005; Taleghani et al., 2023). In the present study, BARI Mistialu-12, BARI Mistialu-16, BARI Mistialu-11, BARI Mistialu-8, BARI Mistialu-2, and BARI Mistialu-13 demonstrated the highest predicted root yields (Figure 2). The use of the BLUP method, which has consistently produced promising results in crops such as rice, corn, cotton, sugarcane, and sugar beet (Barbosa et al., 2014; Baretta et al., 2016; Huang et al., 2021; Vineeth et al., 2022; Taleghani et al., 2023), reinforces its reliability in sweet potato breeding. Choosing sweet potato genotypes with high genetic variance and heritability, especially those resilient to environmental changes, is crucial. Supported by BLUP predictions, this strategy fosters the development of robust cultivars that adapt well to varied conditions, thereby improving yield stability and sustainability within Bangladesh's diverse agroecological settings.

4.3. Genotypic stability and performance analysis

The AMMI analysis showed a nonsignificant error mean sum of squares for root yield, reflecting the model's high accuracy with minimal variation (Table 6) (Omrani et al., 2019; Taleghani et al., 2023). This finding is consistent with Sadabadi et al. (2018), who noted that the first two interaction principal component axes (IPCAs) explained 71.60% of the GEI variability. Conversely, Omrani et al. (2019) and Rajabi et al. (2023) observed that the first four and six IPCAs explained 83% and 98.80% of the GEI variability, respectively. These results highlight the model's effectiveness in evaluating GEI and support the selection of genotypes with stable root yields across diverse environments. The criteria for selecting stable genotypes align with those outlined by Purchase et al. (2000) and are further validated by de Oliveira et al. (2014) and Karuniawan et al. (2021) in their research on passion fruit and sweet potatoes. Unlike AMMI, the WAAS method considers all IPCA scores, not just the first two. WAAS biplot analysis highlighted BARI Mistialu-16 and BARI Mistialu-8 for their low GEI influence and high stability, surpassing the overall yield average (Figure 3). Similar findings were reported by Alam et al. (2024a) using the WAAS biplot.

Bogura, Jashore, and Chattogram were identified as key testing sites, reflecting the genetic potential of the sweet potato clones evaluated (Table 7). This aligns with Karuniawan et al. (2021), who utilized IPCA values from AMMI analysis to select optimal environments for sweet potato cultivation. Genotypic impact on root yield was most pronounced in BARI Mistialu-5, BARI Mistialu-7, BARI Mistialu-10, and BARI Mistialu-14, as evidenced by their lower IPCA values (Table 7). Stability analysis via ASV confirmed the reliability of BARI Mistialu-14, BARI Mistialu-5, BARI Mistialu-10, BARI Mistialu-7, and BARI Mistialu-16, with BARI Mistialu-16 exhibiting an above-average root yield. Sultana et al. (2019) found that BARI Mistialu-8 exhibited the highest stability and root yield among 15 BARI-released sweet potato genotypes using AMMI1 biplot analysis.

The WAASBY index, which evaluates genotypes based on both yield and stability, ranked BARI Mistialu-16, BARI Mistialu-12, BARI Mistialu-7, and BARI Mistialu-8 as top performers (Figure 4). BARI Mistialu-7, in particular, was noted for its stability and potential across various conditions (Table 7; Figures 3 and 4). The effectiveness of the WAASBY index for selecting stable and high-performing genotypes is corroborated by Karuniawan et al. (2021) and Memon et al. (2023). This can assist farmers in choosing reliable, high-yielding sweet potato genotypes that maintain productivity and adaptability in various conditions, ultimately supporting more sustainable farming practices.

4.4. Megaenvironments and genotypic performance analysis

Estimating GEI is crucial for enhancing crop adaptation and performance across varying environmental conditions. The polygonal biplot method, as outlined by Gauch and Zobel (1997), is effective in identifying genotypes best suited for specific environments. Our study used biplot analysis to distinguish two primary megaenvironments. The first megaenvironment, including Gazipur, Bogura, Jashore, and Chattogram, was linked to high-yielding genotypes BARI Mistialu-12 and BARI Mistialu-16. On the other hand, Jamalpur emerged as a separate megaenvironment where BARI Mistialu-11 performed best. Genotypes BARI Mistialu-7, BARI Mistialu-5, and BARI Mistialu-10, situated near the biplot's origin, showed stability across all tested environments, making them suitable for less favorable conditions. Genotypes outside the specific environmental influences in the biplot generally exhibited poorer performance, consistent with findings from other studies on different crops, including sweet potatoes (Nzuve et al., 2013; Nagdeve and Deshmukh, 2018; Karuniawan et al., 2021; Hasani et al., 2021; Saremirad and Taleghani, 2022). Furthermore, Mahmud et al. (2021) found that BARI Mistialu-12, among four BARI-released genotypes, yielded the highest root yield, surpassing the local control cultivar by 57.89% across nine locations and was recognized for its outstanding stability and yield potential.

4.5. Test environments optimization

The GGE biplot method provides a comprehensive evaluation of test environments by balancing discriminativeness and representativeness. Discriminativeness measures how effectively environments can distinguish between superior genotypes, while representativeness assesses how well environments reflect typical conditions (Yan and Tinker, 2006; Oladosu et al., 2017; Khan et al., 2021). A longer environmental vector indicates greater ability to differentiate genotypes, and a smaller angle between this vector and the AEA denotes better representativeness (Yan and Kang, 2002). In the present study, Jamalpur was characterized by high discriminativeness but was less representative of general conditions. Consequently, Bogura was identified as the optimal environment, excelling in both aspects for assessing sweet potato root yield (Figure 6a). The strong correlation observed between Gazipur, Bogura, Jashore, and Chattogram indicates that genotypes responded similarly at these locations. In contrast, Jamalpur exhibited a unique response compared to the other sites (Figure 6b). These findings are consistent with earlier research by Oladosu et al. (2017) and Khan et al. (2021), showcasing the GGE biplot's effectiveness in mapping relationships among locations in METs. Assessing environmental correlations provides valuable insights into their relationships, which can guide future trial designs and optimize resource use (Taleghani et al., 2023).

5. Conclusions

Our study highlights the importance of GEIs for the adaptation and performance of sweet potato genotypes in Bangladesh. Notable genotypes, such as BARI Mistialu-12 and BARI Mistialu-16, were found to offer high storage root yields and stability across various conditions. Bogura, Jashore, and Chattogram were identified as essential testing locations, with Bogura proving particularly effective for both distinguishing and representing optimal yields. Analysis with fixed and random effects models revealed GEI variance, validated the model's accuracy, and supported targeted decision-making to identify high-performing and stable genotypes. Future breeding efforts should prioritize adaptable genotypes with high yield potential. Ongoing research and validation in additional regions will further improve sweet potato cultivation, promoting sustainable practices and enhancing global food security.

Author contributions

Concept, software, resources, formal analysis, visualization, and supervision, Z.A.; methodology, investigation, data curation, and writing—original draft preparation, S.A., and M.A.H.K.; validation, writing—review, revising and editing, U.S., R.R., and S.A. All authors have read and agreed to the published version of the manuscript.

Data availability statement

All of the tables and figures in the text contain the data that were used in the current investigation.

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Conflicts of interest

The authors declare that there are no conflicts of interest.

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