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AMMI and GGE biplot analysis for yield performance and stability assessment of Rice (*Oryza sativa* L.) hybrids under the multi-environmental trials (METs)

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Abstract

Genotype $\times$ environment interaction (GEI) significantly affects grain yield in hybrid rice, making it essential to use robust statistical methods to pinpoint genotypes that are both stable and high-yielding across different environments. This research assessed 67 rice genotypes at three locations using additive main effects and multiplicative interaction (AMMI) and genotype plus genotype-by-environment interaction (GGE) biplot analyses. The AMMI analysis showed that the first interaction principal component axis (IPCA1) accounted for 74.2% of the total GEI, highlighting its substantial role in interaction effects. Genotypes located near the IPCA1 origin demonstrated minimal interaction and greater stability, while those with high IPCA1 scores were specifically adapted. The favourable environment E1 was linked to high-yielding genotypes (G60, G31, G18, G56, G53 and G40), where as E2 and E3 were associated with genotypes that yielded relatively less. The AMMI2 biplot indicated that environment E1 had the strongest interaction effect, followed by E2 and E3, with genotypes G25 and G12 being relatively stable. GGE biplot analysis identified a single mega-environment, with vertex genotypes G23, G42 and G40 showing specific adaptation. The "which-won-where" pattern highlighted G42 as the top-performing genotype in E1, while G40 and G23 excelled in E2 and E3, respectively. Environmental vector analysis showed positive correlations among all test environments, with E2 having the highest discriminating ability. Using the average environment coordination method, genotypes G17, G23, G40, G42 and G55 were deemed ideal, combining high mean grain yield with stability.

Key words: Rice-hybrids, Multi-location trails, $G \times E$ interaction, AMMI, GGE

1. INTRODUCTION

Rice (*Oryza sativa* L.) serves as a fundamental staple food for more than half of the global population, playing a critical role in ensuring food and nutritional security worldwide [1, 2]. In recent years, India has emerged as the largest rice producer, achieving an unprecedented production level of approximately 150 million tonnes, thereby surpassing China and securing the leading position globally [3,4]. Sustaining yield improvements in rice is essential for food security and a comprehensive understanding of genotype-by-environment interaction (GEI) is vital for

developing effective breeding strategies, particularly under diverse environmental conditions [5–7]. GEI complicates the selection process, as genotype rankings may vary across different locations or seasons, which can reduce the effectiveness of breeding programs relying solely on mean performance [8–10].

Multi-environment trials (METs) are integral for assessing genotype performance and stability across a range of agro-ecological conditions [11,12]. While traditional analysis of variance can identify the presence of GEI, it offers limited insights into the underlying patterns of genotype-by-environment (GE) interactions [13]. Consequently, advanced statistical methodologies, including additive main effects and multiplicative interaction (AMMI) models as well as genotype-by-environment (GGE) biplot analysis, have been widely employed to elucidate and visualize GEI in various crops, including rice [14–17]. These models enable breeders to partition variation, quantify stability and identify genotypes with broad adaptability [18,19].

The AMMI model integrates analysis of variance for main effects with principal component analysis for interaction effects, thereby facilitating a robust interpretation of GEI and providing valuable insights into the stability and adaptability of genotypes across METs [20–22]. These analytical tools have demonstrated considerable success in rice and other crops, instilling confidence in breeders engaged in stability assessments [23, 24]. Recent studies emphasize the ongoing relevance and evolution of these methodologies for stability assessment and selection across various crops [25, 26]. For instance, AMMI and GGE biplot analyses have been utilized to identify high-yielding and stable rice genotypes within multi-environment trials and to characterize stability among aromatic rice landraces using multivariate analysis [27, 28]. Moreover, comparative studies of AMMI and GGE models have been applied to other cereals and legumes to illustrate adaptability and environmental discrimination. Such contributions highlight the broad applicability and continued refinement of stability tools within the context of crop improvement under GEI [29–31].

The combined application of AMMI and GGE biplot analyses provides a robust framework for not only detecting significant GEI but also for interpreting complex patterns of genotype performance and stability [32,33]. By synthesizing quantitative and graphical insights, breeders can more effectively identify hybrids with substantial yield potential and adaptability across diverse environmental conditions. Consequently, this study aims to evaluate the grain yield performance of selected rice hybrid genotypes across varied environments, quantify and interpret GEI utilizing AMMI and GGE biplot analyses and identify high-yielding, stable hybrids with broad or specific adaptation for multi-environment cultivation [34].

2. MATERIAL AND METHODS

A panel of (3-Checks, 16-Parents and 48-hybrids) 67 rice genotypes was collected from the germplasm stock at the Indian Institute of Rice Research (IIRR) in Hyderabad (Table.1) and cultivated at three different environments to assess the grain yield performance. The experiments were conducted at the following environments: E1 - ICAR-Indian Institute of Rice Research, Hyderabad; E2 - Regional Agricultural Research Station (RARS), Warangal; and E3 - Regional Sugarcane and Rice Research Station (RS&RRS), Rudrur, Nizamabad (Fig.1 & Table 2). Each field experiment was carried out in a randomized block design with two replications. The 25 days seedlings were planted

with a spacing of 50 cm × 30 cm between rows, with one seedling per hill in each replication. Data on single plant yield were recorded and subjected to further stability analysis based on the stability evaluation system (SES) for rice.

Statistical analysis

Statistical analyses were performed using R software (version 4.5.2) in the R Studio. AMMI & GGE Biplot analysis was conducted using the "metan" package.

3. RESULTS

3.1 Pooled Analysis of variance (Pooled ANOVA) of grain yield across environments

Pooled analysis of variance across three environments revealed highly significant effects of genotypes, environments and their interaction ($G \times E$) for grain yield, indicating differential genotype performance across test environments (Table.3) [35–37]. Genotypic effects accounted for a substantial proportion of the total variation, reflecting the presence of exploitable genetic variability within the evaluated population [38]. The genotype × environment interaction component was also statistically significant when tested against pooled error variance, highlighting the influence of environmental heterogeneity on genotype expression and underscoring the necessity of stability analysis for reliable genotype evaluation [39–41].

3.2 Estimation of stability parameters for grain yield per plant

The additive main effects and multiplicative interaction (AMMI) model was employed to assess the individual and interactive effects of genotype, environment and genotype-by environment interaction on grain yield. The AMMI approach is recognized as a robust analytical framework for dissecting genotype–environment interactions, facilitating the identification of suitable genotypes for specific or broad adaptation, adaptive traits and representative test environments [42–44]. By simultaneously accounting for additive main effects and multiplicative interaction components, the AMMI model enhances the precision of genotype evaluation across diverse environments [45].

Analysis of variance based on the AMMI model revealed that rice grain yield was significantly affected by the main effects of environment (E) and genotype (G), as well as by the genotype × environment ($G \times E$) interaction, indicating differential genotype responses across environments [46, 47]. The interaction principal component analysis showed that the first interaction principal component axis (IPCA1) was statistically significant, capturing the major proportion of GEI variation, whereas the second principal component axis (IPCA2) was non-significant, suggesting that most of the interaction pattern was adequately explained by IPCA1 [48, 49].

3.3 Ammi biplot analysis

The AMMI1 biplot depicts the combined effects of genotype and environment on rice hybrid performance, with mean grain yield represented on the X-axis and the first interaction principal component axis (IPCA1) on the Y-axis. In the present study, thirty hybrid genotypes evaluated across three locations explained 74.2% of the total variation, indicating that the AMMI1 model adequately captured the major patterns of genotype-by-environment interaction (Fig. 2) [50, 51]. The X-axis reflects additive main effects associated with genotype and environment means,

whereas the Y-axis represents the multiplicative interaction effects summarized by IPCA1 [52]. Considerable variation among genotypes was evident in both magnitude and direction along the yield and IPCA1 axes, demonstrating differential responses to environmental conditions [53]. The quadrant distribution of genotypes revealed distinct patterns of adaptability: genotypes positioned in QI (high mean yield with positive IPCA1) and QII (high mean yield with negative IPCA1) exhibited superior performance with specific environmental affinity, whereas genotypes in QIII and QIV were characterized by lower mean yields and stronger genotypes and environments shared the same IPCA1 sign, while opposite signs indicated negative interactions [55]. Genotypes namely, G25, G49, G38 and G61 located close to the horizontal axis ($IPCA1 \approx 0$) expressed minimal interaction effects and were therefore considered more stable across environments [56]. In contrast, genotypes combining high mean yield with large absolute IPCA1 values were identified as specifically adapted to particular environments [57]. Environments E2 and E3, positioned in the left quadrants, were associated with relatively lower-yielding genotypes, such as G37, G7, G28, G14 and G8 with environment interaction effects [54]. Positive genotype–environment interactions were inferred when E1 clustered with high-yielding genotypes, indicating its favourable and discriminative nature [58]. The AMMI2 biplot (Fig. 3), which illustrates only the interaction effects using IPCA1 and IPCA2 axes, further clarified genotype and environment relationships [59]. Genotypes positioned near the origin exhibited low interaction on both axes, reflecting greater stability, whereas those located farther from the origin showed strong responsiveness to environmental variation [60]. Among the test environments, E1 exhibited the longest vector, signifying the strongest interaction force and higher discriminative ability, followed by E2 and E3 [61]. The genotypes (G50, G58, G53 and G28) with longer spokes were more sensitive to environmental changes, while those (G25 and G12) near the origin were less responsive and thus broadly adapted [62].

3.4 GGE biplot analysis: which-won-where

In the polygon view of the GGE biplot, genotypes positioned at the vertices namely G23, G42, G58, G30, G12, G15, G27, G37 and G40-represent the most responsive genotypes to environmental variation (Fig. 4) [63, 64]. The “which-won-where” pattern revealed that all test environments were grouped into a single mega-environment, indicating a similar genotype response pattern across locations [65]. In GGE biplot interpretation, environments falling within the same sector share a common winning genotype, while vertex genotypes are considered either specifically adapted to certain environments or poorly adapted to others [66, 67].

Genotypes G40 and G23 exhibited superior grain yield performance in environments E2 and E3, whereas vertex genotype G42 showed the highest yield in environment E1, demonstrating specific adaptation to that environment [68]. In contrast, genotypes G15 and G12 were consistently positioned away from favourable sectors and displayed inferior performance across most environments, indicating poor adaptability [69]. Based on the polygon biplot analysis, genotype G42 was identified as the overall winning genotype within the single mega-environment, reflecting its high yield potential and adaptability under the tested conditions [70, 71].

3.5 Comparison of environments

In the GGE biplot, an environment forming a small angle with the average environment axis (AEA) is considered more representative of the overall target population of environments, as it more accurately reflects the mean performance of genotypes across test conditions [72, 73]. Representativeness indicates the suitability of a test environment for selecting broadly adapted genotypes and is a key criterion in multi-environment trial evaluation [74]. In the environment vector view of the GGE biplot, vectors drawn from the biplot origin to each test environment represent environment vectors and the cosine of the angle between any two vectors approximates the correlation between those environments [75, 76]. Acute angles indicate positive correlations; obtuse angles suggest negative correlations and right angles imply near-zero correlation [77]. This graphical representation provides a concise summary of inter-environment relationships within the experiment [78].

In the present study, the vector view of the GGE biplot (Fig. 5) revealed that environments E2 and E3 were positively correlated with each other, as indicated by the acute angle between their vectors and both environments also showed positive correlations with E1. These results suggest a similar discriminating pattern among the test environments and support the presence of a common response of genotypes across locations [79, 80].

3.6 GGE biplot environment view for yield

The environment view (Fig. 6), the length of the environment vectors reflects their discriminating ability. The environments E1 and E2 showed relatively long vectors and were positioned away from the origin, indicating that these environments were highly discriminating in differentiating genotype performance for yield. The angle between the environment vectors indicates their correlation, the acute angle between E1 and E2 suggests a positive association, representing both environments tend to rank genotypes similarly [76, 81]. Genotypes located in the direction of the environment vectors, such as G17, G32 and G18 exhibited better yield performance and adoption in those respective environments. In contrast, genotypes located near to the origin displayed average performance across the environments. Overall, the biplot indicates that E1 and E2 were effective environments for identifying high-yielding and environment –specific genotypes [82, 83].

3.7 Discriminating ability and representativeness of test environments

The results of the GGE biplot analysis (Fig. 7) for the grain yield data indicated that each test environment was connected to the biplot origin point with an environment vector, which indicates the discriminating ability of the environment [81, 82]. The results further indicated that the two interaction principal components, IPC1 and IPC2, explained 94.4% of the total variation, and therefore the results could be considered reliable and representative, as the cumulative percentage of the variation explained by the two components was high [83].

The angles between the environment vectors indicated the correlation between the test environments, and acute angles indicated positive correlation [84]. During the course of the present investigation, the test environments E1 and E3, and E1 and E2 were found to be positively correlated, as indicated by the acute angle between the vectors of the respective test environments [85]. The length of the environment vector indicated the discriminating ability of the environment, and longer vectors indicated higher discriminating ability [86, 87]. The vector length for the test

environment E2 was the longest, and therefore the discriminating ability of the environment was the highest, followed by the test environments E1 and E3, which had shorter vectors, indicating lower discriminating ability.

3.8 Varieties relative to an ideal variety

The average environment coordination (AEC) view of the GGE biplot (Fig. 8) provides a concise graphical summary of both mean grain yield and genotype stability across test environments, thereby facilitating simultaneous evaluation of performance and consistency [90, 91]. This approach is particularly effective for multi-environment trials, as it enables breeders to visually identify superior and stable genotypes and supports informed decisions in plant breeding and varietal selection programs [92].

In the present analysis, a single arrowed line drawn from the biplot origin through the average environment represents the AEC abscissa, along which increasing mean grain yield is indicated in the direction of the arrow [93]. A perpendicular axis passing through the origin, referred to as the AEC ordinate, reflects genotype stability, where shorter projections from the abscissa denote greater stability [94]. Genotypes positioned farther along the positive side of the AEC abscissa exhibited higher mean grain yield, whereas those located on the negative side showed inferior mean performance [95]. The arrow direction further establishes the ranking of genotypes in ascending order of yield expression [96].

An ideal genotype is characterized by a high mean performance combined with high stability and is graphically represented near the centre of the concentric circles on the AEC view [97]. Accordingly, genotypes G55, G42, G23, G40 and G17, which were positioned within the innermost concentric circle, were identified as ideal genotypes with superior grain yield and stability across environments [98]. Genotypes located on the subsequent concentric circle were considered desirable, whereas genotypes such as G31, G49, G62 and G24, positioned outside the circles, exhibited higher mean grain yield but comparatively lower interaction with environmental factors, indicating good performance with moderate stability [99, 100].

3.9 Genotype Discrimination by GGE Biplot in Means vs Stability

Genotype positions were identified in the average-environment axis (AEA) or average-environment coordination (AEC) from the GGE biplot (Fig. 9) based on their mean and stabilities. The vertical line (AEC abscissa) and horizontal line (AEC ordinate) from graph were shown on two separate axes [101, 102]. The arrow head direction on the AEA abscissa points towards a higher mean value for grain yield performance. Another axes showing genotypes stability.

The vector having largest length from AEC indicating that high variability or instability in either of the direction. The genotypes namely G58, G43 and G37 were unstable. On the other hand G35, G41, G39 and G42 were regarded as high yielding and stable genotypes and shown small vector length from the AEC axis [88,103].

3.10 Ranking Genotypes

Genotype ranking gives the best and ideal genotype assessment. The ranking genotypes biplot (Fig.10) representing the ideal genotypes from the evaluated genotypes. The ideal genotypes were positioned in centre circular ring [103,

104]. The genotypes G42, G35 and G55 were centric due to their nearness to the arrowhead in the circle for grain yield and these were regarded as ideal genotypes across the tested environment because they were positioned closer of the biplot origin and indicating that they are stable genotypes. Likewise, G40, G63 and G18 were positioned next centric ring. However, in some cases no genotypes were positioned inside the inner circle, consequently, genotypes next closer to the inner circle are considered to be an ideal one [105, 106].

3.11 Ranking of Environment

The GGE ranking environment biplot (Fig. 11) revealed that the concentric circles represent the ideal test environment, while the average environment axis (AEA) indicates representativeness [101,107]. E1 was positioned far away from the origin, high discriminating ability, but its larger deviation from the AEA suggests lower representativeness. In contrast, E2 and E3 were located closer to the AEA, indicating better representativeness of the target environments. Among three environments E3 was comparatively closer to the ideal environment, suggesting a better balance. Therefore, E3 can be considered a relatively ideal test environment, while E1 is useful for discriminating genotypic differences across environments [66, 105].

3.12 Relationship among environment

The GGE biplot (Fig. 12) illustrating the relationship among environment showed that the angles between environment vectors indicates the degree of correlation among them E2 and E3 were formed a small acute angle suggesting a strong positive correlation, explaining that these environments provide similar information regarding genotype performance [72, 73]. Conversely, E1 formed a wider angle with E2 and E3 indicating a weaker correlation and indicating that it represents a relatively different environmental condition. The longer vector of E1 also indicates greater discriminating ability compared to the other environments. Overall, E2 and E3 can be considered similar testing environments, whereas, E1 contributes unique information in genotype evaluation [75, 76].

4. DISCUSSION

Genetic variability forms the foundation of crop improvement programmes, enabling the development of cultivars with enhanced yield potential and reliable performance across diverse agro-climatic conditions. The pooled analysis of variance revealed a highly significant genotype $\times$ environment ($G \times E$) interaction for all traits studied, indicating that phenotypic expression was jointly influenced by genetic constitution and environmental conditions [108,109]. This finding highlights the importance of environment-specific variety evaluation and selection.

Significant variability among genotypes was observed for key agronomic traits, including days to heading, days to maturity, plant height, spike length, number of seeds per spike, thousand-seed weight and grain yield. Similar patterns of genetic variability for these traits have been reported in previous studies, emphasizing their importance in crop improvement programmes [110,111]. Although ANOVA effectively identifies the significance of genotype, environment and their interaction effects, it does not provide insight into the nature or structure of these interactions [112]. Therefore, advanced multivariate approaches are required to dissect $G \times E$ interactions and identify stable and high-performing genotypes.

The stability ANOVA and AMMI analysis further confirmed that both genotypic and environmental effects significantly influenced grain yield per plot. The significant $G \times E$ interaction indicated that genotype rankings were not consistent across environments, reflecting differential responses to ecological variation [105, 113]. Understanding these effects enables breeders to design targeted selection strategies that enhance yield stability and adaptability under diverse environmental conditions, ultimately contributing to sustainable agricultural production and food security [114].

The Additive Main Effects and Multiplicative Interaction (AMMI) model integrates univariate analysis of variance for estimating additive genotype and environment effects with multivariate analysis for interpreting the multiplicative nature of $G \times E$ interactions. This combined approach provides a robust framework for analysing multi-environment trial data and has been widely adopted for grain yield stability assessment [115,116]. The AMMI biplot revealed that genotypes and environments positioned on the right side of the vertical axis were associated with higher grain yield, whereas those on the left exhibited lower performance. This pattern indicates that certain genotypes were better adapted to specific environments, underscoring the role of $G \times E$ interaction in determining yield performance [117].

Genotypes or environments with interaction principal component axis (IPCA) scores close to zero exhibited minimal interaction effects and were therefore considered stable across environments. In contrast, larger absolute IPCA values indicated stronger interactions and specific adaptation [118]. In the present analysis, genotypes G49 and G25 showed both high mean grain yield and relatively high IPCA1 values, indicating superior performance with specific environmental adaptation. Conversely, genotypes with IPCA1 values close to zero demonstrated greater stability across test environments. Genotypes positioned close to the mean axis on the positive side were regarded as stable with satisfactory performance. Based on this criterion, genotype G49 was identified as the most stable genotype with good yield potential. Such genotypes are particularly valuable in breeding programmes aimed at improving yield consistency under variable climatic conditions [119]. The GGE biplot is a powerful graphical tool for analysing genotype $\times$ environment data and is widely used to identify superior genotypes and optimal test environments [120]. In this framework, vertex genotypes represent those with the highest responsiveness to environmental variation and correspond to the best-performing cultivars in specific environments.

In the present study, the first two interaction principal components (IPCA1 and IPCA2) explained 98.2% of the total variation, indicating that the biplot effectively captured the complexity of $G \times E$ interaction patterns [121]. Genotype G6 recorded the highest grain yield in environment E3 and occupied a vertex position, while genotypes G9 and G2 exhibited poor performance across most environments, contributing substantially to the observed GEI. The clustering of all environment markers within a single sector indicated a non-crossover type of interaction, wherein one genotype consistently outperformed others across environments [122]. Accordingly, genotype G6 was identified as the winning genotype across test environments. Similar findings have been reported in earlier studies, reinforcing the utility of GGE biplot analysis in genotype evaluation [108,123]. The environment vector view revealed positive correlations among environments, as indicated by acute angles between their vectors. Environment E3 exhibited the longest vector, reflecting strong discriminating ability, whereas E1 and E2 showed comparatively shorter vectors.

Environments with longer vectors are considered more effective in distinguishing genotypic differences and are therefore valuable for selection purposes [124]. Environment E3 was positioned near the ideal environment and showed both high discriminating ability and representativeness, indicating its suitability as a reliable testing site. Such environments are essential for accurate genotype evaluation and for guiding breeding decisions [125].

Yield stability and adaptability are critical attributes for the successful release of crop cultivars. Breeding programmes therefore prioritize genotypes that maintain consistent performance across diverse environmental conditions [126]. Grain yield, being a complex trait influenced by multiple genetic and environmental factors, serves as the primary selection criterion in crop improvement programmes. Based on stability parameters, genotypes G5, G7 and G10 were identified as the most stable. Genotype G7 exhibited high stability and ranked second in grain yield, whereas genotype G6, despite achieving the highest mean yield, showed comparatively lower stability and ranked third based on the Genotypic Stability Index (GSI). Similar observations, where high-yielding genotypes display reduced stability, have been reported in earlier studies [127].

An ideal genotype is characterized by high mean yield combined with stability across environments. Although identifying such genotypes is challenging, they serve as valuable benchmarks for selection. Genotypes located closer to the ideal genotype in the concentric ring view are considered more desirable, as they combine productivity with adaptability. The present findings highlight the effectiveness of AMMI and GGE biplot analyses in identifying broadly adapted, high-yielding genotypes suitable for diverse production environments [101]. The GGE biplot analysis gave an in-depth understanding of the performance and stability of genotypes and their association with the test environments. The average environment coordination (AEC) perspective of the GGE biplot indicated the average performance and stability of genotypes in the environments. The AEC abscissa indicated the average grain yield performance, with the arrow head showing an increase in performance, while the AEC coordinate indicated the stability of genotypes. The genotypes closer to the AEC axis with shorter projections are more stable. In the present study, genotypes G58, G43 and G37 were shown longer projections from the AEC axis, observed higher variability and unstable performance. The genotypes G35, G41, G39 and G42 are located closer to AEC axis with smaller vectors, indicating stability and higher grain yield. Hence, these genotypes have excellent performance and are suitable for wide adoption [102, 103].

The genotype ranking biplot is another method of determining the ideal genotypes by considering the potential and stable genotypes. From the given biplot, the ideal genotypes were represented at the center of concentric circles. The genotypes located closer to the center are highly desirable. The genotypes G42, G63, and G18 are located on the next circle, indicating average performance with relatively low stability. The evaluation indicates the concentric circles as the optimal test arrangement, with the average environment axis (AEA) indicating how representative the environments. E1 is located far away from the origin, indicating good discriminating. However, the larger distance of E1 from the AEA indicates it is less representative of the target environment. On the other hand, E2 and E3 are located closer to the AEA, indicating better representativeness. Among the two environments, E3 is closer to the ideal environment, indicating better discriminating power [105]. The relationship between the environments was determined by the angle that was created when the vectors intersected. E2 and E3 are positioned close to each other

and creating a angle between them. Moreover, these two environments had similar perspective of genotype performance. Furthermore, E1 had a larger angle between both E2 and E3. This implies a weaker relationship between E1 and both E2 and E3. Moreover, it seems to hint that E1 offers a unique perspective on how well a genotype is able to perform [101, 106].

CHALLENGES AND FUTURE PROSPECTS

Future research should expand multi-location and multi-season trials to enhance the reliability of genotype evaluation. Integration of genomic tools, climate-resilient trait selection and advanced statistical models such as BLUP-based approaches will improve prediction accuracy. Identifying representative and discriminating environments will further strengthen breeding strategies for stable, high-yielding rice hybrids.

CONCLUSION

The pooled ANOVA revealed significant genotype, environment and $G \times E$ interaction effects for grain yield, confirming variable genotype performance across locations. AMMI and GGE biplot analyses effectively partitioned interaction effects and identified differential adaptability among genotypes. Genotypes G42, G23, G40 and G55 were high-yielding and stable, with G42 emerging as the overall winner within the single mega-environment. Some genotypes showed specific adaptation to particular environments. Environment E2 exhibited the highest discriminating ability, while E3 combined good representativeness and discrimination, making it a reliable test site. Positive correlations among E1, E2 and E3 indicated similar genotype ranking patterns across environments.

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Data availability

The datasets generated during the current study are available from the corresponding author on reasonable request.

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Authors' contributions

KRP carried out the experiment, data collection, analyses and manuscript writing. KVR, PSV, SSK and LVS, providing valuable help to input in the experimental design, design of the study, supervised and guidance to identify the research problem and interpretation of results KD, PNR & AS support in the data analysis and manuscript writing, refining the overall data interpretation. All authors reviewed and approved the final manuscript.

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Table 1. Details of Genotypes used in the study

G1	APMS-6B	G35	IR79156A X PSV-49
G2	IR79156B	G36	IR79156A X TCP-950
G3	IR68897B	G37	IR79156A X TCP-951
G4	PUSA-5B	G38	IR79156A X TCP-960
G5	TCP-718	G39	IR79156A X TCP-963
G6	TCP-783	G40	IR79156A X TCP-964
G7	TCP-795	G41	IR68897A X TCP-718
G8	TCP-801	G42	IR68897A X TCP-783
G9	PSV-15	G43	IR68897A X TCP-795
G10	PSV-41	G44	IR68897A X TCP-801
G11	PSV-49	G45	IR68897A X PSV-15
G12	TCP-950	G46	IR68897A X PSV-41
G13	TCP-951	G47	IR68897A X PSV-49
G14	TCP-960	G48	IR68897A X TCP-950
G15	TCP-963	G49	IR68897A X TCP-951
G16	TCP-964	G50	IR68897A X TCP-960
G17	APMS-6A X TCP-718	G51	IR68897A X TCP-963
G18	APMS-6A X TCP-783	G52	IR68897A X TCP-964
G19	APMS-6A X TCP-795	G53	PUSA-5A X TCP-718
G20	APMS-6A X TCP-801	G54	PUSA-5A X TCP-783
G21	APMS-6A X PSV-15	G55	PUSA-5A X TCP-795
G22	APMS-6A X PSV-41	G56	PUSA-5A X TCP-801
G23	APMS-6A X PSV-49	G57	PUSA-5A X PSV-15
G24	APMS-6A X TCP-950	G58	PUSA-5A X PSV-41
G25	APMS-6A X TCP-951	G59	PUSA-5A X PSV-49

G26	APMS-6A X TCP-960	G60	PUSA-5A X TCP-950
G27	APMS-6A X TCP-963	G61	PUSA-5A X TCP-951
G28	APMS-6A X TCP-964	G62	PUSA-5A X TCP-960
G29	IR79156A X TCP-718	G63	PUSA-5A X TCP-963
G30	IR79156A X TCP-783	G64	PUSA-5A X TCP-964
G31	IR79156A X TCP-795	G65	KRH- 2
G32	IR79156A X TCP-801	G66	DRRH-2
G33	IR79156A X PSV-15	G67	JAYA
G34	IR79156A X PSV-41		

Table 2. Physico-chemical properties of experimental soils at different locations

Property	E1 – ICAR-IIRR, Hyderabad	E2 – RARS, Warangal	E3 – RS&RRS, Rudrur (Nizamabad)
Soil order	Alfisol / Vertisol (mixed)	Vertisol	Vertisol / Alfisol
Texture	Clay loam to clay	Clay	Clay loam to clay
Sand (%)	32–38	35.7	30–40
Silt (%)	15–20	14.6	15–22
Clay (%)	42–50	49.7	40–52
Soil pH (1:2.5 soil:water)	7.4–8.1	7.85 ± 0.07	7.2–8.3
EC (dS m⁻¹)	0.40–0.80	0.67 ± 0.07	0.30–0.90
Organic carbon (%)	0.45–0.75	0.70 ± 0.04	0.30–0.70
Available N (kg ha⁻¹)	180–240	209	170–230
Available P₂O₅ (kg ha⁻¹)	35–55	49	30–50
Available K₂O (kg ha⁻¹)	350–550	552	300–500
Zn (mg kg⁻¹)	0.6–1.2	0.75	0.5–1.0
Drainage	Moderately well drained	Moderately drained	Moderately well drained

Table 3: Analysis of variance for yield and yield components for stability in rice

Source	d.f	Grain yield per plant (g)
Varieties	66	26.32**
Envi. + (Var.*Envi.)	134	4.22**
Environments	2	38.49**
Var.* Envi.	132	3.70**
Environments (linear)	1	76.99**
Var.* Envi.(linear)	66	5.32**
Pooled Deviation	67	2.05**
Pooled Error	198	0.66

* Significant at 5% level; ** Significant at 1% level

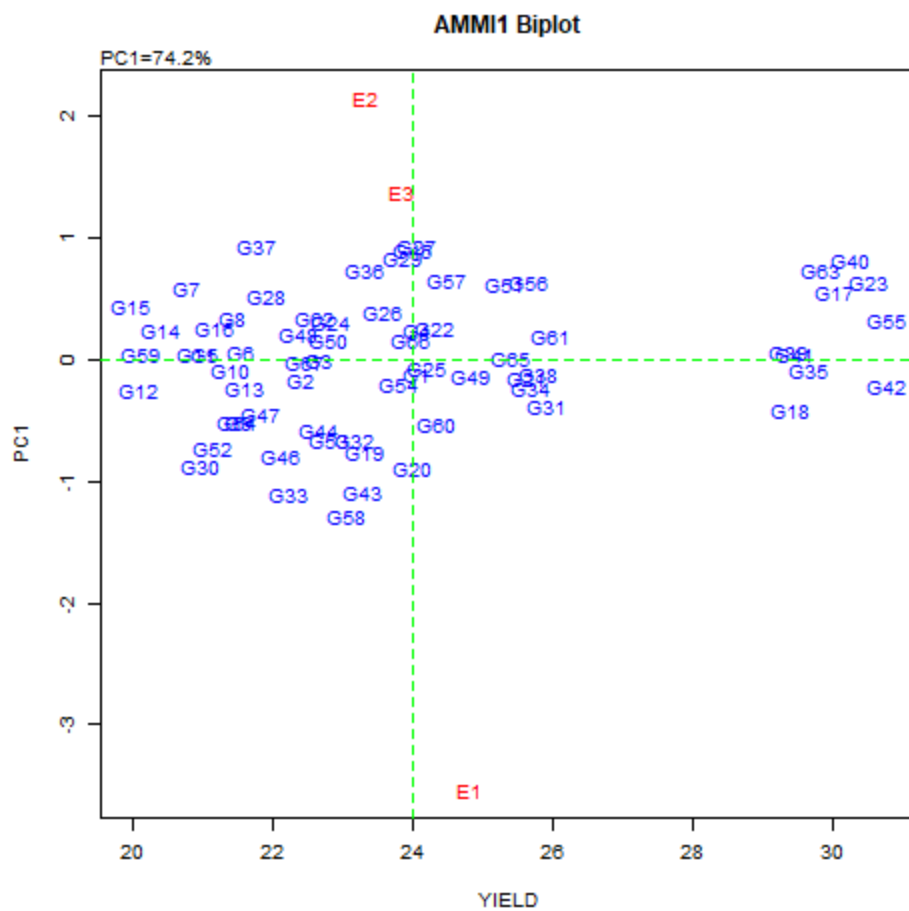


Figure.2. AMMI 1 Biplot of first principal component axis (PCA 1) vs mean grain yield of hybrid rice genotypes over three environments

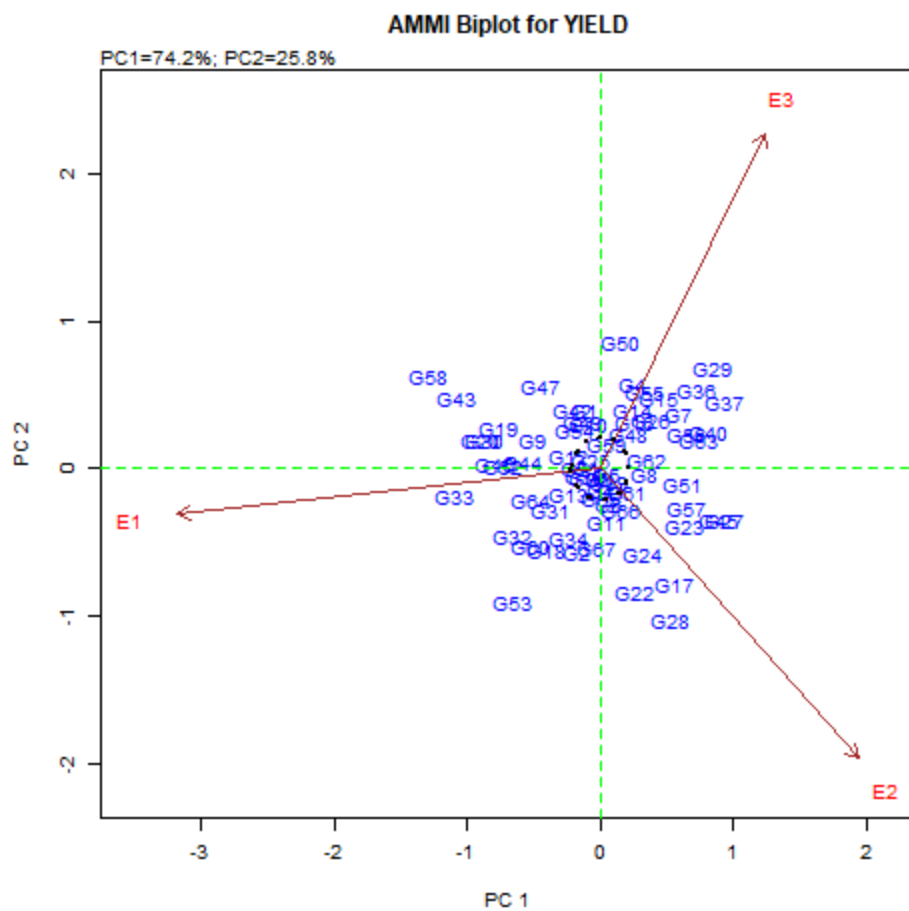


Figure.3. The AMMI biplot of first principal component axis (PCA 1) vs. Second principal component axis (PCA 2) of hybrid rice genotypes over three environments.

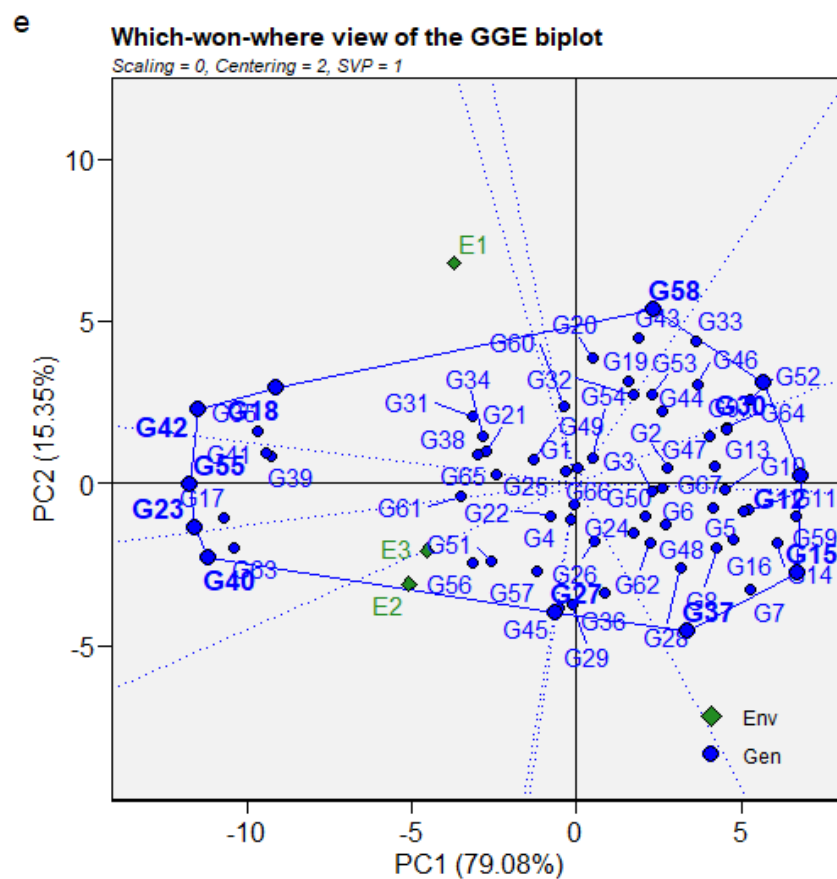


Figure 4. Which-won-where GGE biplot of rice hybrids over three environments

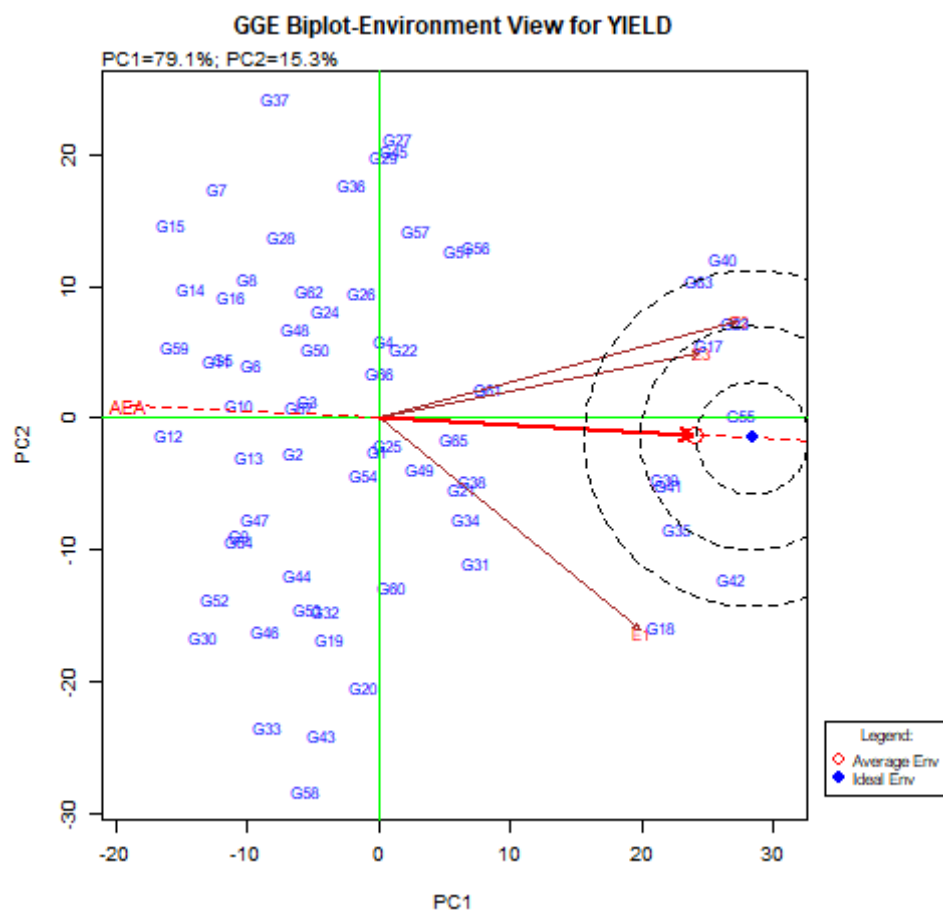


Figure 5: The GGE biplot- Environment vector view for the grain yield of rice hybrids

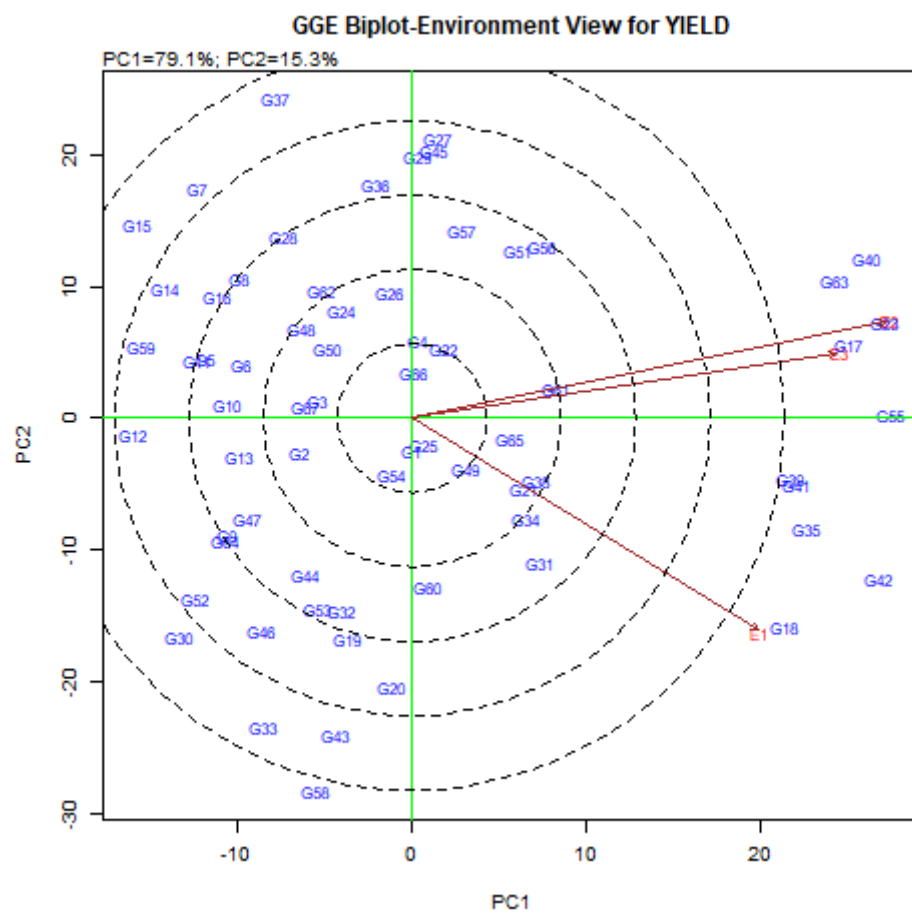


Figure 6: The GGE biplot- Environment vector view showing the relationships among three environments.

g

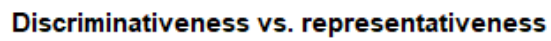


Figure 7: The GGE biplot Discriminating vs. Representativeness pattern for genotypes comparison

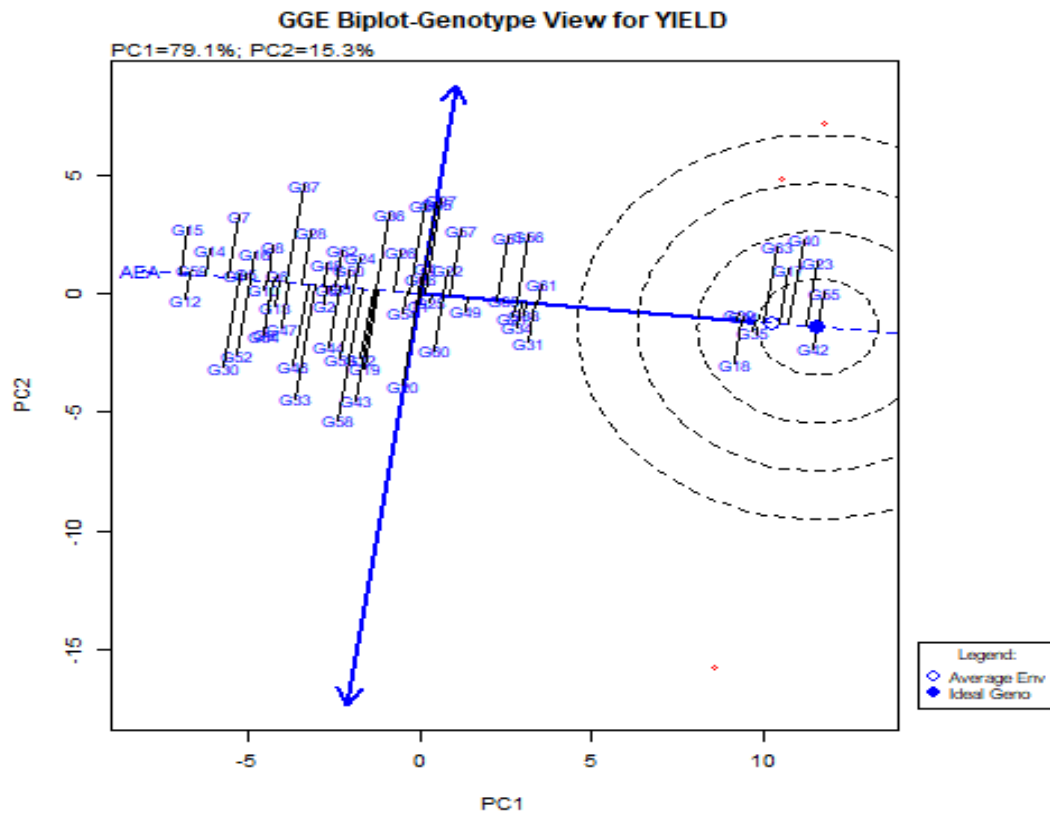


Figure 8: The GGE biplot of stability and mean performance of rice hybrids across average environments.

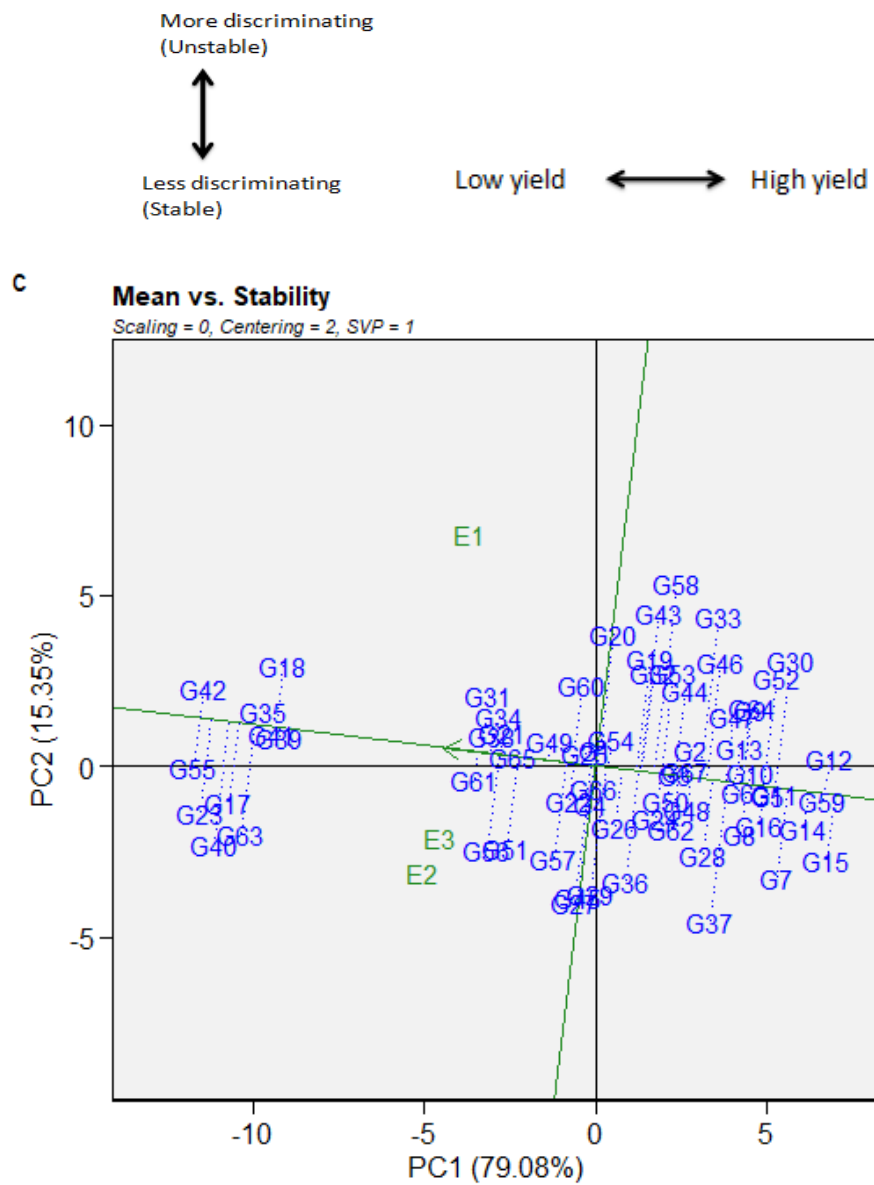


Figure 9: The GGE biplot showing mean performance vs stability of vector view for rice genotypes

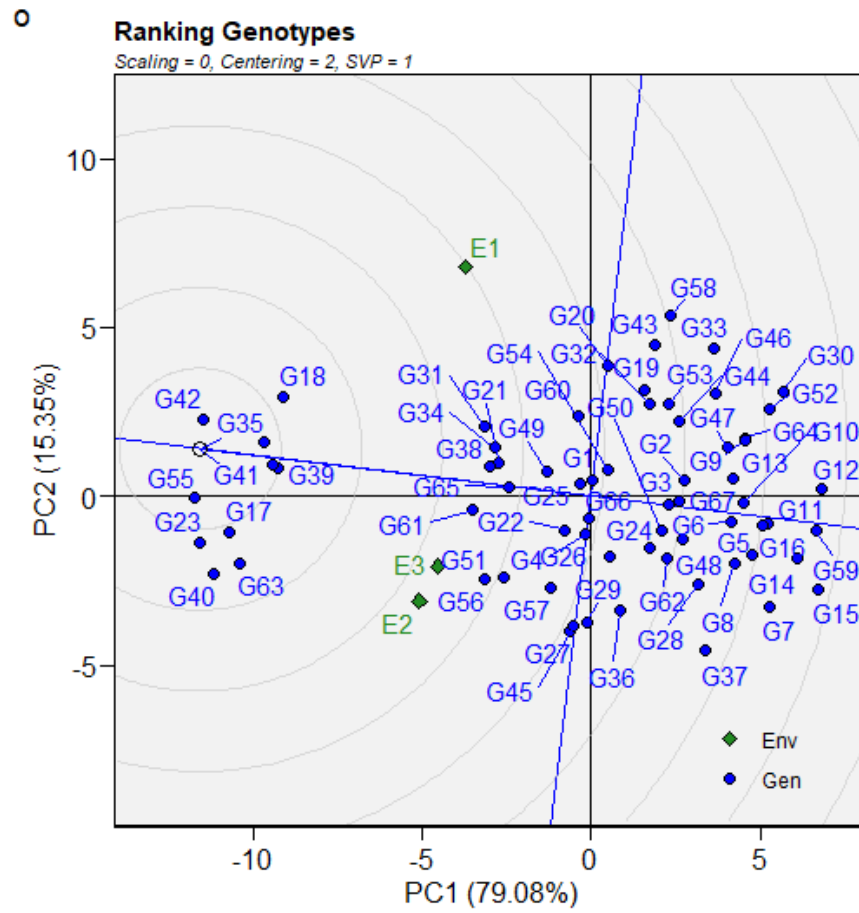


Figure 10: GGE biplot for ranking ideal rice genotypes

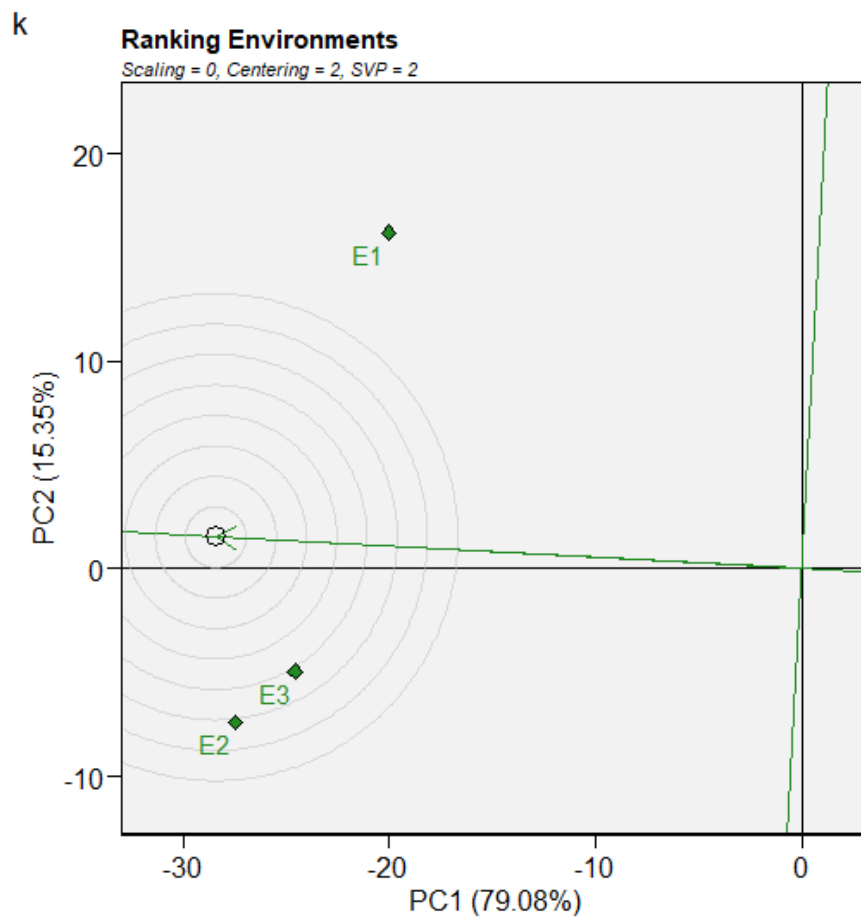


Figure 11: The GGE biplot Environment ranking pattern for environment comparison

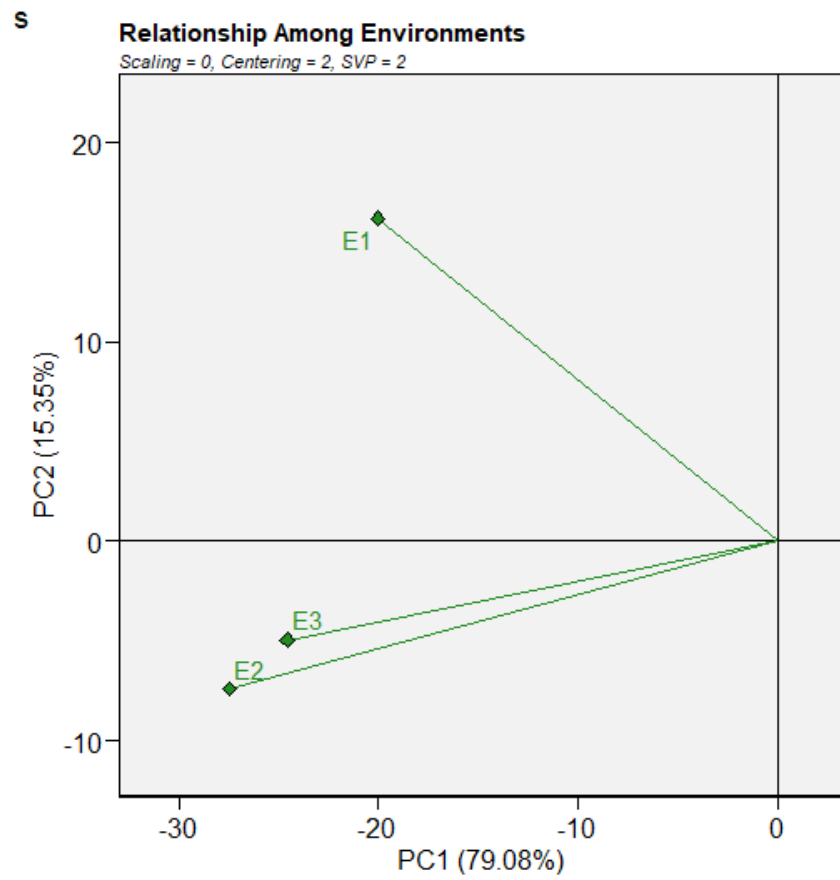


Figure 12: Vector view of GGE biplot showing the relationship among environments