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RESEARCH ARTICLE

Multi environment stability analysis of maize (*Zea mays*) inbreds using AMMI and GGE biplot models

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Abstract

This study investigates the impact of heat stress on the stability and adaptability of maize genotypes across three environments Odisha, Jharkhand and Bihar during 2022-2023. A total of 54 maize inbred lines, along with two check varieties (56 genotypes), were evaluated using an alpha-lattice design with two replications. Data were recorded for 18 quantitative traits and stability analysis was conducted using both Additive Main Effects and Multiplicative Interaction (AMMI) and Genotype plus Genotype × Environment interaction (GGE) biplot models. Pooled ANOVA revealed significant effects for genotypes and environments across all traits, except anthesis-silking interval and brown husk. The mean squares due to genotypes were notably high for grain yield per plant (94058.26), grain weight (23656.84), plant height (1962.3), ear height (691.99), kernel per row (245.06) and chlorophyll content (53.8). Similarly, environments showed significant contributions, with grain weight (11034.5), grain yield per plant (1522), kernel per row (737.15), anthesis-silking interval (603.26), plant height (411.6) and brown husk (350.26) exhibiting substantial variation. The G × E interaction was highly significant for most traits, with grain weight (453.3), grain yield per plant (282.3), brown husk (24.99), plant height (22.76), days to silking (16.91) and days to anthesis (14.36) being particularly important contributors. Partitioning of G × E revealed that IPCA I was significant for traits such as days to 50 % anthesis, days to silking, ears per plant, chlorophyll content, plant aspect, grain yield per plant, cob length, grain weight, kernels per row and kernel rows per cob, while IPCA II was non-significant across traits (values ranging from 0.018 for brown husk to 59.63 for grain weight) and PC3 was zero for all traits. GGE biplot analysis identified genotypes VL1010764, KL155991, KL156009 and KL155979 as high performing under heat stress conditions, whereas VL143892, VL143905, KL155989, KL156003, VL13853, KL155739, VL18333, VL18334, VL143891 and KL153072 demonstrated consistent stability across all environments. These findings provide critical insights into the identification of heat-resilient and stable maize genotypes. The integration of AMMI and GGE biplot models strengthens the precision of selection under heat stress, thereby supporting breeding programs aimed at enhancing climate resilience and ensuring maize productivity in the face of rising global temperatures.

Keywords: ANOVA; food security; grain yield per plant; G × E interactions; heat-resilient

Introduction

The surging global demand for maize, driven by its diversified uses in animal feed, biofuel production and direct human consumption, presents substantial challenges for global agriculture. This demand is expected to intensify, with global maize consumption projected to rise by 23 million tons by 2029, a significant portion of which will be met by sub-Saharan Africa (SSA) (1, 2). SSA, where maize serves as both a staple food crop and an economic driver, is increasingly under pressure to boost production amidst worsening climatic and agronomic constraints.

Despite its importance, maize cultivation in SSA remains vulnerable to a multitude of biotic (e.g., diseases and pests) and abiotic (e.g., drought, heat and nutrient deficiency) stresses that cause substantial yield losses annually (3, 4). The situation is further aggravated by global climate change, which is leading to rising temperatures and erratic rainfall patterns, especially during critical phenological stages such as flowering and grain filling. These high-temperature stress episodes can lead to pollen sterility, reduced kernel set and ultimately drastic yield reductions (5, 6).

Recent IPCC reports and regional climate models indicate that SSA is likely to experience more frequent and intense heatwaves over the next few decades, exacerbating the production challenges for temperature-sensitive crops like maize. Consequently, there is an urgent need to develop heat stress-resilient maize genotypes capable of sustaining productivity under such conditions. Conventional breeding methods, though effective, require robust multi-environment testing (MET) to accurately identify and select genotypes that demonstrate stable performance across variable environments, especially under heat stress conditions.

To address this critical need, the present study aims to conduct a comprehensive stability analysis of maize genotypes under heat stress. Advanced statistical tools such as the Additive Main Effects and Multiplicative Interaction (AMMI) model and the Genotype plus Genotype x Environment Interaction (GGE) biplot analysis are utilized. These models not only assess the genotypic performance across diverse environments but also help visualize and interpret the genotype-by-environment (G×E) interactions, providing critical insights into the stability and adaptability of different maize lines (1, 7).

Recent studies have demonstrated the effectiveness of GGE and AMMI models in screening heat-tolerant maize varieties across South Asia and SSA, making them indispensable tools in modern plant breeding programs (8, 9). Moreover, integrating phenotypic data with environmental covariates and possibly genomic selection tools in future studies can further enhance the predictive accuracy and efficiency of selection.

Thus, the outcomes of this research are expected to guide breeding programs in developing climate-resilient maize varieties, contributing not only to regional food security but also to the global maize value chain, particularly under the impending threat of climate change.

Materials and Methods

The experimental material used in the present investigation consisted of 54 inbred lines of maize (*Zea mays*) and 2 check varieties (Table 1.) which were obtained from ARS, Peddapuram. The experimental trial was sown in alpha lattice design with two replications during the spring, 2022-23 to carry out the stability analysis by evaluating the stable inbreds in relation to the environmental effects. The experiments were conducted at Post Graduate Farm, Centurion University of Technology and Management (CUTM), Paralakhemundi, Odisha as well as two additional locations in Narayan Institute of Agricultural Sciences, Rohtas, Bihar and Birsa Agricultural University (BAU), Jharkhand during spring, 2023 to determine their stable performance across the 3 locations. The observations were recorded to understand the extent of genetic variability, diversity and stability of inbred lines for eighteen quantitative traits. The observations *viz.,* plant height, ear height, ears per plant, ear aspect, plant aspect, leaf death, number of kernel rows per ear, number of kernels per row, 1000 grain weight, cob length and cob girth were taken from 5 random selected plants of each genotype. Further observations such as days to 50 % anthesis, days to 50 % silking, anthesis silking interval, tassel blast, grain yield were taken on plot basis in three different environments under heat stress as per the standards of abiotic stresses. Data were recorded on individual plant and plot basis for grain yield, yield attributing characters and stress related traits at the appropriate growth stage of the crop. The GGE biplots have been interpreted for four major yield-attributing traits like grain yield per plant, kernels per row, kernel rows per cob and 1000 grain weight. These measurements provided the basis for assessing genotypic performance and stability across environments.

Statistical analysis

Analysis of variance over the environments

The pooled analysis of variance can be further extended in which the total mean squares may be partitioned into various components. In this model, the total variance is first divided into two components, *i.e.*,

i) genotype and

ii) environment plus interaction (E + (G × E)).

The second component is further sub-divided into three components, *viz.,* (a) environment linear, (b) genotype x environment (linear) and (c) pooled deviations. The variance due to pooled deviations is further divided into variance due to individual genotype.

The additive main effect and multiplicative interaction (AMMI) model

It can effectively explain G × E interaction, identify genotypes for specific and wide adaptation and measures the genetic gain in plant breeding programmes. The AMMI model analyses the additive effect of genotype and environment (location) by a

Table 1. List of genotypes used in the study

S. No	Genotypes	S. No	Genotypes	S. No	Genotypes	S. No	Genotypes
1	VL1110501	15	VL107406	29	VL143892	43	KL153241
2	VL1110514	16	VL109452	30	VL154632	44	KL154688
3	VL1110517	17	VL109457	31	VL162206	45	KL155738
4	VL1110519	18	VL109499	32	VL144234	46	KL155739
5	VL1110532	19	VL109501	33	Vl143891	47	KL154714
6	VL1110458	20	VL18444	34	KL154678	48	KL153072
7	VL111341	21	VL18211	35	KL155993	49	KL153092
8	VL111341	22	VL18327	36	KL155994	50	KL155978
9	VL1017169	23	VL18333	37	KL155988	51	KL155973
10	VL1016417	24	VL13692	38	KL155989	52	KL155974
11	VL1016452	25	VL13853	39	KL155991	53	KL155979
12	VL1016977	26	VL18523	40	KL156003	54	KL153093
13	VL1017223	27	VL143903	41	KL156009	55	VL13691
14	VL1010764	28	VL143905	42	KL154685	56	VL18334

standard analysis of variance (ANOVA) and the multiplicative effects of the GEI by using a multivariate technique *i.e.* principal component analysis (PCA). The numbers of AMMI family are identified according to number of PCA axis. One PCA axis, it is defined as AMMI1 and two PCA axis, it is defined as AMMI2 and so on. The multivariate analyses reveal the structure of data, summarize the data and eliminate the noise from data pattern. AMMI combines analysis of variance (ANOVA) and principal component analysis (PCA) into a single model with additive and multiplicative parameters. AMMI analysis was carried out using R software v4.0.2.

GGE Biplot (Genotype + Genotype × Environment interaction)

The GGE biplot methodology originates from graphical analysis of multi-environment variety trials (MET) data. The GGE Biplot model was introduced based on biplots, which are an effective tool for visualizing two-way data and are frequently used for the analysis of MET data (10) . A GGE biplot can simultaneously display genotype main effects (G) and genotype × environment effects (GE) from a two-way data table (10). here, it depicts 4 main components, those are discriminativeness vs representativeness, mean Vs stability, which won where biplot, relationship among the environments. The GGE biplots have been interpreted for four major yield-attributing traits like grain yield per plant, kernels per row, kernel rows per cob and 1000 grain weight.

Using both AMMI and GGE biplot approaches together enhances insights: while AMMI rigorously quantifies component effects (G, E, GEI), GGE biplot adds a powerful, intuitive graphical representation. Studies have shown that combining these methods is particularly effective for comprehensive genotype selection and environment evaluation in maize breeding.

Results and Discussion

In this study, fifty-six maize genotypes were evaluated across the 3 locations (Odisha, Jharkhand and Bihar) to carry out the stability analysis by evaluating the stable inbreds in relation to the environmental effects using pooled analysis of variance based on the Additive Main Effects and Multiplicative Interaction (AMMI) model. Comparable results were also reported, emphasizing the importance of coefficient of variation (CV) in assessing environmental consistency in breeding trials (8).

Pooled analysis of variance based on AMMI model

The pooled analysis of variance of fifty-six maize genotypes for eighteen characters using the AMMI model is presented in Table 2. The mean squares due to genotypes were significant for all traits except anthesis-silking interval and brown husk, while environments showed significance across all characters studied. The G × E interaction was highly significant for most traits, except ear aspect, chlorophyll content, anthesis-silking interval, leaf death, tassel blast, cob length, cob girth and kernel rows per cob (11). This interaction was partitioned into three interaction principal component analysis (IPCA) axes, with IPCA-1 being significant for traits such as days to 50 % anthesis, days to silking, anthesis-silking interval, brown husk, ears per plant, chlorophyll content, plant aspect, grain yield per plant, cob length, grain weight, kernels per row and kernel rows per cob, confirming the discriminative capacity of IPCA-1 for major agronomic traits (12, 13).

In contrast, IPCA-II was non-significant for all traits, with values ranging from 0.018 (brown husk) to 59.63 (grain weight), while PC3 values remained zero. Residuals ranged from 0.017 (ears per plant) to 236.21 (grain weight). Variance analysis across various traits indicated maximum variance for grain weight (892.54), followed by grain yield per plant (557.01), brown husk (49.26), plant height (44.92), days to silking (33.27) and days to anthesis (28.29), reflecting their major contributions.

Environmental mean sums square further emphasized significant effects, particularly for grain weight (11034.5), grain yield per plant (1522), kernels per row (737.15), anthesis-silking interval (603.26), plant height (411.6) and brown husk (350.26). Comparable studies in maize and wheat reported similar outcomes, where IPCA-I captured core interaction effects and grain yield traits exhibited the highest variance, validating their role in selection across environments (14, 15). In multi environment maize trials, IPCA-II also failed to achieve statistical significance, while grain yield and weight consistently displayed maximum variance, underscoring their importance in breeding programs (11).

Table 2. Pooled analysis of variance for eighteen quantitative traits in maize

Sources of variation	ENV	GEN	ENV*GEN	PC1	PC2	Residuals
DTA	247.34	18.81	14.36	26	2.29	9.52
DTS	331.5	19.25	16.91	31.74	1.53	12.73
ASI	603.26	5.55	10.68	20.46	0.54	10.78
BHK	350.26	20.77	24.99	44.23	5.03	16.56
LDT	1.17	3.12	0.05	0.09	0.02	1.09
EHT	97.52	691.99	7.95	10.87	4.93	6.24
PHT	411.6	1962.3	22.76	39.12	5.8	38.58
EPP	0.008	0.4	0.01	0.03	0	0.01
EAT	3.92	7.72	0.17	0.31	0.03	0.38
CHC	10.95	53.8	0.86	1.38	0.33	0.91
PLA	0.53	6.423	0.032	0.058	0.004	0.02
GPP	2.33	7.34	0.12	0.23	0.01	0.17
TBT	11.77	35.88	1.7	2.74	0.62	1.56
COL	10.12	20.9	0.76	0.94	0.57	0.67
COG	11034.5	23656.84	453.3	832.91	59.63	236.21
GWT	737.15	245.06	12.95	23.21	2.3	6.65
KPR	113.44	46.92	2.28	3.69	0.83	1.92
KRC	1522.26	94058.26	282.8	514.77	42.24	145.88

DTA=Days to Anthesis, DTS=Days to silking, ASI=Anthesis-silking interval, BHK=Brown husk, LDT=Leaf death, EHT=Ear height, PHT=Plant height, EPP=Ears per plant, EAT=Ear Aspect, CHC=Chlorophyll content, PLA=Plant Aspect, GPP=Grain yield per plant, TBT=Tassel Blast, COL=Cob length, COG=Cob girth, GWT=Grain weight, KPR=Kernel per row, KRC=Kernel rows per cob.

The mean sum squares due to genotypes highlighted strong contributions from grain yield per plant (94058.26), grain weight (23656.84), plant height (1962.3), ear height (691.99), kernels per row (245.06) and chlorophyll content (53.8), whereas anthesis silking interval and brown husk were non-significant. Similar environmental effects on grain traits and plant architecture were reported earlier in multi-environment trials (16, 17). The G × E interaction also revealed notable contributions for grain weight (453.3), grain yield per plant (282.3), brown husk (24.99), plant height (22.76), days to silking (16.91) and days to anthesis (14.36), reaffirming their importance in genotype evaluation. These findings are consistent with earlier studies highlighting the significance of these traits in dissecting G × E interactions (9, 11).

Interpretation of GGE biplots and its components

The graphical representation provides insight into genotype and genotype × environment interaction. It comprises four primary components: discriminativeness versus representativeness, mean versus stability, which-won-where biplot and relationship among the environments. The GGE biplots have been analysed specifically for four major yield-contributing traits: grain yield per plant, kernels per row, kernel rows per cob and 1000 grain weight.

Grain yield per plant

Discriminativeness vs representativeness

The GGE biplot (Fig. 1) illustrates discriminativeness through concentric circles representing the standard deviation within each environment, where longer vectors signify greater discriminatory power. Among the test sites, Bihar exhibited the highest discriminative ability. Representativeness was assessed using the average environmental axis (AEA), with environments positioned closer to this axis considered more representative. Bihar and Jharkhand were found to be more representative than Odisha, making them optimal for genotype selection. Similar findings were reported by (18, 19), where environments with both high discriminative ability and representativeness such as certain eastern Indian states were identified as most effective for selecting stable, high-yielding maize hybrids using GGE biplot analysis.

Mean vs stability

The "Mean vs. Stability" biplot (Fig. 1) evaluates both genotype performance and stability. Genotypes positioned farther to the right indicate higher yield potential, whereas those on the extreme left reflect poor performance. Along the y-axis, higher values represent greater variability, while lower values denote

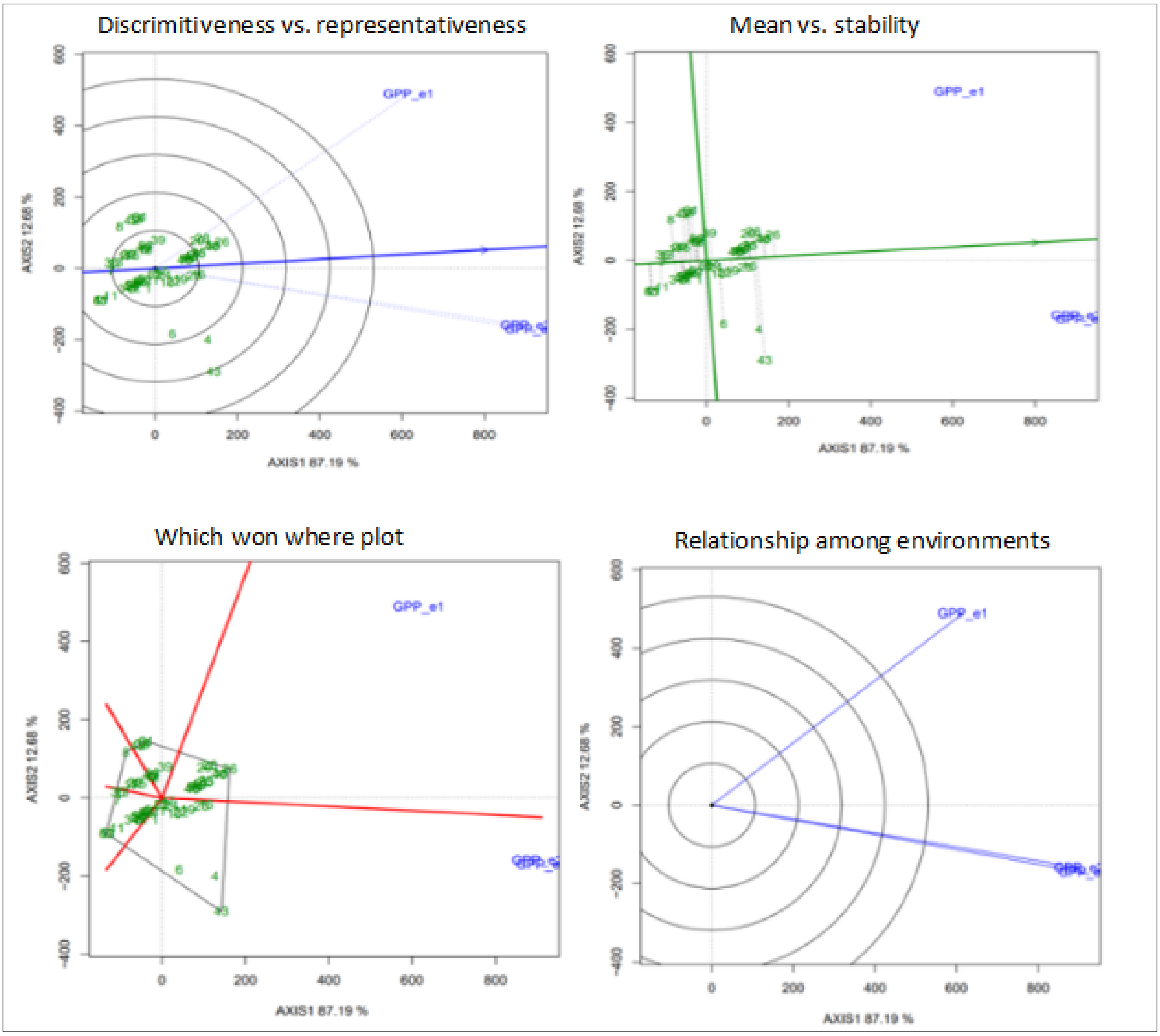

Fig. 1. GGE biplot of grain yield per plant in maize genotypes.

stability. Genotype VL18523 recorded the highest yield potential, while KL155994 performed poorly. In contrast, genotypes such as KL155991, with lower y-axis values, demonstrated greater stability. Similar observations were reported in maize (20), where high-yielding and stable genotypes were identified through GGE biplots. This method was also successfully applied in wheat for recognizing multi-environment stable performers under diverse climatic zones (21).

Which won where biplot

The biplot (Fig. 1) highlights the top-performing genotypes in each environment and their adaptability across locations. Genotypes located at the polygon vertices represent the best performers in specific environments. For grain yield per plant, VL18523 was superior in Odisha, while KL153241 performed best in Jharkhand and Bihar. Additional genotypes such as VL1110519 and VL1110458 also exhibited promising performance in certain environments. Similar findings were reported where GGE biplots were applied in rice to assess regional adaptability and in maize to identify climate-resilient genotypes (22, 23).

Relationship among environments

The relationship among environments was assessed through the angles between vectors, which indicate correlation coefficients smaller angles suggesting stronger correlations. The analysis revealed positive correlations among Odisha, Jharkhand and Bihar, with the strongest relationship observed between Jharkhand and Bihar, followed by Odisha. This indicates consistent performance patterns across environments. Comparable results were documented in wheat studies, where strong inter-environmental correlations were observed across the Indo-Gangetic Plain (12). Likewise, clustering of environments in GGE biplots has been shown to aid mega-environment identification and regional breeding strategies in rice (24).

Kernels per row

Discriminativeness vs representativeness

The GGE biplot (Fig. 2) illustrates the discriminative and representative capacities of the three environments Odisha, Jharkhand and Bihar based on the angle between the Average Environmental Axis (AEA) and environment vectors. Jharkhand demonstrated both high discriminativeness and representativeness, making it ideal for selecting generally adapted genotypes for the kernel per row trait. In contrast, Odisha was discriminative but lacked representativeness, while Bihar, though highly representative, was non-discriminative and offered limited information for genotype differentiation. Similar outcomes were reported in earlier studies on multi-environment GGE analyses of maize kernel traits (18).

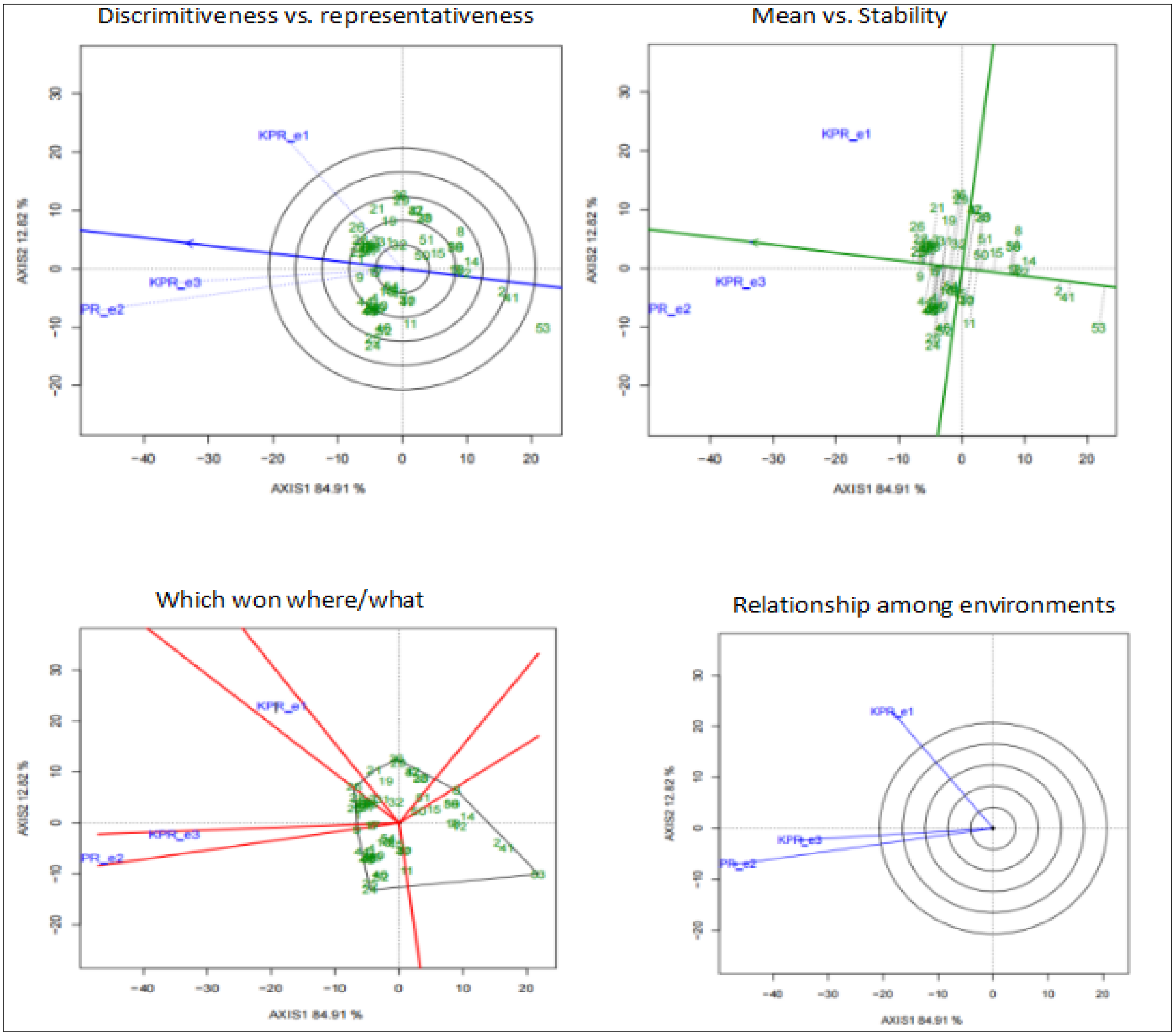

Fig. 2. GGE biplot of kernels per row in maize genotypes.

Mean vs stability

The biplot (Fig. 2) presents genotypes based on their variability and stability. Genotype KL155979 recorded the highest number of kernels per row, confirming its superiority, whereas VL1017169 showed the lowest count, indicating poor performance. Genotypes KL15594 and KL15591 displayed high variability, while VL144234 emerged as a stable genotype. Similar findings were reported in earlier studies examining genotype-by-environment interaction in maize hybrids (25).

Which won where biplot

The vertices of the polygon in the biplot (Fig. 2) represent the best-performing genotypes in each environment. In Bihar, KL155979 was identified as the top performer, followed by VL111341, whereas VL1017169 showed poor performance. In Odisha, KL155994, VL143892 and VL18523 emerged as winning genotypes, while in Jharkhand, VL13692 and VL13853 exhibited superior performance. Similar observations were reported in earlier studies on maize trials where location-specific winners were identified using the polygon view approach (26).

Relationship among environments

The relationship among environments revealed that Bihar formed the smallest angle with the average environmental axis, indicating the strongest positive correlation with other environments, followed by Jharkhand and then Odisha. This alignment suggests consistent performance trends across the environments.

Kernel row per cob

Discriminativeness vs representativeness

Analysis of the GGE biplot (Fig. 3) shows that Odisha is the most discriminative environment, followed by Bihar and then Jharkhand. However, in terms of representativeness, Jharkhand ranks highest, ahead of Bihar and Odisha. This trend highlights Bihar as both discriminative and representative, making it the most suitable environment for evaluating generally adapted genotypes. Jharkhand contributes discriminative but less representative insights, whereas Odisha, despite being relatively representative, provides limited genotype information. Similar findings were reported in a multi-location maize breeding program in eastern India, where Bihar was emphasized for its dual utility in selection (27).

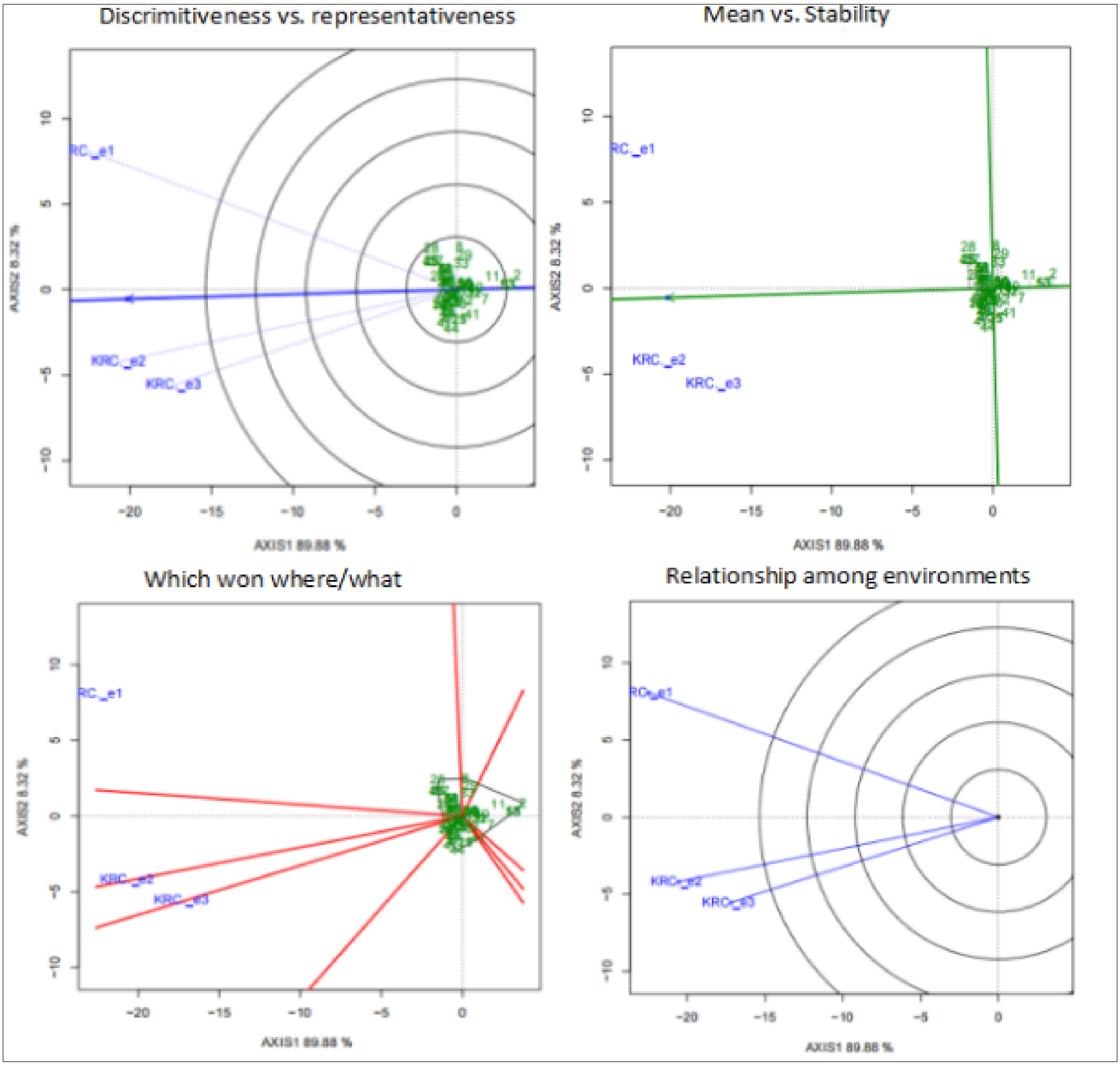

Fig. 3. GGE biplot of kernel row per cob in maize genotypes.

Mean vs stability

From the mean vs. stability plot (Fig. 3), genotype VL1110514 recorded the highest kernel rows per cob in Jharkhand, followed by KL155979 and VL1016452. In Odisha, VL111341 showed the highest magnitude, with VL143892 and VL143891 also performing strongly, though with greater variability. In contrast, KL155978 emerged as the most stable genotype, while several other variants performed poorly, particularly in Bihar. Similar findings were reported earlier, where specific genotypes demonstrated both high performance and stability across states in eastern India (28).

Which won where biplot

In the "which won where" biplot (Fig. 3), genotypes VL1110514, VL111341, VL143905 and KL154688 occupy the polygon vertices. Among these, VL1110514 recorded the highest kernel rows per cob, making it the top-performing genotype. Similar findings were reported where vertex genotypes were identified as environment-specific winners for kernel traits in maize (29).

Relationship among environments

The relationship among environments Odisha, Jharkhand and Bihar also shows positive correlations, as indicated by the biplot. The angles between environment vectors are less than 90°, suggesting that improvement in kernel rows per cob in one environment positively influences performance in the others. This direct proportionality reflects consistent performance trends across environments. Similar results were observed in maize and sorghum trials conducted across multiple Indian locations (12).

Grain weight

Discriminativeness vs representativeness

In the graph (Fig. 4), Odisha displayed the widest angle among the environments, identifying it as the most discriminative, followed by Bihar and then Jharkhand (Odisha > Bihar > Jharkhand). In terms of representativeness, Jharkhand ranked highest, followed by Bihar and Odisha. Notably, Odisha was also reported as a strongly discriminative environment in multi-environment maize trials conducted in eastern India (21).

Mean vs stability

In the graph (Fig. 4), genotype KL156009 recorded the highest grain weight, while KL155979 exhibited the highest magnitude along the y-axis in both Jharkhand and Bihar. In Odisha, VL1010764 was identified as the most stable genotype. Similar findings were reported, where high yielding but moderately stable maize genotypes were considered preferable for breeding programs targeting eastern India (27).

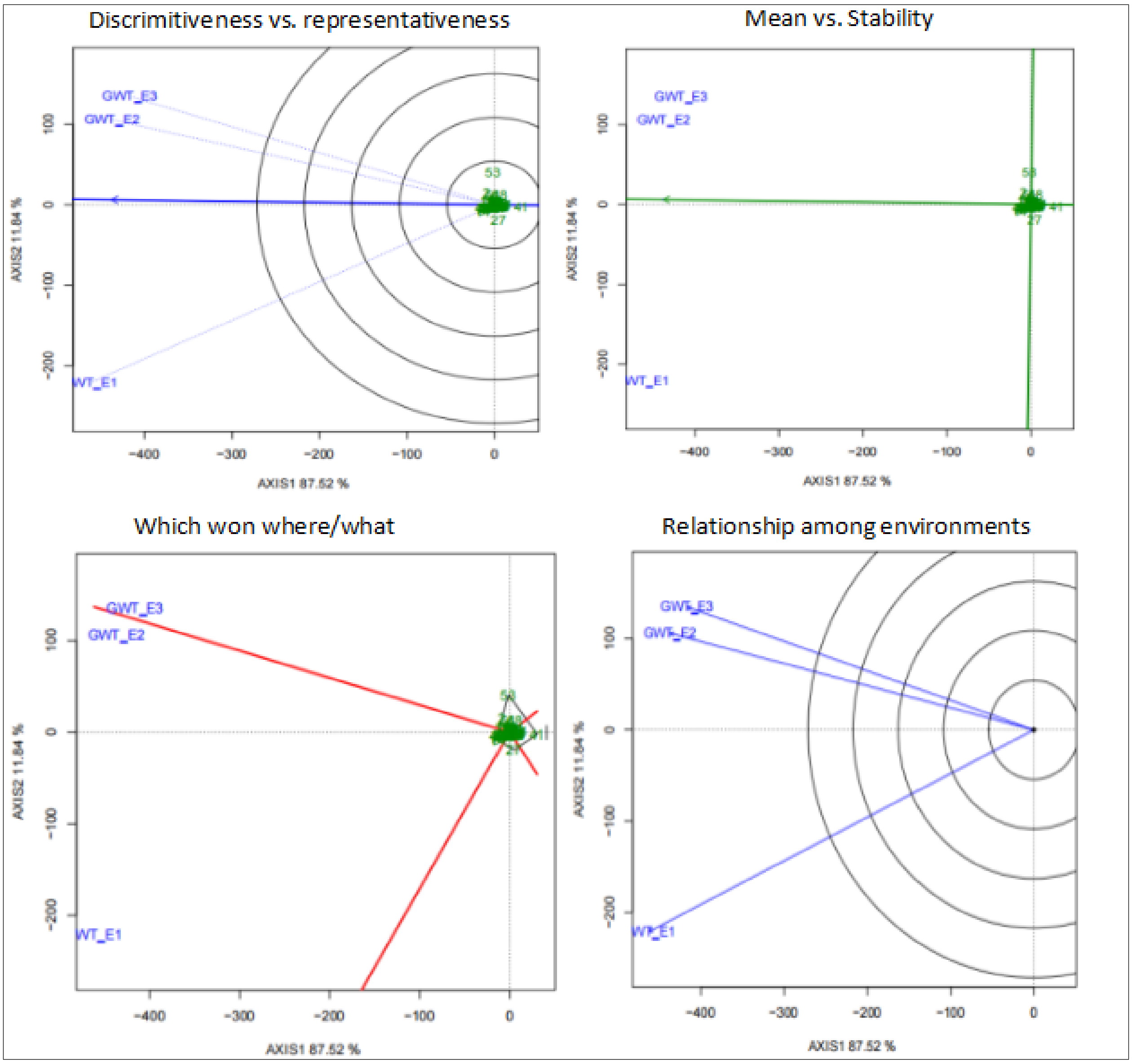

Fig. 4. GGE biplot of grain weight in maize genotypes.

Which won where biplot

In which won where biplot, Fig. 4 the genotypes KL155979, KL156009, VL111341, VL143903 were joined along the vertices of the polygon which represented the winning genotype, however KL156009 showed the highest grain weight.

Relationship among environments

The relationship among the environments showed a positive correlation between three environments Odisha, Jharkhand and Bihar as the angle were less than 90°. It means that grain weight in Odisha is directly proportional to grain weight in Jharkhand and Bihar.

The results highlight the differential sensitivity of maize genotypes to heat stress, underscoring the importance of genetic factors in plant responses. Several genotypes showed strong performance under stress across variable environments. Notably, VL1010764, KL155991, KL156009 and KL155979 demonstrated superior resilience, marked by reduced tassel blast, lower leaf death and better overall plant and ear health. Bihar emerged as the most effective environment for discriminating genotype performance. Similar findings reported maize genotypes with enhanced tolerance under high-temperature stress in eastern India, characterized by reduced tassel blast and leaf senescence (28).

Mean vs. stability plots identified KL156003, VL143892, VL143905, VL13853 and KL155738 as high-yielding and stable across environments, while the GGE biplot recognized genotypes VL18523, KL153241, KL155979 and VL111341 as robust performers. Additionally, genotypes VL143892, VL143905, KL155989, KL156003, VL13853, KL155739, VL18333, VL18334, VL143891 and KL153072 consistently demonstrated stability across all test locations. Similar outcomes were reported where maize hybrids combined high yield with environmental stability across multi location trials in eastern and central India (12).

The study's findings align with earlier research on genotype-environment (G × E) interactions, validating the utility of AMMI and GGE biplot models in stability analysis. Comparable to previous studies (11), this works also revealed significant environmental influences on maize yield, with grain yield and related traits contributing strongly to G × E interactions. GGE interpretations on discriminativeness, representativeness and stability further corroborate earlier reports on maize hybrids and other crops (29, 30). "Which-won-where" biplot analyses confirmed environment-specific winners, consistent with earlier observations that highlighted the role of regional adaptability in breeding (11, 31, 32).

These parallels reinforce the robustness of AMMI and GGE biplot models as tools for interpreting G × E interactions and guiding the selection of stable, high-yielding genotypes across environments (14, 15, 33). The identification of environment-specific and broadly adapted heat-tolerant maize hybrids, as also demonstrated in other studies across South Asia's climate-vulnerable zones (29, 19), offers valuable opportunities for developing climate-resilient varieties. Such findings hold strong implications for advancing breeding strategies and ensuring global food security (34, 35).

Conclusion

The GGE biplot analysis highlights that among the three test environments, Bihar (E3) emerged as the most discriminative and representative site, making it the most reliable for selecting generally adapted inbreds. Jharkhand also correlated strongly with Bihar in terms of grain yield, while Orissa showed superiority specifically in grain weight. Overall, positive correlations across environments were evident for yield-related traits. Key inbreds showing trait-specific superiority included VL18523 for grain yield per plant, KL155979 for kernels per row, VL1110514 for kernel rows per cob and KL156009 for grain weight, while KL155991, VL144234, KL155978 and VL1010764 displayed strong stability across environments. The "Which-Won-Where" analysis further confirmed inbreds such as KL155979, VL111341, KL155994 and VL143892 as strong performers in specific environmental niches. Importantly, the study identified highly resilient and heat-tolerant inbreds VL1017223, VL1010764, VL144234, KL155993, KL155991, KL156009 and KL155979 based on key stress indicators like tassel blast, leaf death and plant and ear traits. Vertex inbreds VL18523, KL153241, KL155979 and VL111341 were additionally marked as robust performers across environments. In terms of yield stability combined with adaptability, inbreds KL156003, VL143892, VL143905, VL13853 and KL155738 demonstrated high productivity while maintaining stability, with VL143892, VL143905, KL155989, KL156003, VL13853, KL155739, VL18333, VL18334, VL143891 and KL153072 consistently stable across all environments. In conclusion, E3 (Bihar) stands out as the most effective environment for selection, while specific high-performing inbreds such as VL18523, KL155979, KL156009 and VL1110514, alongside stress-resilient lines like KL155991, VL1010764 and VL144234, represent valuable genetic resources for maize breeding under heat stress and multi-environment conditions. The study effectively demonstrated the utility of AMMI and GGE biplot models in dissecting G × E interactions and identifying stable, high-yielding maize genotypes under heat stress across eastern India. Significant genotypic and environmental effects were observed, particularly for grain yield and grain weight. Genotypes like KL156003, VL143892 and VL13853 emerged as both high-performing and stable across diverse environments. These insights are valuable for breeding climate-resilient maize varieties suited for stress-prone regions, thereby supporting sustainable crop improvement and food security.

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Authors' contributions

The research work was conceptualized and designed by BSP and SK. Field and laboratory experiments, along with data collection, were executed by BSP, SK, PK and DVS. Data analysis and interpretation were conducted by LKM, VKS, SR, RKS, DKR and MKS. Reference articles were collected by VKS, RKS, DKR and LKM. The manuscript was prepared by BSP, SK, PK, MKS and DVS. All authors read and approved the final manuscript.

Compliance with ethical standards

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

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References

1. FAO. OECD-FAO Agricultural Outlook 2020-2029. Paris: OECD Publishing; 2020.
2. Shiferaw B, Prasanna BM, Hellin J, Banziger M. Crops that feed the world 6. Past successes and future challenges to the role played by maize in global food security. Food Secur. 2011;3(3):307-27. https://doi.org/10.1007/s12571-011-0140-5
3. Prasanna BM, Cairns JE, Zaidi PH. Addressing abiotic stresses in maize: Challenges and opportunities. Agronomy. 2021;11(8):1577.
4. Cairns JE, Prasanna BM. Developing and deploying climate-resilient maize varieties in the developing world. Curr Opin Plant Biol. 2018;45:226-30. https://doi.org/10.1016/j.pbi.2018.05.004
5. Lobell DB, Gourdji SM. The influence of climate change on global crop productivity. Plant Physiol. 2012;160(4):1686-97. https://doi.org/10.1104/pp.112.208298
6. Djanaguiraman M, Perumal R, Jagadish SVK, Prasad PVV. High temperature stress and its impact on maize (*Zea mays* L.) productivity. Plants. 2020;9(12):1790.
7. Gauch HG, Zobel RW. AMMI analysis of yield trials. In: Genotype by Environment Interaction. Madison: CSSA; 1996:85-122.https://doi.org/10.1201/9781420049374.ch4
8. Makumbi D, Atlin GN, Tumusiime S, Njoroge K. Assessment of maize genotype stability under heat stress conditions in sub-Saharan Africa using GGE biplot analysis. Field Crops Res. 2023;294:108891.
9. Cairns JE, Bänziger M, Prasanna BM, Magorokosho C. Enhancing heat and drought tolerance in maize through integrated breeding approaches. Plant Physiol. 2021;185(2):507-20.
10. Yan W, Hunt LA, Sheng Q, Szlavnics Z. Cultivar evaluation and mega-environment investigation based on the GGE biplot. Crop Sci. 2000;40:597-605.https://doi.org/10.2135/cropsci2000.403597x
11. Kumar R, Yadav VK, Kumar M. AMMI analysis for stability and adaptability of maize genotypes under heat stress environments. Int J Agric Sci. 2012;8(2):319-24.
12. Sharma L, Choudhary M, Singh M. Genotype × environment interaction analysis for yield and its attributes in maize (*Zea mays* L.). J Pharmacogn Phytochem. 2018;7(1):1674-80.
13. Adugna A. Analysis of genotype × environment interaction and stability for grain yield of maize hybrids in mid-altitude sub-humid agro-ecology of Ethiopia. J Plant Breed Genet. 2019;7(1):1-10.
14. Yan W, Tinker NA. Biplot analysis of multi-environment trial data: Principles and applications. Can J Plant Sci. 2007;86(3):623-45. https://doi.org/10.4141/P05-169
15. Bänziger M, Lafitte HR. Efficiency of secondary traits for improving maize for low-n input and drought stress environments. Crop Sci. 2006;42(3):1117-24.
16. Mohammadi R, Haghparast R, Amri A, Ceccarelli S. The use of AMMI and GGE biplot analysis for interpreting genotype × environment interaction in durum wheat. Crop Sci. 2009;49(4):1545-51. https://doi.org/10.2135/cropsci2008.09.0537
17. Singh RK, Pal S, Kumar A. AMMI and GGE biplot analysis for stability and adaptability of maize hybrids across environments. Electron J Plant Breed. 2020;11(2):468-75.
18. Singh AK, Yadav RK, Kumar A. Identification of stable and high-yielding maize hybrids for Eastern India using GGE biplot. J Agric Sci. 2022;14(2):156-65.
19. Singh D, Mohanty TA, Kushwaha N, Kumar A, Kumar R, Singh MK, et al. Assessment of genetic diversity in quality protein maize (QPM) inbreds using principal component analysis. Pharma Innov J. 2021;10(7):1726-31.
20. Choudhary M, Sharma L, Singh M. Evaluation of maize genotypes for heat tolerance and stability using GGE biplot. Indian J Genet Plant Breed. 2021;81(1):40-7.
21. Kumar A, Sharma V, Singh D. Multi-environment evaluation of wheat genotypes under changing climate using GGE biplot. Agric Res J. 2023;60(1):75-82.
22. Patel D, Yadav M, Meena RK. Identification of stable and climate-resilient maize genotypes using AMMI and GGE biplots. J Cereal Res. 2024;16(1):33-42.
23. Kumar A, Swapnil, Perween S, Singh RS, Singh DN. Prospects of molecular markers in precision plant breeding. In: Jha AK, Kumar U, editors. Recent advances in chemical sciences and biotechnology. New Delhi: New Delhi Publishers; 2020:132-42.
24. Sahu R, Kumari S, Mishra AK. GGE biplot analysis of rice genotypes under varied climatic zones. Oryza. 2023;60(2):181-7.
25. Yadav M, Patel D, Kumar R. Multi-environment GGE biplot analysis for kernel traits in maize. Indian J Genet. 2024;84(2):245-53.
26. Thakur A, Mehta P, Sharma P. GGE biplot analysis for yield and yield attributing traits in maize hybrids. J Pharmacogn Phytochem. 2022;11(3):339-44.
27. Mehta P, Roy A, Sharma L. Genotype by environment interaction studies in maize for Eastern India using GGE biplot. Int J Curr Microbiol Appl Sci. 2023;12(3):1005-17.
28. Roy A, Mehta P, Sharma L. Stability analysis for yield and its component traits in maize using AMMI and GGE biplot. J Pharmacogn Phytochem. 2022;11(5):112-20.
29. Hussain M, Singh D, Rathi S. Stability analysis of maize genotypes using AMMI and GGE biplot across environments. Plant Genome. 2024;17(1):e20134.
30. Mehta P, Sharma L, Choudhary M. Multi-location stability analysis in maize using AMMI and GGE biplot models. Electron J Plant Breed. 2021;12(2):565-74.
31. Swapnil, Rashmi K, Sahay S, Mandal SS, Sinha S, Singh B, et al. Stability analysis in quality protein maize (*Zea mays*) by Eberhart and Russell model and GGE biplots. Indian J Agric Sci. 2024;94(9):929-34. https://doi.org/10.56093/ijas.v94i9.144431
32. Singh D, Swapnil, Kushwaha N, Mohanty TA, Kumar A, Kumar R. Morphological diversity analysis for quantitative traits in quality protein maize (QPM). Int J Res Agron. 2024;7(2):524-8. https://doi.org/10.33545/2618060X.2024.v7.i2g.466
33. Singh D, Swapnil, Kushwaha N, Mohanty TA, Kumar A, Kumar R. Multivariate analysis for yield and its component traits in quality protein maize (QPM). Int J Adv Biochem Res. 2024;8(2):736-41. https://doi.org/10.33545/26174693.2024.v8.i2i.807
34. Singh D, Kushwaha N, Swapnil, Parveen R, Mohanty TA, Suman SK. Assessment of quality protein maize (QPM) inbreds for genetic diversity using morphological characters and simple sequence repeat markers. Electron J Plant Breed. 2023;14(3):1276-84. https://doi.org/10.37992/2023.1403.145
35. Swapnil, Jaishreepriyanka R, Singh D, Mandal SS. Principal component analysis in maize (*Zea mays* L.) under normal sown condition of Bihar. Pharma Innov J. 2021;10:641-4.

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