



## Stability analysis for yield and yield components through AMMI and GGE biplot techniques in germplasm of finger millet (*Eleusine coracana*)

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### ABSTRACT

An experiment was conducted during the winter (*rabi*) season of 2022–23 and 2023–24 to evaluate the stability and adaptability of 35 diverse finger millet (*Eleusine coracana* L. Gaertn.) germplasm across three environments, namely Odisha ( $E_1$ ), Bihar ( $E_2$ ), and West Bengal ( $E_3$ ). The experiment was laid out in a randomised complete block design (RCBD) with three replications. Data on 15 quantitative traits were recorded to assess genotype  $\times$  environment ( $G \times E$ ) interactions using AMMI and GGE biplot models. AMMI analysis revealed significant  $G \times E$  interactions for key traits such as biological yield/plant, harvest index and grain yield/plant, indicating differential genotype responses across environments. GGE biplot analysis showed that the first two principal components (PC1 and PC2) explained 91.05% of the total yield variation, effectively capturing genotype performance and stability.  $E_1$  (Odisha) emerged as the most discriminative environment, while  $E_2$  (Bihar) was both discriminative and representative, making it suitable for selecting widely adaptable genotypes. Genotypes Badatara, FM 1213, Chillika and FM PR 1731 exhibited stable and superior yield performance across environments. The “which-won-where” biplot identified VL 410, Badatara and FM 1213 as top performers in Odisha, Bihar and West Bengal, respectively. Positive associations among environments, inferred from acute angles between environment vectors in the GGE biplot, indicated consistent genotype performance across locations. Overall, the study demonstrated that both AMMI and GGE biplot approaches are effective for selecting high-yielding and stable finger millet genotypes.

**Keywords:** AMMI model, GGE biplot, Genotype  $\times$  environment interaction, Principal components

Finger millet (*Eleusine coracana* L. Gaertn.) is an important small millet crop cultivated primarily in Africa and Asia, valued for its adaptability to marginal environments and low-input agriculture. It is a nutrient-dense cereal, rich in dietary fibre, essential amino acids, calcium, iron, and other micronutrients, making it suitable for nutritional security and climate-smart agriculture (Gaikwad 2024). Finger millet is a self-pollinating crop grown for human consumption, fodder, brewing, and traditional medicinal uses (Bisht and Mukai 2000).

It is an allotetraploid species ( $2n = 4x = 36$ ) with an estimated genome size of approximately 1,593 Mb. The cultivated subspecies *coracana* is classified into four races i.e. *elongata*, *plana*, *compacta* and *vulgaris*

while the wild subspecies *africana* includes two races, *africana* and *spontanea*. The genus *Eleusine* comprises 13 species, including nine annual and four perennial species, predominantly native to Africa, with *E. tristachya* being the only species indigenous to the New World.

India remains the largest producer of millets, contributing nearly 38.4% of global production in 2025, with finger millet an important component of small millets production (APEDA 2025, Millets National Media Portal 2025). In Odisha, finger millet production reached over 2.26 lakh tonnes in 2022–23 with yields above 1,200 kg/ha (Times of India 2024). It is also widely cultivated in eastern states such as Bihar and West Bengal, contributing to national output and highlighting regional production diversity in India’s millet sector. Despite its adaptability to poor soils and moisture-limited conditions, the national average productivity of finger millet remains low, reflecting limited genetic improvement and high environmental variability. These constraints are particularly evident in hilly and tribal regions, where finger millet plays a critical role in food and nutritional security but is cultivated under low-input conditions with minimal access to improved varieties and technologies (Anuradha *et al.* 2022).

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In crop improvement programmes, the simultaneous achievement of high grain yield and yield stability across diverse environments is a major breeding objective. Grain yield is strongly influenced by environmental factors and genotype  $\times$  environment interaction (GEI). The presence of significant GEI complicates genotype evaluation, as varietal performance often varies across locations and seasons. Therefore, understanding and effectively modelling GEI through multi-environment trials (METs) is essential for identifying genotypes with wide or specific adaptation (Ghazvini *et al.* 2018, Vaezi *et al.* 2018, 2019). Several statistical approaches have been developed to analyse GEI and assess phenotypic stability, among which the Additive Main Effects and Multiplicative Interaction (AMMI) model and Genotype plus Genotype  $\times$  Environment (GGE) biplot analysis are widely used. The AMMI model integrates analysis of variance (ANOVA) for estimating genotype and environment main effects with principal component analysis (PCA) of the GEI, enabling effective partitioning and interpretation of interaction effects (Gauch 1988). Complementarily, GGE biplots focus on genotype main effects and GEI, providing a powerful graphical tool to visualize genotype performance, stability and the identification of mega-environments, as well as superior genotypes within each environment (Yan *et al.* 2000, Yan and Hunt 2002, Yan and Kang 2002).

Although finger millet is increasingly recognised for its nutritional and agronomic importance, systematic stability studies integrating AMMI and GGE biplot analyses across diverse agro-ecological environments remain limited, particularly for recently developed or region-specific genotypes. In this context, the present study was carried out to evaluate the magnitude and nature of genotype  $\times$  environment interaction for grain yield in finger millet, to assess the yield stability and adaptability of finger millet genotypes using AMMI and GGE biplot approaches, and to identify stable and high-performing genotypes and representative testing environments to support future breeding and varietal deployment strategies.

## MATERIALS AND METHODS

An experiment was conducted during the winter (*rabi*) season of 2022–23 and 2023–24. The study utilised 35 diverse genotypes (Table 1) of finger millet, which were obtained from AICRP Small Millet Research Station, Mandya, Karnataka; Indian Institute of Millets Research, Hyderabad and M S Swaminathan Research Foundation, Jeypore, Odisha. This experiment was laid out in randomised complete block design (RCBD) with three replications to assess genotype stability in response to environmental variation. Data on 15 quantitative traits were recorded to evaluate genotype  $\times$  environment (G $\times$ E) interactions and identify stable genotypes. The experiment was conducted across three distinct environments, viz. Ranadevi Farm, Centurion University of Technology and Management, Paralakhemundi, Odisha (E<sub>1</sub>); Research Farm, Narayan Institute of Agricultural Sciences, Sasaram,

Rohtas, Bihar (E<sub>2</sub>); and Zonal Adaptive Research Station, Birbhum, West Bengal (E<sub>3</sub>).

The statistical analyses were performed on mean values calculated for each genotype in each replication. All analyses were carried out using R statistical software (R Core Team). Pooled analysis of variance was conducted to test the significance of genotype, environment and genotype  $\times$  environment interaction effects for all 15 traits. AMMI analysis and associated biplots were generated using the agricolae package in R. The AMMI model utilises singular value decomposition (SVD) to partition the residual matrices after accounting for genotype and environment main effects, thereby effectively capturing non-linear genotype  $\times$  environment interactions. The AMMI analysis for grain yield was conducted using the model described by Gauch *et al.* (1996):

$$Y_{ij} = \mu + G_i + E_j + \sum_{k=1}^r \lambda_k \alpha_{ik} \beta_{jk} + \epsilon_{ij}$$

Where  $Y_{ij}$ , Mean yield of genotype  $i$  ( $i = 1, 2, \dots, 35$ ) in the environment  $j$  ( $j = 1, 2, 3$ );  $\mu$ , General mean;  $G_i$ ,  $i^{\text{th}}$  genotypic effect;  $E_j$ ,  $j^{\text{th}}$  environment effect;  $\lambda_k$ , Eigen value of the principal component analysis (PCA) axis  $k$ ;  $\alpha_{ik}$  and  $\beta_{jk}$  are the  $i^{\text{th}}$  genotype in  $j^{\text{th}}$  environment PCA scores for the PCA axis  $k$ ;  $\epsilon_{ij}$ , Residual. The GGE biplot approach, which partitions variation into genotype main effects and genotype  $\times$  environment interaction effects, was employed following the methodology described by Yan and Hunt (2002) and Yan *et al.* (2002). The GGE biplot model is expressed as:

$$Y_{ij} - \beta_j = \lambda_1 \xi_{i1} \eta_j + \lambda_2 \xi_{i2} \eta_{j2} + \epsilon_{ij}$$

Where  $Y_{ij}$ , Observed mean of genotype ‘ $i$ ’ in environment ‘ $j$ ’;  $\beta_j$ , Average yield across all genotypes in environment ‘ $j$ ’;  $\lambda_1$  and  $\lambda_2$ , Singular values for PC1 and PC2, respectively;  $\xi_{i1}$  and  $\xi_{i2}$ , PC1 and PC2 scores, respectively for genotype ‘ $i$ ’;  $\eta_j$  and  $\eta_{j2}$ , PC1 and PC2 scores, respectively for genotype ‘ $j$ ’;  $\epsilon_{ij}$ , Residual of the model associated with genotype ‘ $i$ ’ in environment ‘ $j$ ’.

The estimation and graphical visualisation of GGE biplots including discriminativeness vs. representativeness, mean vs. stability, which-won-where and relationships among environments were performed using the “GGE Biplot GUI” package (Frutos *et al.* 2014) implemented in R.

## RESULTS AND DISCUSSION

*Pooled analysis of variance based on AMMI model:* The AMMI analysis was conducted to evaluate the performance of 35 genotypes for 15 traits in three different environments. This approach efficiently distinguishes between additive main effects genotypes and environments and multiplicative components of genotype  $\times$  environment (G  $\times$  E) interaction through principal component analysis, thereby providing a comprehensive understanding of genotype responses across environments.

The combined analysis of variance (Table 2) revealed that environmental effects were highly significant for all traits except plant height. Traits such as biological yield/plant (2098.65), peduncle length (1858.99), days

Table 1 List of the finger millet genotypes assessed under three test environments during *rabi* 2023–24

S. No.	Genotypes	S. No.	Genotypes	S. No.	Genotypes	S. No.	Genotypes	S. No.	Genotypes
1	VL376	8	VR 1194	15	BR 14 28	22	Madli Muskuri	29	Bagadadli
2	IIMR 7028	9	VL 410	16	FM 1213	23	Muskuri	30	Telugu Mandia
3	FM PR 1731	10	VR 1238	17	VR 1200	24	Lalsuru Mandia	31	Chillika
4	VL 408	11	VR 1223	18	VR 1152	25	Bada Kumnda	32	Lala
5	FM WN 566	12	VR 1192	19	IIMR 7066	26	Badatara	33	Mami Mandia
6	KOPN 1055	13	IIMR 7202	20	KMR 1151	27	Dangardli	34	Bhairabi
7	VR 1174	14	VR 1184	21	Taya	28	Bada Mandia	35	KMR 301

Source: AICRP Small millet Research Station, Mandya, Karnataka; Indian Institute of Millets Research (IIMR), Hyderabad; and M S Swaminathan Research foundation, Jeypore, Odisha.

to maturity (1069.78) and 50% flowering (1513.74) were predominantly influenced by environmental variation, whereas plant height (236.98) showed non-significant variations. The analysis of genotype effects also indicated significant variability for all traits, with especially high values observed for biological yield/plant (189.22), plant height (39.27) and days to maturity (35.17). Furthermore, significant genotype-by-environment ( $G \times E$ ) interactions were found for all traits, highlighting differential genotype responses across environments. The magnitude of  $G \times E$  interaction was particularly high for traits such as biological yield/plant (97.03), plant height (39.67), 50% flowering (17.04), harvest index (14.471) and grain yield/plant (12.122). These results underscore that genotype performance for yield and its associated traits is strongly environment-dependent, emphasising the necessity of multi-environment testing for identifying stable and adaptable genotypes. Contrary to the present findings, several studies in finger millet have reported that environmental effects contributed the largest proportion of total variation in grain yield and related traits. Environmental effects accounting for the majority of yield variation, along with significant genotype  $\times$  environment interaction leading to inconsistent genotype performance across locations, have been reported in finger millet (Birhanu *et al.* 2016). A dominant contribution of environmental effects to total variation coupled with significant GEI was also observed in multi-environment evaluations of finger millet (Lakew *et al.* 2017). Similarly, strong environmental influence and significant  $G \times E$  interaction for grain yield, highlighting the necessity of stability analysis and multi-environment testing, have been reported in finger millet (Seyoum *et al.* 2019). Significant  $G \times E$  interactions have been reported in sorghum (Gudadinni *et al.* 2017), pearl millet (Govindaraj *et al.* 2019) and foxtail millet (Prakash and Reddy 2016). Likewise, strong  $G \times E$  interactions have also been documented in barnyard millet (Sood *et al.* 2015). Comparable trends highlighting the predominance of  $G \times E$  interaction have been reported in other field crops such as wheat (Dehghani *et al.* 2006), field pea (Tolessa *et al.* 2013) and maize (Swapnil *et al.* 2021, Swapnil *et al.* 2024). The observed variability in the relative contribution of genotype, environment and  $G \times E$  interaction across studies may be

attributed to differences in genetic material, number of test environments and environmental heterogeneity.

*GGE biplot analysis:* The highly significant  $G \times E$  interaction for grain yield across the three test environments highlighted the importance of multi-environment evaluation for identifying stable genotypes. The GGE biplot served as an efficient tool for precisely assessing genotype performance. In this framework, the horizontal axis (PC1) represents the main effect of genotypes, capturing the variation in yield, whereas the vertical axis (PC2) reflects the  $G \times E$  interaction, indicating the stability of genotypes across the tested environments. PC1 accounted 68.21% and PC2 showed 22.84%, thereby together accounting for 91.05% of the total yield variability (Fig. 1). This high proportion of explained variation demonstrates the effectiveness of the GGE biplot in reliably identifying high-yielding and stable genotypes while clearly differentiating test environments. Similar findings on the effectiveness of GGE biplots in assessing genotype performance, stability, and discriminative and representative test environments have been reported earlier (Yan and Tinker 2006). In finger millet, significant  $G \times E$  interaction for grain yield, with the first two principal components of the GGE biplot explaining more than 85% of the total variation and enabling the identification of high-yielding and stable genotypes, was also reported (Ishwarya *et al.* 2025). In the present experiment the biplot illustrated four key features: discriminativeness vs. representativeness, mean vs. stability, which-won-where biplot and relationship between the environments for grain yield/plant.

*Discriminativeness vs. Representativeness:* In the three environments, Odisha was the most discriminative, while West Bengal, with the shortest vector, was the most representative compared to Bihar and Odisha (Fig. 1). The trend, Odisha > Bihar > West Bengal, revealed that Bihar was both discriminative and representative, making it a suitable test environment for identifying generally adapted genotypes. Odisha, on the other hand, provided discriminative but not representative information about the genotypes, whereas West Bengal, though highly representative, offered limited information on genotype differentiation. These results indicated that Bihar can be considered an ideal environment for selecting widely

Table 2 Pooled analysis of variance (ANOVA) based on AMMI model for 15 traits in finger millet genotypes

Traits	Source of variation						Residuals	Total
	ENV	REP (ENV)	GEN	GEN × ENV	PC1	PC2		
FF	1513.74**	100.3**	11.78**	17.04**	22.89**	10.84**	4.01	18.76
FLBL	340.251**	12.705**	21.834**	8.423**	14.468**	2.013**	0.901	7.405
FLBW	3.110647**	0.012895**	0.157445**	0.071302**	0.11893**	0.02079**	0.000849	0.05634
PL	1858.992**	2.627**	3.488**	4.905**	7.338**	2.325**	0.179	11.927
EHL	69.4024**	0.8951**	0.5352**	0.2516**	0.4113**	0.0823**	0.0409	0.5365
FL	91.1436**	0.9392**	0.3479**	0.1467**	0.2088**	0.0808**	0.0378	0.5953
FW	0.772511**	0.009274**	0.080642**	0.038339**	0.05465**	0.02104**	0.000732	0.025408
NFME	4.4781**	0.238**	1.1667**	0.3753**	0.3892**	0.3605**	0.0229	0.2769
PH	236.98	108.79**	39.27**	39.67**	61.92**	16.06**	7.13	24.38
TTP	16.3261**	0.1997**	1.8178**	1.1314**	1.9777**	0.2337**	0.0194	0.6635
1000-GW	2.2875**	0.07459**	0.22399**	0.10226**	0.11868**	0.08484**	0.00398	0.07162
DM	1069.78**	156.85**	35.17**	31.87**	46.42**	16.44**	8.38	27.02
BYPP	2098.65**	138.21**	189.22**	97.03**	148.27**	42.7**	7.28	68.43
HI	80.215**	9.405**	15.033**	14.471**	20.353**	8.233**	0.604	7.381
GYPP	52.628**	10.086**	17.037**	12.122**	19.956**	3.812**	0.652	6.614

\*\* Significant at 1% level of probability. ENV, Environment; REP(ENV), Replication within each environment; GEN, Genotype; GEN × ENV, Interaction between genotype and environment; PC, Principle component; FF, Days to 50% flowering; FLBL, Flag leaf blade length (cm); FLBW, Flag leaf blade width (cm); PL, Peduncle length (cm); EHL, Ear-head length (cm); FL, Finger length (cm); FW, Finger width (cm); NFME, No. of fingers on main ear; PH, Plant height at maturity (cm); TTP, Total tillers/plant; 1000-GW, 1000-grain weight; DM, Days to maturity; BYPP, Biological yield/plant (g); HI, Harvest index (%); GYPP, Grain yield/plant (g).

adapted genotypes, whereas Odisha was more effective for identifying specifically adapted genotypes and West Bengal primarily served as a representative reference environment with limited discriminative capacity.

*Mean vs. Stability:* This biplot illustrates the mean grain yield and stability of genotypes across three different environments, which are marked in red- 1 (Odisha), 2 (Bihar) and 3 (West Bengal). Genotypes performing well

in Odisha were located along the rightward arrow, with genotype no. ‘9’ (VL 410) showing the highest yield potential in this environment (Fig. 2). For Bihar, genotypes such as ‘26’(Badatara) and ‘6’ (KOPN 1055), positioned with the diagonal pointing to the upper left, demonstrate better yield potential, indicating they are well-adapted to this environment. In West Bengal, genotypes like ‘26’

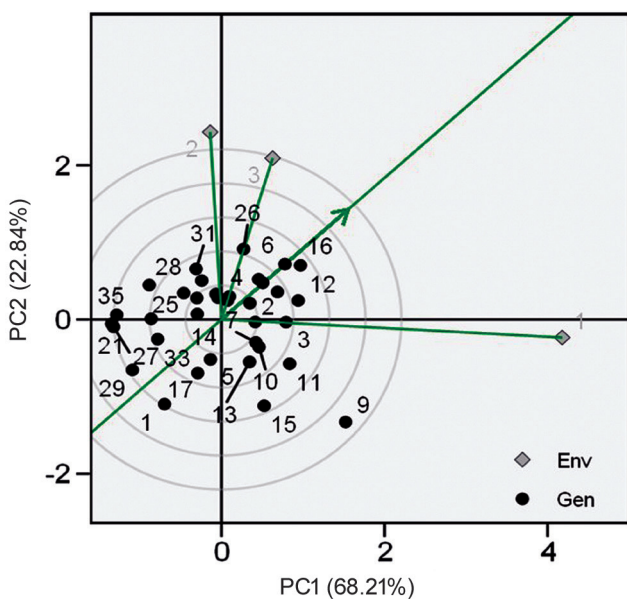


Fig. 1 GGE biplot representing “discriminativeness vs. representativeness”.

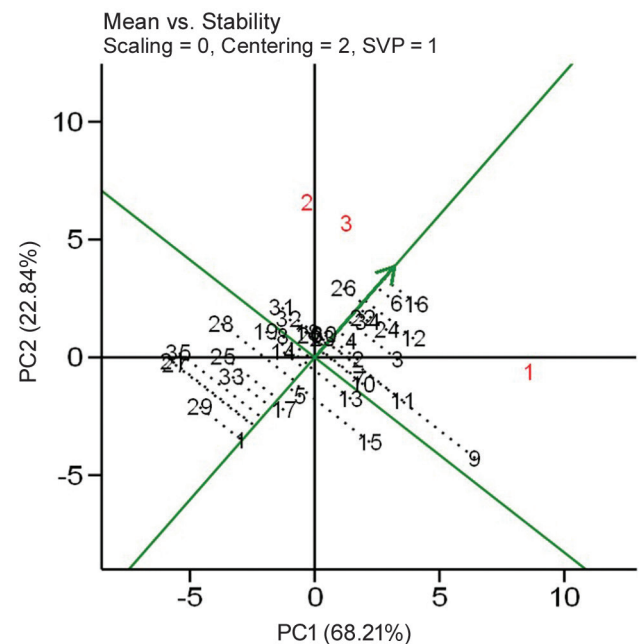


Fig. 2 GGE biplot representing “mean vs. stability”.

(Badatara) and ‘3’ (FM PR 1731), positioned along the upper-right diagonal, performed the best, showing higher grain yield potential. In terms of stability, genotypes closer to the centre of the biplot were considered more stable as they show less variability across different environments. For instance, genotypes ‘16’ (FM 1213), ‘31’ (Chillika), ‘3’ (FM PR 1731) were located near the centre, indicating consistent grain yield performance across the three environments. On the other hand, genotypes positioned farther away from the origin, such as genotype ‘9’ (VL 410) and ‘26’ (Badatara), showed greater variability, meaning their performance is more specific to particular environments and they may not perform consistently across all conditions.

**Which-won-where biplot:** The genotypes that performed best in each environment and which were the most appropriate for a given environment were identified through the "Which-won-where" GGE biplot. In the biplot, genotypes positioned at the vertices of the polygon represented either the highest or lowest performers in one or more of the environments (Fig. 3). All remaining genotypes were present within the polygon, which was designed to include those that were the farthest from the biplot origin. The polygon for grain yield per plant showed that in Odisha, the genotype ‘9’ (VL 410) showed the superior genotype along with ‘11’ (VR 1223), ‘13’ (IIMR 7202) and ‘15’ (BR 14 28), as they were along the vertices of the polygon. Whereas in Bihar, ‘26’ (Badatara) showed the superior performance and in West Bengal, the genotypes ‘16’ (FM 1213) and ‘6’ (KOPN 1055) were along the vertices showed the superiority followed by the genotypes like ‘26’ (Badatara), ‘22’ (Madli Muskuri), ‘24’ (Lalsuru Mandia) and ‘34’ (Bhairabi), respectively. GGE biplot analysis of finger millet genotypes across multiple locations revealed distinct environment-specific winning genotypes, where the which-won-where polygon delineated three mega-environments with different superior genotypes, and PF8 was identified as the most desirable genotype

based on high mean yield and stability (Bandhyopadhyay *et al.* 2023).

**Relationship among environments:** The angles between environment vectors in a GGE biplot represent the correlation among environments, with acute angles (<90°) indicating positive correlations and smaller angles reflecting stronger associations. In the present study (Fig. 4), the environments Odisha, Bihar, and West Bengal exhibited acute angles between their vectors, indicating a positive correlation for grain yield performance across locations. This suggests that finger millet genotypes responded in a broadly similar manner across these environments, and genotypes performing well in one location are likely to perform well in the others. Similar positive relationships among environments inferred from acute angles in the GGE biplot, indicating consistent genotype performance patterns across locations, have been reported in finger millet evaluated across agro-climatic zones of Andhra Pradesh (Madhavalatha *et al.* 2023).

The pooled AMMI analysis revealed that environmental effects were highly significant for most traits, while genotype and G × E interactions were significant for all traits, particularly grain yield, biological yield, harvest index, and flowering traits, highlighting differential genotype responses. GGE biplot analysis explained 91.05% of total variation (PC1 = 68.21%, PC2 = 22.84%), with Odisha being the most discriminative, West Bengal the most representative, and Bihar both discriminative and representative, identifying Bihar as the ideal test environment for broadly adapted genotypes. Genotypes ‘16’ (FM 1213), ‘31’ (Chillika), and ‘3’ (FM PR 1731) were highly stable across environments, while ‘26’ (Badatara) combined high yield with moderate stability. The which-won-where biplot confirmed environment-specific superior genotypes, and acute angles among environment vectors indicated positive correlations, suggesting consistent genotype performance

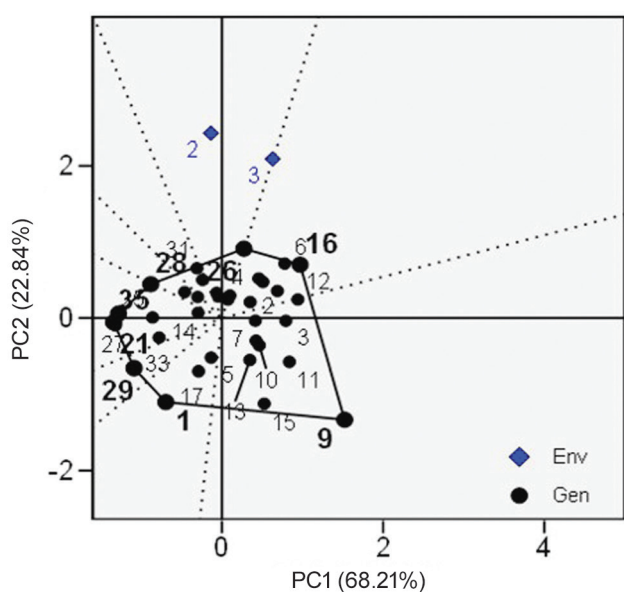


Fig. 3 “Which-won-where biplot” GGE biplot of the genotype × environment interaction.

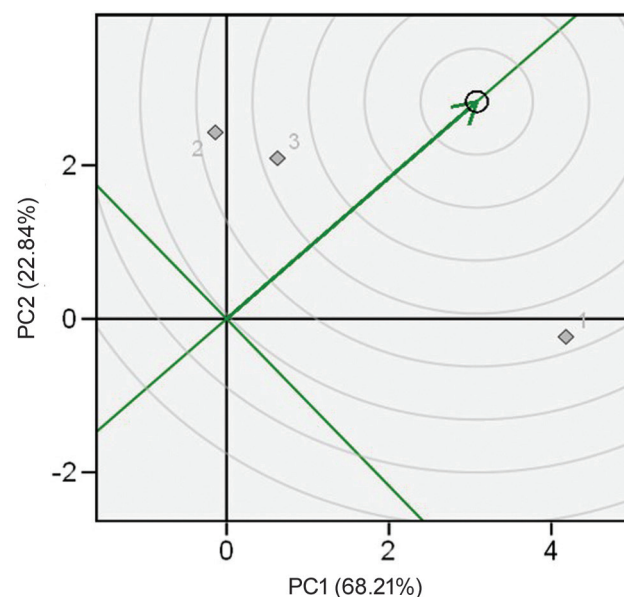


Fig. 4 GGE biplot representing “relationship among environments”.

across locations. Overall, AMMI and GGE biplot analyses effectively identified high-yielding, stable genotypes and suitable test environments for targeted finger millet breeding.

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