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RESEARCH ARTICLE

Multi-environment evaluation of yield stability in finger millet (*Eleusine coracana* (L.) Gaertn.) using AMMI, GGE, WAASBY and MTSI

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Abstract

Genotype × environment interaction (GEI) strongly influences finger millet yield and agronomic performance, making multi-environment testing essential for identifying stable, high-yielding genotypes. This study aims to identify high-yielding and stable finger millet genotypes using complementary stability analyses. A total of 57 finger millet genotypes were evaluated in a randomised complete block design (RCBD) with 2 replications across three environments at Dr. Rajendra Prasad Central Agricultural University, Pusa (Dholi and Pusa), Bihar, India during 2024–25. The GEI was significant for grain yield and for all agronomic traits ($p < 0.001$). Therefore, genotype performance and stability were assessed using additive main effects and multiplicative interaction (AMMI), the genotype plus genotype × environment (GGE) biplot, the weighted average of absolute scores of the best linear unbiased predictions of the GEI effects (WAASB) with its superiority index (WAASBY) and the multi-trait stability index (MTSI). Based on the WAASBY, PR 202 (17.82 g per plant), IE 2082 (17.08 g), IE 96 (16.92 g), IE 2097 (16.57 g), GPU 26 (16.15 g), IE 510 (14.49 g) and IE 2062 (11.02 g) genotypes were identified as high yielding and most stable genotypes. Considering all nine traits jointly, MTSI selected IE 2097, MR 6, IE 817, IE 2082, IE 510, PR 202, IE 2062, IE 886 and GPU 28, with a selection differential of +29.82 % for grain high-yielding and stable performers. These genotypes represent promising candidates for multi-environment cultivation and may serve as valuable parental material in finger millet breeding programs.

Keywords: AMMI stability value; finger millet; genotype × environment interaction; genotype plus genotype × environment biplot; multi-trait stability index; WAASBY

Introduction

Finger millet (*Eleusine coracana* (L.) Gaertn.) is a nutritionally rich, resilient cereal that is widely cultivated across the semi-arid and arid regions of Asia and Africa, where it serves as a critical food-security crop during periods of drought (1). Despite this adaptability, finger millet productivity remains low relative to other cereals, largely due to the limited availability of well-adapted, stable varieties suited to diverse growing environments. Characterising genotype × environment interaction (GEI) and genotype stability is therefore essential for understanding genotypic response to changing environments and for identifying material with stable performance across environments as well as high yield (2, 3).

Genotype × environment interaction studies on finger millet have identified genotypes exhibiting stable and consistent performance across diverse test environments (4). Similarly, both genotype × environment (GGE) biplot and additive main effects and multiplicative interaction (AMMI) approaches were applied to assess adaptability and yield stability of genotypes of finger millet across diverse environments, to identify stable genotypes with high agronomic and yield performance (2). In the humid lowland areas of Ethiopia, the combined application of AMMI, GGE and multi-trait stability index (MTSI) has been used to assess GEI and yield stability, converging on a similar set of stable, high-yielding genotypes (3). Collectively, these studies underscore the effectiveness of GGE, AMMI and MTSI based stable genotype performance in finger millet studies. However, few studies have integrated AMMI, GGE, WAASBY and MTSI within a single analytical framework to effectively identify broadly adapted finger millet genotypes across multiple environments, highlighting the needs for present study.

The AMMI model combines additive main effects with multiplicative interaction effects in genotype × environment analyses (5). Biplot methodology led to the AMMI biplot (6–8) and the GGE biplot (9, 10). The AMMI biplot represents the interaction pattern and facilitates stability assessment, whereas the GGE biplot combines the genotype main effect with the GEI, providing a genotype-focused visualisation of which-won-where patterns, mega-environment differentiation and genotype stability (11, 12).

The genotype × yield × trait biplot later addressed GGE biplot limitations (13) and MTSI was proposed for simultaneous selection of stability and performance of agronomic traits (14, 15). Weighted average of absolute scores based on BLUPs (WAASB) provides a best linear unbiased prediction (BLUP)-based measure of genotype stability, whereas WAASBY integrates stability with mean performance to facilitate simultaneous selection for high yield and stability (14). In the present study, AMMI, GGE biplot, WAASB/ WAASBY and MTSI were applied jointly to identify stable, high-yielding finger millet genotypes and to characterise the test environments.

Materials and Methods

The present study was conducted at two different locations in Bihar, Dholi (25.98° N, 85.60° E) and Pusa (25.98° N, 85.67° E), across three environments (E1 = summer 2024 at Dholi; E2 = summer 2025 at Dholi; E3 = kharif 2025 at Pusa with mean maximum and minimum temperatures of 32.6/19.4 °C (E1), 32.9/19.2 °C (E2) and 32.0/22.5 °C (E3), with seasonal rainfall of 263.8 mm over 19 rainy days, 163.1 mm over 20 rainy days and 876.3 mm over 50 rainy days respectively, during study period in the middle Gangetic Plains on alluvial soil. The material comprised 57 accessions (50 germplasm accession and 7 high yielding released varieties) obtained from International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) minicore collection (Supplementary Table 1). Weather data, including rainfall and; minimum and maximum temperatures were recorded at the Pusa Observatory of Dr. Rajendra Prasad Central Agricultural University during the study (Fig. 1).

The experiment was conducted in a randomised complete block design (RCBD) with 2 replications. Each entry was planted in two rows of 3 m each, with plant-to-plant distance of 10 cm), row spacing of 50 cm and a plot size of 3 m^2. The recommended fertiliser dose of 60 : 30 : 30 kg nitrogen, phosphorus and potassium (NPK) ha^{-1} was applied, irrigation was provided at sowing and critical growth stages and two hand weedings were carried out during the crop cycle, following standard agronomic practices for irrigated finger millet. days to 50 % flowering (DFL), days to maturity (DTM) were recorded on whole plot basis. For the remaining traits five plants were randomly selected per plot and data were recorded on agro-morphological trait namely, plant height (PH), number of basal tillers (BT), ear length (EL), finger length (FL), number of fingers per ear (FNo), grain yield per plant (GYPP) and test weight (TW).

Analysis of variance

Analysis of variance (ANOVA) was carried out on 57 genotypes of finger millet in three environments (E1, E2 and E3) separately for each environment and on the combined data, following standard general linear mixed-model procedures. Homogeneity of error variance across environments was assessed with Hartley's F-max test (16), computed as the ratio of the largest to the smallest environment-wise error mean square; for grain yield the F-max ratio was 5.66 and because the AMMI and GGE analyses were based on genotype × environment means the combined analysis was carried out across all three environments. Fisher's least significant difference (LSD) at 5 % probability was used to compare genotype means and experimental precision expressed as the coefficient of variation (CV).

AMMI analysis and construction of the GGE biplot

The stability and adaptability of each genotype were examined using the AMMI model (5) and the genotype plus GGE biplot (9). The AMMI ANOVA was computed using Gollob's *F*-test, which tends to be liberal in the number of interaction axes declared significant; with only two estimable axes in the present design this has limited consequence (17). Because three environments were tested, the G × E interaction was partitioned into a maximum of two interaction principal component axes, IPCA1 and IPCA2 [N = min (g - 1, e - 1) = 2]. The AMMI model is:

$$Y_{ge} = \mu + \alpha_g + \beta_e + \sum_{n=1}^{N} \lambda_n \gamma_{gn} \delta_{en} + \varepsilon_{ge}$$

where

Y_{ge} = yield of genotype g in environment e

μ = grand mean

α_g and β_e = deviations of genotype g and environment e respectively from the grand mean

λ_n= singular value of nth IPCA

γ_{gn} and δ_{en}= genotype and environment scores respectively for nth IPCA

ε_{ge}= residual error (Gollob)

The GGE biplot model, in which the genotype main effect and the GEI are jointly decomposed after removing the environment main effect, is:

$$Y_{ij} - \mu - \beta_j = \sum_{n=1}^{N} \lambda_n \xi_{in} \eta_{jn} + \varepsilon_{ij}$$

where,

Y_{ij} = mean yield of genotype i in environment j

μ = overall mean

Bj= main effect of environment j

λ_n = singular value of nth principal component

$\xi_{in}$and η_{jn}= genotype and environment scores respectively for nth eigenvector

ε_{ij} = residual

The AMMI stability value (ASV) was computed from the IPCA1 and IPCA2 scores (18):

$$ASV = \sqrt{\left[\frac{SS_{IPCA1}}{SS_{IPCA2}} \times \text{IPCA1 score}\right]^2 + (\text{IPCA2 score})^2}$$

where,

SSIPCA1 = sum of squares of IPCA1

SSIPCA2 = sum of squares of IPCA2

A lower ASV indicates a more stable genotype. The genotype selection index (GSI), which combines stability and productivity, was computed (19):

$$GSI = RASV + RY$$

where

RASV = rank of a genotype based on ASV and RY is its rank based on mean grain yield across environments (a lower GSI denotes a genotype that is both high-yielding and stable).

Fig. 1(A). Maximum and minimum temperature and cumulative rainfall during finger millet growing period – Environment 1 (E1) – 2024, Summer season



Fig. 1(B). Maximum and minimum temperature and cumulative rainfall during finger millet growing period – Environment 2 (E2) – 2025, Summer season



Fig. 1(C). Maximum and minimum temperature and cumulative rainfall during finger millet growing period – Environment 3 (E3) – 2025, Kharif season

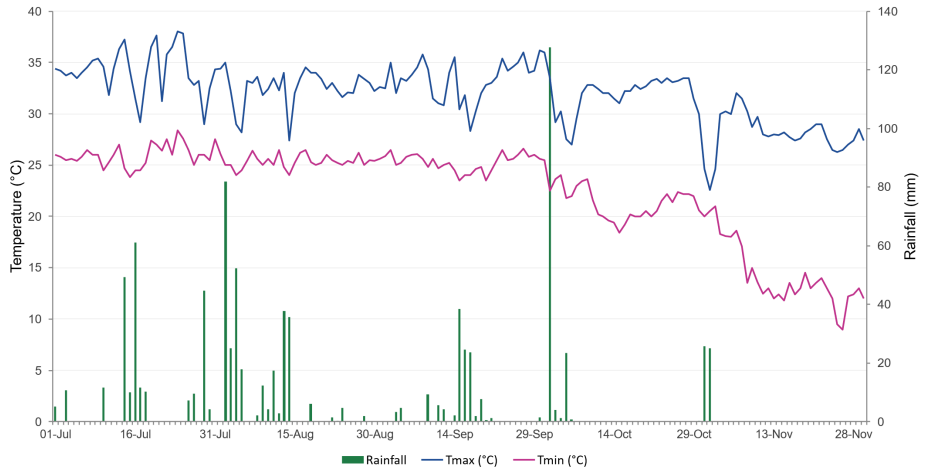


Fig. 1. Weather data (maximum and minimum temperature and rainfall) recorded during the study period: (A) E1, summer 2024, Dholi; (B) E2, summer 2025, Dholi; (C) E3, kharif 2025, Pusa.

Multi-trait stability index

Genotype stability across all nine measured traits was further evaluated with the MTSI. For every character, WAASB values were obtained from the singular value decomposition of the matrix of best linear unbiased predictions of the GEI effects estimated from a linear mixed model; WAASB quantifies stability (lower = more stable). The WAASBY index then combined stability (WAASB) with mean performance to allow simultaneous stability and yield selection. Following standard procedure, WAASBY was computed as a weighted combination of the rescaled mean yield (rG) and the rescaled WAASB (rW), each placed on a 0–100 scale, with weights assigned to yield and stability; equal weights (50 each) were adopted so that higher WAASBY values mark genotypes that are simultaneously high-yielding and stable (14). The WAASBY-derived factor scores were then used to compute the MTSI as the genotype–ideotype Euclidean distance (14):

$$MTSI_i = \left[\sum_{j=1}^{f} (F_{ij} - F_j)^2 \right]^{0.5}$$

where

$MTSI_i$ = multi-trait stability index of the ith genotype

F_{ij} = is the jth factor score of genotype i

F_j = j^{th} score of the ideotype

F = number of retained factors

A lower MTSI value indicates closer proximity to the ideotype and, therefore, higher combined mean performance and stability across traits and environments. Genotypes were selected at a selection intensity of 15 %, a value commonly adopted in MTSI (15).

Trait correlation and principal component analysis

Pearson correlation coefficients among genotype means were computed for all nine traits to assess trait associations. Principal component analysis (PCA) of the genotype-mean matrix was also performed to summarise overall patterns of trait covariation, with components having eigenvalues greater than 1 retained for interpretation.

Statistical analysis

All statistical analyses, including combined and individual-environment ANOVA, AMMI analysis, AMMI-based stability statistics, BLUP-based WAASB and WAASBY indices, MTSI and construction of AMMI and GGE biplots, were performed in R version 4.4.2 (20) using the metan package version 1.19.0 (21). The functions performs_ammi(), ammi_indexes(), waasb(), mtsi () and gge() were used for AMMI analysis, computation of AMMI-based stability statistics including ASV and GSI, estimation of BLUP-based WAASB and WAASBY indices, calculation of the MTSI and construction of GGE biplots respectively.

Results

Combined AMMI analysis of variance

The combined AMMI ANOVA indicated highly significant differences ($p < 0.001$) among environments, genotypes and GEI for grain yield per plant and all eight agronomic traits evaluated (Table 1). For grain yield per plant, the environment mean square (MS = 1568.61) was substantially larger than the genotype (MS = 58.10) and GEI (MS = 29.21) mean squares, expressed as a proportion of the total sum of squares of the sources listed in Table 1, however, the environment (31.30 %), the genotype (32.47 %) and the GEI (32.64 %) accounted for almost equal shares of the variation in grain yield, with the residual accounting for 3.59. Significant GEI for all traits demonstrated that genotype performance differed among environments, warranting stability analyses to identify broadly adapted and high-yielding genotypes.

The GEI for grain yield was partitioned into two interaction principal components (IPCA). Interaction principal component 1 (IPCA1) captured 75.80 % of the GEI sum of squares, while IPCA2 explained the remaining 24.20 %. For the other traits, IPCA1 and IPCA2 together explained substantial proportions of GEI variation: DFL (78.67 % and 21.33 %), DTM (77.25 % and 22.75 %), plant height (66.54 % and 33.46 %), basal tillers (73.75 % and 26.25 %), ear length (72.47 % and 27.53 %), finger length (62.42 % and 37.58 %), number of fingers per ear (75.23 % and 24.77 %) and test weight (87.23 % and 12.77 %). The significance of both IPCA axes for most traits ($p < 0.001$) confirmed the complex nature of GEI and justified the use of multiple stability assessment approaches.

AMMI stability value and genotype selection index

The ASV quantified genotype stability based on IPCA1 and IPCA2 scores, with lower ASV values indicating greater stability. Among the ten most desirable genotypes (Table 2), IE 510 recorded the lowest ASV (0.316), followed by IE 2062 (ASV = 0.529) and IE 3101 (ASV = 0.563), indicating that these genotypes contributed least to the GEI. However, high stability did not always correspond to high yield, necessitating the GSI which combines stability rank (rASV) and yield rank (rY).

Based on GSI, 10 most desirable genotypes for grain yield were IE 510, IE 96, PR 202, GPU 26, IE 3101, IE 954, IE 2062, IE 2097, IE 2082 and IE 817 (Table 3). IE 510 ranked first with GSI = 8 (yield rank = 6, ASV rank = 2), while PR 202 (GSI = 18) and IE 96 (GSI = 14) demonstrated the best combination of stability and high yield despite moderate ASV ranks (17 and 11 respectively). The AMMI1 biplot visually confirmed these findings: genotypes with high yield

Table 1. Combined AMMI analysis of variance for grain yield and eight related traits of 57 finger millet genotypes across three environments

Source	DF	GYPP (MS)	DFL (MS)	DTM (MS)	PH (MS)	BT (MS)	EL (MS)	FL (MS)	FNo (MS)	TW (MS)
Environment	2	1568.61***	53448.87***	128065.27***	81554.30***	5.63***	22.48*	24.81**	33.47*	4.49***
Genotype	56	58.10***	809.09***	855.62***	489.29***	1.53***	9.38***	4.91***	2.69***	0.43***
GEI	112	29.21***	156.88***	167.76***	103.28*	1.06***	4.32***	2.23***	1.73***	0.10***
IPCA1	57	43.51***	209.36***	210.81***	118.70**	1.24***	5.39***	2.36***	2.54***	0.19***
IPCA2	55	14.39***	102.50***	123.14***	87.31 ns	0.87***	3.21***	2.09***	0.89 ns	0.01 ns
Residual	168	2.14	34.29	25.64	70.82	0.26	1.54	0.84	0.97	0.03

[a]DF degrees of freedom; MS mean square; GEI: genotype × environment interaction; IPCA1, IPCA2 interaction principal component axes 1 and 2; ns: non-significant. *, ** and *** significant at $p < 0.05$, $p < 0.01$ and $p < 0.001$ respectively; GYPP: grain yield per plant (g); DFL: days to 50 % flowering; DTM: days to maturity; PH: plant height (cm); BT: basal tillers; EL: ear length (cm); FL: finger length (cm); FNo: number of fingers per ear; TW: test weight.

Table 2. Overall mean and range of genotype means for the nine traits

Trait	Mean	Minimum	Maximum
DFL (days)	85.37	61.83	110.17
DTM (days)	118.81	94.0	145.5
PH (cm)	82.22	61.62	103.67
BT	3.64	2.63	4.93
EL (cm)	8.95	5.98	11.52
FL (cm)	7.26	4.82	9.65
FNo	7.49	5.87	9.07
GYPP (g)	10.14	3.88	17.82
TW	1.9	0.4	2.54

GYPP: grain yield per plant (g); DFL: days to 50 % flowering; DTM: days to maturity; PH: plant height (cm); BT: basal tillers; EL: ear length (cm); FL: finger length (cm); FNo: number of fingers per ear; TW: test weight.

Table 3. Ten most desirable genotypes ranked by the genotype selection index (GSI) for grain yield

Genotype	Mean GY (g)	rY	ASV	rASV	GSI	rGSI
IE 510	14.49	6	0.316	2	8	1
IE 96	16.92	3	1.132	11	14	2
PR 202	17.82	1	1.424	17	18	3
GPU 26	16.15	5	1.379	14	19	4
IE 3101	11.41	15	0.563	5	20	5
IE 954	12.94	9	1.203	12	21	6
IE 2062	11.02	20	0.529	4	24	7
IE 2097	16.57	4	1.774	22	26	8
IE 2082	17.08	2	2.06	26	28	9
IE 817	11.38	16	1.342	13	29	10

[a]rY rank by mean yield; rASV: rank by AMMI stability value; rGSI: rank by genotype selection index.

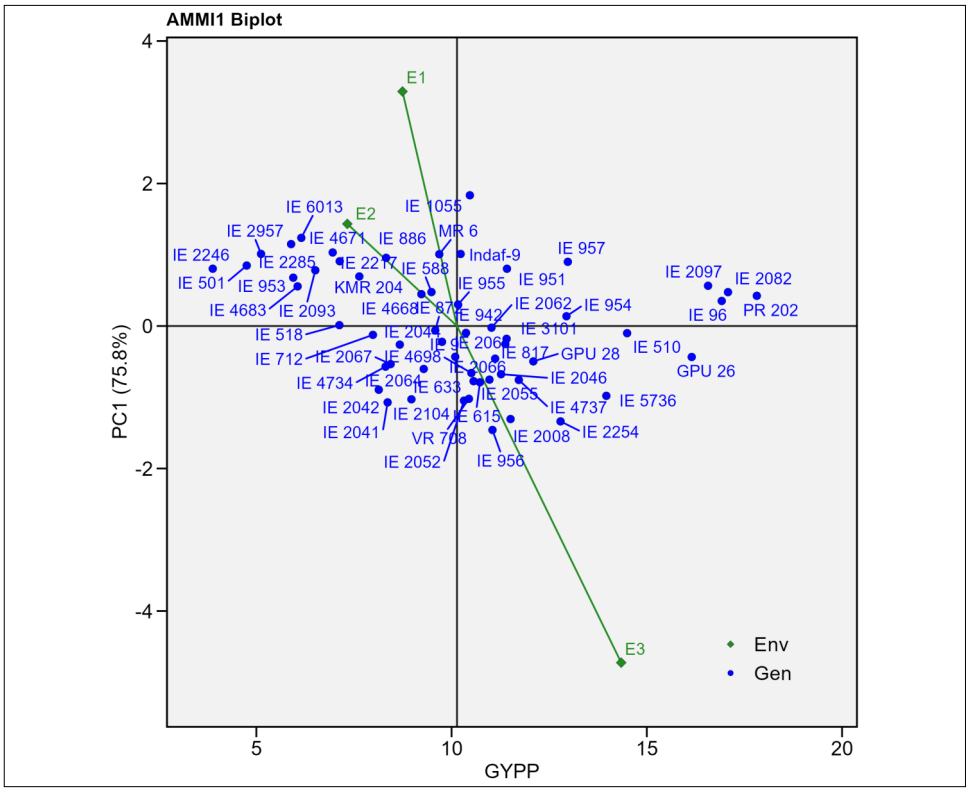


Fig. 2. AMMI1 biplot of grain yield (mean GYPP vs. IPCA1) for 57 finger millet genotypes across three environments.

and low IPCA1 scores clustered near the upper portion of the biplot close to the origin, indicating both high productivity and stability (Fig. 2). Genotypes positioned far from the origin showed adaptation to specific environments, with IE 9, IE 2246 and IE 5736 exhibiting strong positive IPCA1 scores suggesting adaptation to specific environmental conditions.

GGE biplot analysis

For grain yield, the GGE biplot explained 90.46 % of the G + GE variation, with PC1 accounting for 58.57 % and PC2 for 31.89 % of the total variation. The which-won-where plot view partitioned the 57 genotypes into distinct sectors and identified the vertex genotypes for each environmental group (Fig. 3). The three environments formed two distinct mega-environments: E1 (summer 2024, Dholi) and E2 (summer 2025, Dholi) clustered together, while E3 (kharif 2025, Pusa) separated distinctly, indicating significant seasonal and/or locational effects on genotype performance. The genotypes at vertex for the two mega-environments were PR 202 (for the Dholi summer environments) and IE 2082 (for the Pusa kharif environment), representing the highest-yielding genotypes within each environmental group.

The mean-versus-stability view of the GGE biplot highlighted the genotypes closest to the ideal genotypes (high mean yield and high stability). PR 202, IE 96 and IE 2097 positioned

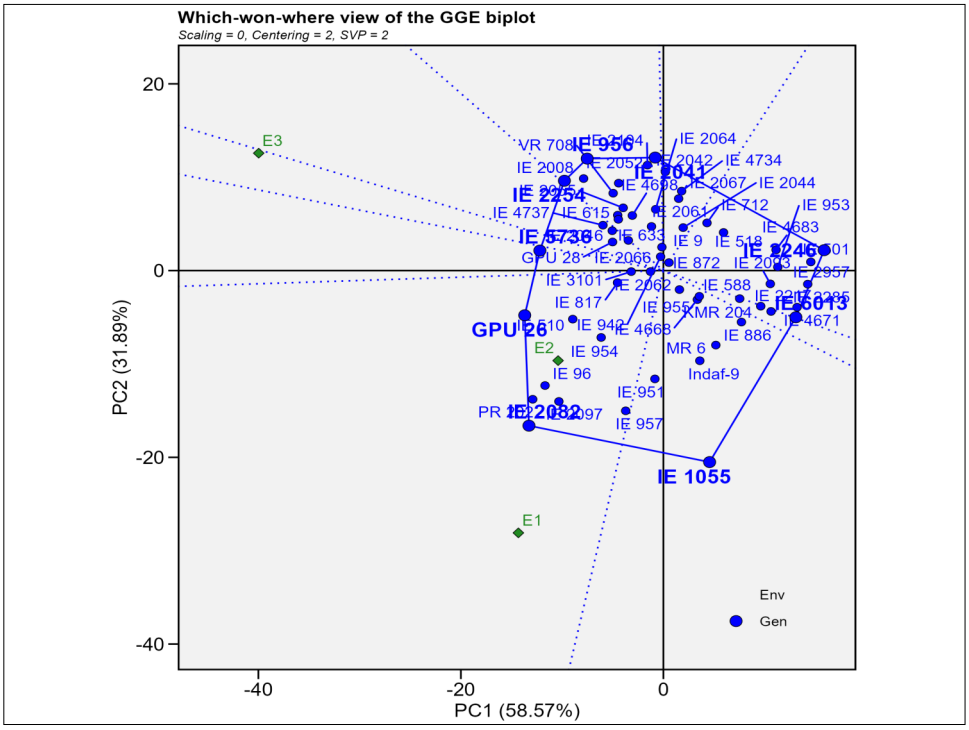


Fig. 3. Which-won-where view of the genotype plus genotype × environment (GGE) biplot for grain yield. GYPP: grain yield per plant (g).

nearest to the ideal genotype, followed by IE 510 and GPU 26. Genotypes such as IE 9, IE 2246 and IE 5736 exhibited high stability but below-average yield, while IE 956 and IE 957 showed high yield but poor stability. The discriminating power and representativeness assessment indicated that E1 was identified as the most discriminating environment, whereas E3 was most representative of the average environment, suggesting its potential utility for selecting broadly adapted genotypes.

WAASB and WAASBY indices

The WAASB index, derived from singular value decomposition of the BLUP-based GEI matrix, quantified stability with lower values indicating greater stability. Across the 57 genotypes, IE 872 exhibited the highest stability (WAASB = 0.068), followed by IE 2062 (WAASB = 0.097) and IE 3101 (WAASB = 0.175). Conversely, IE 9 (WAASB = 1.017) and IE 5736 (WAASB = 0.965) were the most unstable genotypes.

The WAASBY index, which integrates stability and mean performance with equal weighting, identified the most desirable genotypes. PR 202 achieved the highest WAASBY score (92.43), reflecting its exceptional yield (17.82 g) and good stability (WAASB = 0.304). IE 96 (WAASBY = 89.76), IE 2097 (WAASBY = 83.01) and IE 510 (WAASBY = 80.52) followed closely (Table 4). The yield × WAASB biplot effectively classified genotypes into four quadrants: the upper-left quadrant (high yield, high stability) contained PR 202, IE 96, IE 2097, IE 2082, GPU 26 and IE 510, confirming their superior combined performance (Fig. 4). The lower-left quadrant (low yield, high stability) included genotypes such as IE 2062, IE 3101 and IE 872, while the upper-right quadrant (high yield, low stability) comprised IE 956 and IE 957. The lower-right quadrant (low yield, low stability) contained predominantly poor-performing genotypes including IE 9 and IE 2246.

Multi-trait stability index

Considering all nine traits simultaneously at a selection intensity of 15 %, the MTSI selected nine genotypes: IE 2097, MR 6, IE 817, IE 2082, IE 510, PR 202, IE 2062, IE 886 and GPU 28 (Table 5; Fig. 5). IE 2097 exhibited the lowest value of MTSI (3.05), indicating closest proximity to the ideotype, followed by MR 6 (MTSI = 3.31) and IE 817 (MTSI = 3.84). The MTSI values for selected genotypes ranged from 3.05-7.43 (GPU 28). The radar confirmed that selected genotypes consistently outperformed the population mean across most traits, particularly for GYPP, DFL, DTM, EL and FL view (Fig. 6) .

Selection differentials demonstrated significant improvements for most traits (Table 5). Grain yield per plant showed the highest positive selection differential (+29.82 %), increasing from the original population mean of 10.14-13.16 g among selected genotypes. DFL (+11.56 %) and DTM (+9.92 %) also exhibited substantial increases, indicating selection favoured slightly later-maturing genotypes. The TW (+5.89 %), EL (+4.28 %), FL (+3.56 %), PH (+2.32 %) and FNo (+0.70 %) all

Table 4. Ten genotypes with the highest WAASBY for grain yield

Genotype	Mean GY (g)	WAASB	WAASBY
PR 202	17.82	0.304	92.43
IE 96	16.92	0.287	89.76
IE 2097	16.57	0.458	83.01
IE 510	14.49	0.304	80.52
IE 2082	17.08	0.668	78.13
GPU 26	16.15	0.637	75.8
IE 2062	11.02	0.097	74.67
IE 954	12.94	0.326	74.25
IE 3101	11.41	0.175	73.56
IE 872	9.58	0.068	70.45

GY: grain yield; WAASB: weighted average of absolute scores; WAASBY: weighted average of absolute scores and grain yield.

Table 5. Selection differentials from the multi-trait stability index (MTSI) (15 % selection intensity)

Trait	Factor	Xo	Xs	SD (%)
DFL	FA 1	85.37	95.24	+11.56
DTM	FA 1	118.81	130.59	+9.92
EL	FA 1	8.95	9.33	+4.28
FL	FA 1	7.26	7.52	+3.56
GYPP	FA 2	10.14	13.16	+29.82
TW	FA 2	1.9	2.02	+5.89
PH	FA 3	82.22	84.13	+2.32
BT	FA 3	3.64	3.61	−1.02
FNo	FA 3	7.49	7.54	+0.70

[a]Xo: mean of the original population; Xs: mean of the selected genotypes; SD (%): selection differential; GYPP: grain yield per plant (g); DFL: days to 50 % flowering; DTM: days to maturity; PH: plant height (cm); BT: basal tillers; EL: ear length (cm); FL: finger length (cm); FNo: number of fingers per ear; TW: test weight.

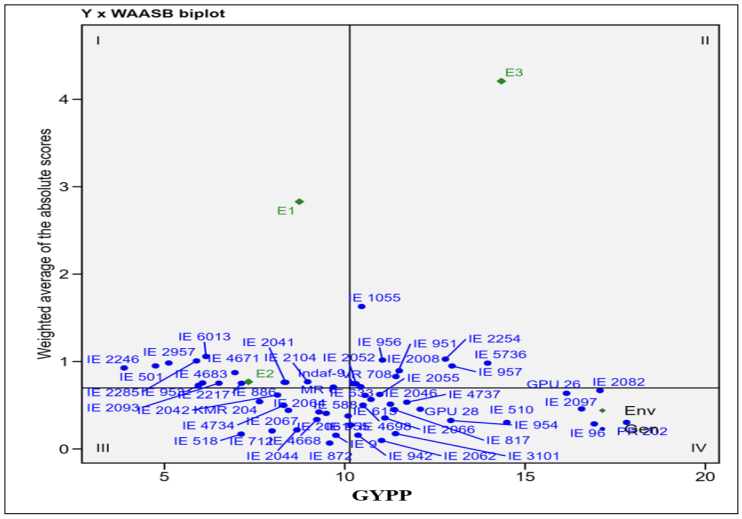


Fig. 4. Yield × WAASB biplot for the simultaneous selection of high-yielding and stable genotypes.



Fig. 5. Multi-trait stability index (MTSI) ranking of 57 genotypes (lower is better). Genotypes to the left of the dashed selection threshold were selected at 15 % intensity.

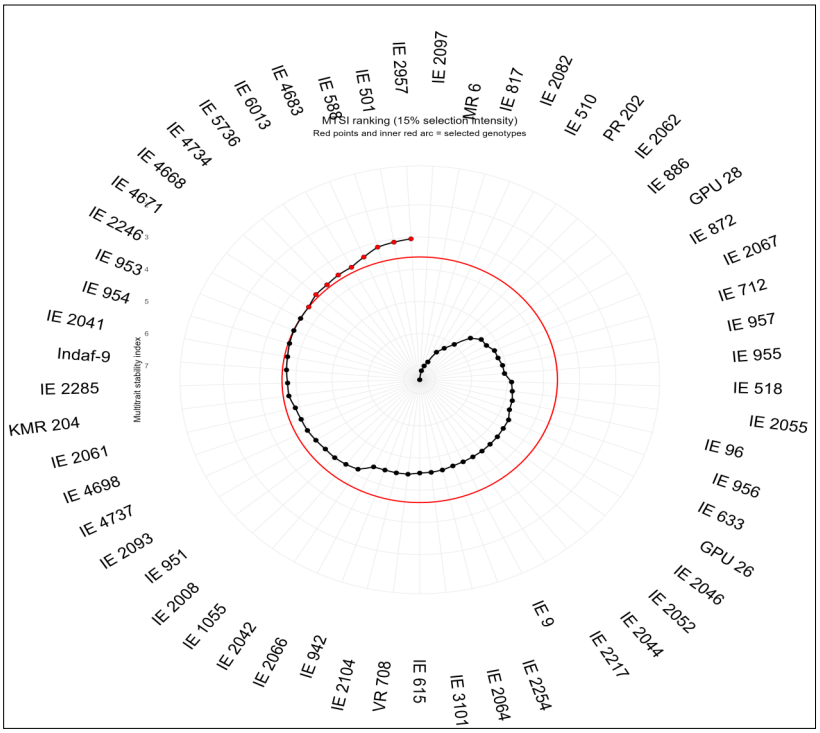


Fig. 6. Radar view of the multi-trait stability index (MTSI) ranking; red points and the inner red arc mark the selected genotypes (15 % selection intensity).

exhibited positive selection differentials. Only basal tillers showed a marginal negative selection differential (-1.02 %), suggesting minimal impact on tillering capacity.

Trait correlations and principal component analysis

Pearson correlation analysis among genotype means revealed strong positive associations within phenological and panicle trait groups (Fig. 7). The DFL and DTM were very closely correlated ($r = 0.98$, $p < 0.001$), as were EL and FL ($r = 0.89$, $p < 0.001$). The DFL showed moderate correlations with PH ($r = 0.53$), EL ($r = 0.68$), FL ($r = 0.64$) and TW ($r = 0.31$). Similarly, DTM correlated moderately with PH ($r = 0.48$), EL ($r = 0.60$), FL ($r = 0.56$) and TW ($r = 0.33$).

Principal component analysis (PCA) of genotype means extracted three components with eigenvalues > 1, together explaining 72.58 % of the total variation. Principal component 1 (PC 1) accounted for 41.63 % of the variation and loaded strongly on phenological and panicle traits: DFL (eigenvector = 0.42), DTM (0.41), EL (0.39) and FL (0.38). PC2 explained 16.86 % of variation and was defined primarily by GYPP (eigenvector = 0.43) and test weight (0.42). PC3 accounted for 14.09 % of the variation and loaded heavily on PH (0.65) and BT (0.57). The distinct separation of phenology–panicle traits (PC1) from yield–test weight traits (PC2) indicated that these trait groups varied independently,

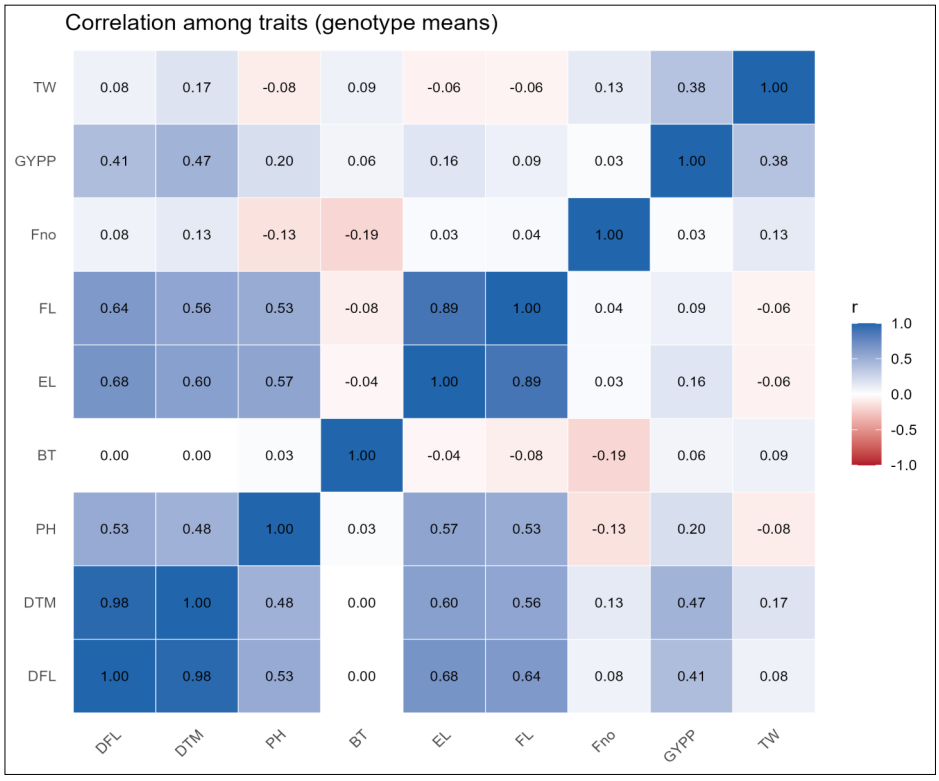


Fig. 7. Pearson correlation among traits (genotype means).

suggesting that selection for earliness would not necessarily compromise grain yield potential.

Congruence among stability methods

Comparison of rankings across the different stability methods revealed consistent identification of superior genotypes. PR 202, IE 2097, IE 510 and IE 2082 were consistently ranked among the top performers across the GSI, WAASBY and MTSI analyses. Specifically, PR 202 ranked 3rd in GSI, 1st in WAASBY and 6th in MTSI; IE 2097 ranked 8th, 3rd and 1st; IE 510 ranked 1st, 4th and 5th; and IE 2082 ranked 9th, 5th and 4th. IE 96 ranked 2nd by both GSI and WAASBY but fell outside the nine genotypes retained by MTSI at the 15 % selection intensity, reflecting the additional weight that MTSI places on the remaining eight traits. This high degree of concordance among methods strengthens confidence in identifying these genotypes as possessing stability across environments and high yield.

Notably, genotypes such as IE 2062 and IE 3101 exhibited excellent stability (low ASV and WAASB values) but moderate yields, making them valuable as stable parents in breeding programs. Conversely, genotypes like IE 956 and IE 957 showed higher yield potential but poor stability, suggesting environment specific suitability rather than broad adaptation.

Discussion

The significant GEI for GYPP and all agronomic traits shows that genotype performance in finger millet varied considerably across the growing conditions tested. This agrees with earlier multi-environment work in finger millet and confirms that stability assessment is needed to identify genotypes with broad adaptation (2, 3). The greater environmental contribution to yield variation likely reflects seasonal and location-specific climatic differences among the test environments (1). The significant IPCA axes for most traits indicate that the GEI arose from more than one source, so several complementary stability models were employed rather than relying on a single approach.

The AMMI analysis partitioned the GEI and identified low-ASV genotypes, including IE 510, IE 2062 and IE 3101, as highly stable as highly stable. Stability on its own is not enough for a breeding programme, so the GSI which combines yield and stability ranks, provided a more practical foundation for selection. The top GSI genotypes IE 510, IE 96, PR 202 and GPU 26 showed that high yield and stability can occur together, as also reported in wheat (19) and other millets. In the AMMI1 biplot, genotypes near the origin had high mean yield and low IPCA1 scores, a sign of broad adaptation, whereas genotypes far from the origin, such as IE 9 and IE 2246, were adapted to particular environments. This crossover pattern points to the presence of more than one mega-environment, which the GGE biplot then clarified.

The GGE biplot provided a more comprehensive, genotype -focused view by decomposing both the genotype main effect and the GEI. It's which-won-where view showed that the three test environments formed two mega-environments: the two summer seasons at Dholi (E1 and E2) grouped together and the kharif season at Pusa (E3) stood apart. This split probably reflects differences in temperature, photoperiod and rainfall between the summer and kharif seasons, together with soil differences between locations. PR 202 and IE 2082 were the vertex genotypes of the two mega-environments, which marks their strong specific adaptation. In the mean-versus-stability view, PR 202, IE 96 and IE 2097 lay closest to the ideal genotype, in agreement with the AMMI rankings. The GGE biplot explained a high proportion of the variation (90.46 %), which adds confidence to these interpretations. Comparable AMMI and GGE agreement has been reported in finger millet, which supports the reliability of these biplot methods for stability (22, 23).

The WAASB and WAASBY indices combine BLUP-based stability with mean performance and have some methodological advantages over the traditional ASV. With yield and stability weighted equally, WAASBY identified genotypes that performed consistently across environments and PR 202, IE 96 and IE 2097 ranked highest. The yield × WAASB biplot separated genotypes into four quadrants and so allowed stable, high-yielding genotypes to be selected in one step. The method has been used more often in recent finger millet stability studies because it shows stability and yield on a single plot and avoids the need to reconcile two separate indices (3). IE 872 and IE 2062 showed good stability based on their low WAASB values but only moderate yields, indicating their potential value as stable germplasm for further breeding evaluation, while IE 956 and IE 957 had higher yield but poor stability and are therefore suited only to specific environments.

The MTSI extends stability assessment beyond grain yield to encompass all nine agronomic traits simultaneously. The MTSI selected 9 genotypes - IE 2097, MR 6, IE 817, IE 2082, IE 510, PR 202, IE 2062, IE 886 and GPU 28 that collectively represent the best compromise across phenology, plant architecture, yield components and grain quality. The positive selection differentials for most traits, especially the remarkable +29.82 % gain for grain yield, confirm the effectiveness of MTSI in improving the population mean for multiple traits. The slight negative differential for basal tillers indicates that selection did not compromise tillering capacity, while the moderate gains in earliness-related traits suggest that the selected genotypes tend to be slightly later-flowering, which may be advantageous for biomass accumulation and yield potential in the target environments. This multi-trait approach addresses a critical limitation of single-trait stability analyses, which often overlook trade-offs among traits (14, 15). The convergence of MTSI-selected genotypes with those identified by GSI and WAASBY particularly IE 2097, IE 510, PR 202 and IE 2082 provide strong validation for recommending these genotypes as parental material.

The genotypes identified here can be used in the breeding programme in three complementary ways. PR 202, IE 2097, IE 510 and IE 2082, which combined high mean yield with low WAASB and low MTSI, are the most suitable candidates for direct use as parents in crossing blocks aimed at broad adaptation. IE 2062, IE 3101 and IE 872, which were highly stable but only moderately productive, are better deployed as stability donors in crosses with high yielding but unstable material such as IE 956 and IE 957, so that the yield potential of one parent may be recombined with the buffering capacity of the other. Because the three test environments resolved into two mega-environments, a single variety is unlikely to be optimal across both; parallel selection streams targeting the Dholi summer and Pusa kharif niches, using PR 202 and IE 2082 respectively as

vertex genotypes, should therefore be more efficient than selection on average performance alone.

The remarkable concordance among the four stability methods AMMI, GGE, WAASB/WAASBY and MTSI in identifying the same set of superior genotypes (PR 202, IE 2097, IE 510 and IE 2082) is noteworthy. The repeated selection of these genotypes across methods suggests that their superior performance is not an artefact of any single analytical technique but reflects genuine genetic potential for high yield and stability across diverse environments. This multi-method consensus has been similarly reported in recent finger millet studies and reinforces the recommendation to use complementary stability indices in breeding programmes (2, 3).

Conclusion

The joint application of additive main effects and multiplicative interaction (AMMI), the genotype plus genotype × environment (GGE) biplot, weighted average of absolute scores/ weighted average of absolute scores and grain yield (WAASB/WAASBY) and multi-trait stability index (MTSI) identified finger millet genotypes that combine high grain yield with stability across environments. PR 202, IE 96, IE 2097, IE 510, IE 2082, GPU 26 and IE 2062 were the most promising for grain yield stability, while IE 2097, MR 6, IE 817, IE 2082, IE 510, PR 202, IE 2062, IE 886 and GPU 28 were superior when all nine traits were considered jointly, with a selection differential of +29.82 % for grain yield. Because the three test environments resolved into two mega-environments, these genotypes are recommended as parental material for programmes targeting either broad adaptation or specific adaptation to the summer and kharif niches. As the results derive from three environments over two years, the genotypes identified require further validation across additional locations and seasons before large-scale recommendation. Future work should extend the evaluation to a wider set of environments, characterise the selected accessions with molecular markers to establish their genetic relationships and test whether the stability observed here is transmitted to derived progenies. These genotypes represent promising candidates for further multi-location evaluation and potential cultivation in environments similar to those examined in the present study. The complementary nature of the stability methods employed here provides a robust framework for genotype evaluation that can be extended to other crops and breeding programmes. Although the present evaluation was conducted across three environments, further validation over additional years and diverse agro-ecological regions would strengthen recommendations for varietal release. The genotypes are recommended as parental material and required for the validation across additional locations and seasons before large scale recommendation.

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Authors' contributions

RB carried out the investigation, data curation and manuscript drafting. SM contributed to conceptualisation, methodology, resources, supervision, funding acquisition and drafting of the original manuscript. MKS contributed to data curation and supervision. SK contributed to methodology, supervision and data curation. MKT contributed to formal analysis and manuscript drafting. MC contributed to data curation. All authors read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interest to declare.

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