Research Article

An analytical approach integrating GGE-Biplot and AMMI techniques for assessing genotype-environment interactions and yield stability in rice (*Oryza sativa* L.) genotypes

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Abstract

A study was conducted during the Kharif 2020 season in Eastern Uttar Pradesh, India, to investigate the interaction between genotype and environment (GxE) for 55 rice genotypes grown at three different locations. The analysis employed GGE Biplot and AMMI tools to evaluate and graphically visualize these locations for grain yield response to their interrelationships, discrimination ability, and representativeness. AMMI ANOVA revealed significant genotype-environment interactions. A lower value of ASV led to the most stable genotypes HL19WS-33B-369, HL19WS-33A-16, and HL19WS-33B-128, which produced the higher grain yield of all genotypes. The combined use of AMMI and GGE biplot approaches helped identify stable genotypes viz., BRRI Dhan 64, HL19WS-33B-171, HL19WS-33B-317, Samba Mahsuri, and HL19WS-33B-77, which can be proposed in the national testing programs to release new varieties. GGE biplots analysis depicted that all three locations fall under one mega environment. The genotypes, HL19WS-33B-359 and HL19WS-33A-51 exhibited the best yields in the mega-environment. In terms of genotype selection, E1 and E3 demonstrated effective genotypes with general adaptability and specific adaptability for yield, respectively. The mean v/s stability view shows genotype HL19WS-33B-359 to be ideal and most desirable among all other screened genotypes.

Keywords AMMI, GGE biplot, G x E interaction, rice, stability

Introduction

Rice is the chief food for approximately 4 billion individuals worldwide, and contributes 27% of the total calorie intake in low and middle-income nations. Over 90% of the global rice production takes place in Asia, often called the "Rice Basket" of the world since it is home to 60% of the world's population [1]. India being self-sustained in food production, stands second globally in rice production; cultivated on 45.07 resulting in a remarkable production of 122.27 million tons and a productivity rate of 2713 kg/ha [2]. However, productivity is low and it needs to be increased owing to population growth and climate change. Despite the release of over 900 rice varieties in India, the majority of them were phased out within a few years of cultivation due to variable performance under different environments. Only a few reliable varieties are consistently

being used in regular cultivation 15 to 20 years after their release [3]. Grain yield, a dynamic quantitative trait, is influenced by various genetic and environmental factors. An ideal stable genotype exhibits a high average yield and performs consistently across a diverse array of agroecological conditions with a low degree of fluctuation. The study of genotype interactions with locations would aid in obtaining information on the genotype's adaptability and stability performance [4]. Hence, G x E interaction is crucial in plant breeding programs linked to genotype stability and also to determine the post-breeding adaptability analysis of improved lines before making them available for commercial cultivation. The AMMI model, short for Additive Main Effects and Multiplicative Interaction, combines the additive and multiplicative components of a two-way data structure. This model provides breeders with the ability to accurately predict the potential of genotypes and understand the impact of environmental factors on them [5]. ANOVA is used in AMMI to examine the main effects of genotype and environment, while PCA is employed to analyze residual multiplicative interactions between genotypes and environments [6-8]. AMMI analysis allows for the estimation of a genotype's interaction effect in each location and helps in identifying genotypes that are well-adapted for specific locations [9-11].

GGE biplots demonstrate the concurrent effect of G and GE for genotypic and test environment assessment by using a key mathematical method called SVD (singular value decomposition) to represent both sources of variation [12-14]. The primary change between both models is that the AMMI analysis relies on double-centered principal components analysis, whereas the GGE biplot analysis uses environment-centered principal components analysis. Both techniques produce comparable results and are equally acceptable [15-17]. It also facilitates the accurate identification of location groups with the least amount of crossover interactions, specifically to the best performing genotype [18-19]. Keeping the above aspects in view, we used both biplot tools to study GxE interaction in determining the adaptability and stable behavior of 55 rice genotypes for grain yield response grown over three different locations in Eastern Uttar Pradesh.

Methodology

The experiment consisted of fifty-five genotypes including five checks (Table 1), obtained from the IRRI South Asia Hub, Hyderabad. During the Kharif 2020 season, genotypes were tested at three different places in Uttar Pradesh namely the Agricultural research farm of BHU (Location 1), Bhikaripur (Location 2) of Varanasi, and Rampur (Location 3) of Mirzapur. A geographical map of the three locations is depicted in Figure 1. Alpha Lattice Design was used to conduct the field experimentation at every location, with three replications. Each replication consisted of five blocks, and within each block, there were 11 plots. The study involved sowing the seeds of 55 genotypes on raised nursery beds, and 21-day-old seedlings of each genotype were subsequently transplanted to the main field, with a spacing of 20 x 15 cm between each plant. To ensure consistent, uniform, and healthy crop growth, regular agronomic practices and plant protection measures were implemented in all three experimental locations. All plants were harvested distinctly from each plot after field maturity, and grains were separated, dried for 5-6 days, and then weighed on an electronic balance. The grain yield plot-1 was noted in kilograms and was converted to grain yield hectare^{-1}. In the AMMI analysis, the relationship between genotypes, locations, and genotype by environment (G × E) interaction was assessed using adjusted mean grain yield, as described by Zobel et al., [6] and Crossa [9]. The method proposed by Purchase et al., [20] was utilized to calculate the AMMI Stability Value (ASV). Stability alone may not always be the sole criterion for selection, as highly stable genotypes may not necessarily exhibit the highest yield reported by Mohammadi and Amri [21]. To classify stable genotypes, we decided to combine stability and yield into a single index. The genotype stability index (GSI) took into account genotype yield rankings over different environments, along with their corresponding AMMI stability values. It is calculated as the sum of the rank of ASV (RASV) and the rank of the mean genotype yield across all environments (RY). Yan and Tinker described GGE

Table 1. List of genotypes along with their mean and stability parameters for grain yield

SN.	Genotype	Grain yield per hectare					
		Mean	Mean rank	IPCA 1	IPCA 2	ASV	ASV rank	GSI
G1	HL19WS-33A-1	2161.11	44	-1.66861	-0.15607	2.95	4	48
G2	HL19WS-33A-12	2020.37	46	-19.7042	-7.46204	35.55	54	100
G3	HL19WS-33A-16	3709.88	10	2.318917	-0.53903	4.13	8	18
G4	HL19WS-33A-26	1933.33	48	5.157379	6.691375	11.29	24	72
G5	HL19WS-33A-39	3023.46	27	13.57149	-4.03335	24.28	48	75
G6	HL19WS-33A-40	2517.9	40	-0.14041	17.81454	17.82	37	77
G7	HL19WS-33A-49	3324.07	18	9.003015	18.94588	24.72	49	67
G8	HL19WS-33A-51	4117.9	6	-13.2014	-4.5787	23.74	47	53
G9	HL19WS-33A-59	2349.38	41	0.789035	0.698466	1.56	1	42
G10	HL19WS-33A-60	4160.49	4	9.995148	-0.67928	17.65	36	40
G11	HL19WS-33A-61	2863.58	28	-4.5541	-9.42272	12.38	27	55
G12	HL19WS-33A-66	2345.06	42	-17.3402	18.05289	35.52	53	95
G13	HL19WS-33A-133	3416.05	15	7.967291	0.730563	14.07	30	45
G14	HL19WS-33A-135	3341.36	17	-9.78875	-6.26376	18.37	40	57
G15	HL19WS-33A-137	2819.14	31	-5.08178	-3.46429	9.61	20	51
G16	HL19WS-33A-139	2625.31	36	1.510115	5.800405	6.38	14	50
G17	HL19WS-33A-232	2704.32	33	-9.29296	-13.3488	21.14	44	77
G18	HL19WS-33A-332	2728.39	32	-12.5836	-2.00545	22.29	46	78
G19	HL19WS-33A-358	3123.46	24	-18.3725	-7.00275	33.16	51	75
G20	HL19WS-33A-359	3183.95	21	-6.51714	-3.60921	12.05	26	47
G21	HL19WS-33A-367	2156.17	45	-17.7145	-11.5044	33.3	52	97
G22	HL19WS-33A-401	4061.11	7	6.742316	3.79588	12.49	28	35
G23	HL19WS-33A-491	2013.58	47	3.024635	-4.18307	6.78	16	63
G24	HL19WS-33A-589	3841.98	8	3.661948	13.12533	14.63	31	39
G25	HL19WS-33A-604	2653.7	34	11.04592	10.60935	22.19	45	79
G26	HL19WS-33A-625	4138.27	5	5.475732	-0.32697	9.67	21	26
G27	HL19WS-33A-628	3532.1	13	-5.67567	6.619573	12	25	38
G28	HL19WS-33B-2	1240.74	53	-4.07558	2.021561	7.47	17	70
G29	HL19WS-33B-6	1206.17	55	-2.09338	1.442426	3.96	7	62
G30	HL19WS-33B-36	1841.36	49	0.820416	2.056018	2.51	2	51
G31	HL19WS-33B-43	3196.3	19	15.43208	-2.15807	27.31	50	69
G32	HL19WS-33B-75	1436.42	52	-2.01609	0.073861	3.56	6	58
G33	HL19WS-33B-77	2653.7	35	1.544439	3.160495	4.17	9	44
G34	HL19WS-33B-127	3146.3	23	38.10375	-27.8736	72.77	55	78
G35	HL19WS-33B-128	4356.79	2	3.690134	-5.97621	8.84	19	21
G36	HL19WS-33B-171	3185.19	20	3.471151	-1.70155	6.36	13	33
G37	HL19WS-33B-182	1546.91	51	-1.34635	9.494011	9.79	22	73
G38	HL19WS-33B-224	3166.67	22	-4.48617	-1.18032	8	18	40
G39	HL19WS-33B-225	4322.84	3	9.424205	-6.44053	17.83	38	41
G40	HL19WS-33B-239	2565.43	38	5.911818	14.83934	18.14	39	77
G41	HL19WS-33B-246	3083.33	25	-11.5394	1.836387	20.44	42	67
G42	HL19WS-33B-249	2336.42	43	3.948851	14.48103	16.07	35	78
G43	HL19WS-33B-252	3630.25	11	8.652027	3.224129	15.6	34	45
G44	HL19WS-33B-317	2622.84	37	-1.26624	-3.70826	4.33	10	47
G45	HL19WS-33B-324	1754.32	50	-7.34132	-8.62775	15.56	33	83
G46	HL19WS-33B-359	4987.04	1	6.116116	-10.7557	15.24	32	33
G47	HL19WS-33B-361	2538.89	39	-9.6519	-11.3683	20.47	43	82
G48	HL19WS-33B-369	3797.53	9	-1.46132	-0.78467	2.69	3	12
G49	HL19WS-33B-405	1233.95	54	1.088969	4.835039	5.2	12	66
G50	HL19WS-33B-439	3406.79	16	-2.14794	-3.30234	5.03	11	27
G51	Samba Mahsuri	2843.21	29	-3.67622	-0.14531	6.49	15	44
G52	MTU1010	3536.42	12	10.74095	6.169628	19.93	41	53
G53	BRRI Dhan 64	3033.95	26	1.480156	-1.47389	3	5	31
G54	DRR Dhan 48	2824.07	30	7.375257	2.054615	13.17	29	59
G55	HUR 105	3417.28	14	-5.32549	-4.49639	10.42	23	37

biplots, which graphically interpret the GxE interaction to categorize genotypes that exhibit stability and adaptability across different environments. Biplots were made by integrating the initial two PCAs while excluding centering, scaling, or SVP (singular value partitioning).
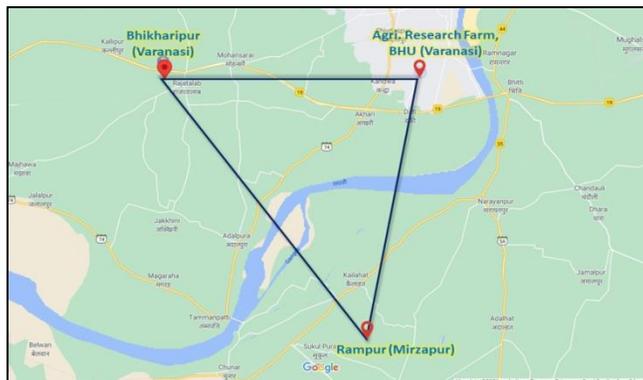
Figure 1. Map of 3 different Locations used for the study in Uttar Pradesh, India

In the biplot, the environment vectors are represented as lines joining the test locations to the origin. The cosine angle between the vectors roughly indicates the correlation between the two locations/environments [22]. To obtain AMMI ANOVA, ASV, and GSI, META-R version 6.04 was utilized. GGE biplots were generated using PB Tools Version 1.4.

Results and Discussion

The genotype HL19WS-33B-359 recorded the highest grain yield hectare^{-1} with 4987.04 kg followed by HL19WS-33B-128 (4356.79kg), HL19WS-33B-225 (4322.84kg). The grain yield hectare^{-1} ranged from 1206.17 kg to 4987.04 kg with a mean of 2905.02 kg (Table 1). However, HL19WS-33B-6 had the lowest grain yield hectare-1 with 1206.7 kg, followed by HL19WS-33B-405 (1233.95 kg).

Analysis of variance
The AMMI ANOVA conducted on fifty-five genotypes tested evaluated at three locations indicated that 69.58% of the total sum of squares (SS) was accounted for by genotypes, 5.93% by environments (E), and 24.49% by the effects of GxE interaction (Table 2).

Table 2. AMMI analysis of variance for grain yield of 55 rice genotypes across 3 environments

Source of variation	Degrees of freedom	Sum of squares	Mean sum of squares	Explained SS (%)
ENV	2	30599515.39	15299757.7	5.93245
GEN	54	358897377.7	6646247.735	69.58089
ENV*GEN	108	126301893.1	1169461.973	24.48666
PC1	55	79864430.24	1452080.55	63.63478
PC2	53	45639933.27	861130.8164	36.36522
Residuals	330	20169877.46	61120.8408	

Analysis results demonstrated significant GxE interactions and MSS (mean sum of squares) attributed to genotype and environment were also found to be highly significant. The significance of G x E interaction is a prerequisite for stability analysis, which indicates that genotypes and environments differ significantly. The high SS attributed to genotypes suggests a diverse range of genotypes, with the majority of grain yield variation resulting from genotypic differences. This finding aligns with the studies conducted by Akter et al., [5] and Hasan et al., [23]. MSS of the GxE interaction was lower compared to genotypes, indicating that the predominant effect was due to genotypes, signifying that the existing difference was due to genotypes. Certainly, the environment influenced the genotype's potential for character expression. In contrast, Ashwini et al., [24] and Reddy et al., [25] found that when rice genotypes were examined in different locations, MSS due

to environment were higher than the genotypic main effects for grain yield. The multiplicative variance due to genotype-environment interaction was partitioned into two significant (IPCA1 and IPCA2) interaction principal component axes. These axes explained 63.63% and 36.28% of the interaction, respectively, with a combined total of 100 percent interaction mean sum of squares. Notably, there were no residual effects observed, indicating that the first interaction axis accounted for a variance that was equal to or greater than the variance explained by the additive terms.

Stability parameters

AMMI stability values (ASV) were estimated for all genotypes based on the individual contributions of the principal component axis scores *viz.*, IPCA I and IPCA II, to the sum of squares of the genotype-environment interaction, following the method proposed by Purchase et al. Additionally, the Genotypic Selection Index (GSI) or Yield Stability Index (YSI) was determined (Table 1) by summing the rankings based on ASV and rankings of yield performance. YSI incorporates yield and stability as the sole criterion. Lower values of stability parameters help to identify stable and desirable genotypes. Accordingly, genotype HL19WS-33A-59 exhibited a high degree of grain yield stability followed by HL19WS-33B-36 and HL19WS-33B-369. Cultivation of these genotypes is recommended across locations. The genotypes HL19WS-33B-127 and HL19WS-33A-12 reported the highest ASV levels and were most unstable across locations. The genotype HL19WS-33B-369 recorded a low GSI value for grain yield, found stable with a better mean performance followed by HL19 WS-33A-16, HL19 WS-33B-128, and HL19 WS-33B-439. Hence, HL19 WS-33B-369 and HL19 WS-33A-16 were the top genotypes due to their higher mean yields and are stable for yield across the three locations. So, these can be suitable for general cultivation as they reported better mean yield and low ASV. The findings are consistent with previous studies or in line with existing research [3, 26].

AMMI biplot display

AMMI1 biplot describes the interaction between genotypes and environments by displaying the main effects in the abscissa while IPCA1 scores on the ordinate. A displacement in the abscissa, also known as the X-axis signifies the main effects difference, wherein ordinate represents variances in the interaction effects. The genotypes G53, G36, G38, G33, G51, G44, G20, and G54 were stable genotypes due to their position near the biplot's origin as shown in Figure 2. A similar type of findings has been reported in the literature on rice crops by Bose et al., [3] and Akter et al., [27]. A genotype that shows a smaller AMMI stability value or AMMI stability index (Di) value will generally be considered stable. The low degree of interaction between these genotypes and the environment makes them least affected by the environment. In contrast, the G7, G12, G2, G19, G17, G47, and G34 genotypes were the most unstable. Hence, their adaptations seemed to be environment-specific due to their distant location from the biplot origin (Figure 2A and 2B). Akter et al., [27] reported similar findings on hybrid rice genotypes. The genotype G46 was adjudged as the best genotype owing to its highest yield response with greater adaptability among all genotypes with a yield of 4987.04 kg/ha per hectare followed by G35 and G39. According to the AMMI 1 biplot, environments E1 and E3 have high yields exhibiting significant additive genotypic main effects; in contrast E2 has a lower yield.

GGE biplot

The graphical representation of GGE biplots for grain yield per hectare (Figure 3) showed 90.9 percent of total G + GE variation which represents an adequate amount of variation among different genotypes under three environments. *"What-won-where" view* The genotypes viz., G46 (HL19WS-33B-359), G8 (HL19WS-33A-51), G19 (HL19WS-33A-358), G2 (HL19WS-33A- 12), G28 (HL19WS 33B-2), G49 (HL19WS-33B-405), and G34 (HL19WS-33B-127) were observed to be responsive genotypes and unstable for grain yield hectare-1 owing to their position on vertices of the polygon as shown in the Figure 3A. All three environments were falling under one group by the radiating straight lines interconnecting the verges of the polygon at 900. The genotypes HL19WS-33B-359 (G46)
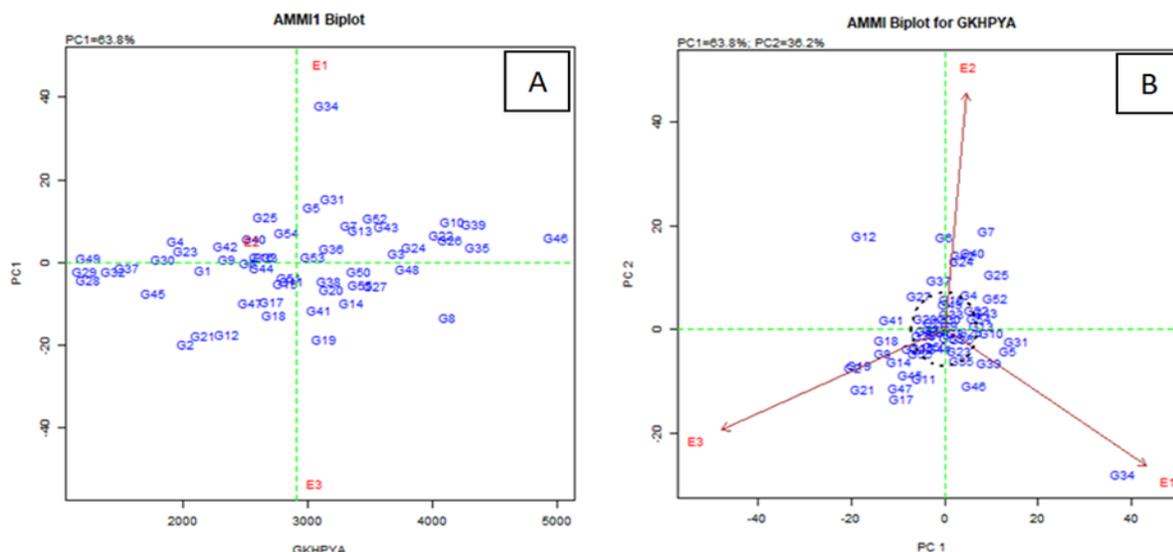
Figure 2. (A) AMMI-1 model biplot for grain yield of rice genotypes across the environments (B) AMMI 2 biplot for grain yield (tha^{-1}) showing the interaction of IPCA2 against IPCA1 scores of 55 rice genotypes

and HL19WS-33A-51 (G8) were winners in all three environments. The genotypes BRRI Dhan 64 (G53), HL19WS-33B-171 (G36), HL19WS-33B-317 (G44), Samba Mahsuri (G51), and HL19WS-33B-77 (G33) were stable according to GGE biplots, based on their proximity to the origin. The stable genotypes with higher yields can be recommended for cultivation and also use as parents to improve yield. The obtained results align with the findings reported by different researchers [16, 19, 28-29]. These studies have also observed similar patterns or trends, reinforcing the consistency and reliability of the current research findings.

Mean v/s stability

The ranking of 55 genotypes in the GGE biplot genotype view depends on the mean yield and stability. It was noted that if PC1 of a GGE bi-plot approximates the genotype's mean performance, PC2 must approximate the GE effects linked to each genotype, which is an indicator of instability [12]. The genotypes G35 and G39, being closer to the "ideal genotype" G46, are considered more desirable than the other screened genotypes (Figure 3B). Their proximity to the ideal genotype suggests that they possess favorable traits and characteristics that align with the desired breeding objectives. Conversely, the genotypes G28, G29, G49, G32, and G37 are regarded as poor performing or inferior since their placement at a considerable distance from the ideal genotype G46, indicates that they exhibit characteristics or traits that are undesirable. Additionally, genotypes having shorter vector lengths are deemed more stable, while genotypes having longer vector lengths are considered less stable. Consequently, G34, G19, G8, and G2 were the least stable, whereas G35, G26, G24, G3, G53, G50, and G39 were with greater stability. However, stability alone is desirable when it is associated with a high mean yield. Thus, G46, G35, and G39 were identified as high-yielding and stable genotypes. These observations provide valuable insights for selecting the most desirable and stable genotypes for further cultivation and breeding programs. Hashim et al., [30] reported that G1 exhibited the highest grain yield but lacked stability, while G15 displayed high stability despite having a lower grain yield. "*Discriminativeness vs. Representativeness*" *view* The environment view of the GGE biplot (Figure 3C) showed the short vector found in Bhikaripur (E2) so this environment was not able to discriminate the genotypes while longer vectors than E2 were found in the locations *viz*., Agricultural research farm, BHU (E1) and Rampur (E3) signifying that these environments were

able to discriminate between different genotypes for grain yield. Agricultural research farm, BHU (E1) had the longest vector and short angle with AEA, indicating the best representative place or location for distinguishing genotypes, while Rampur (E3) has the long vector and larger angle with AEA, so these locations may not be utilized for discriminating the genotypes but can be advantageous in rejecting unstable genotypes.
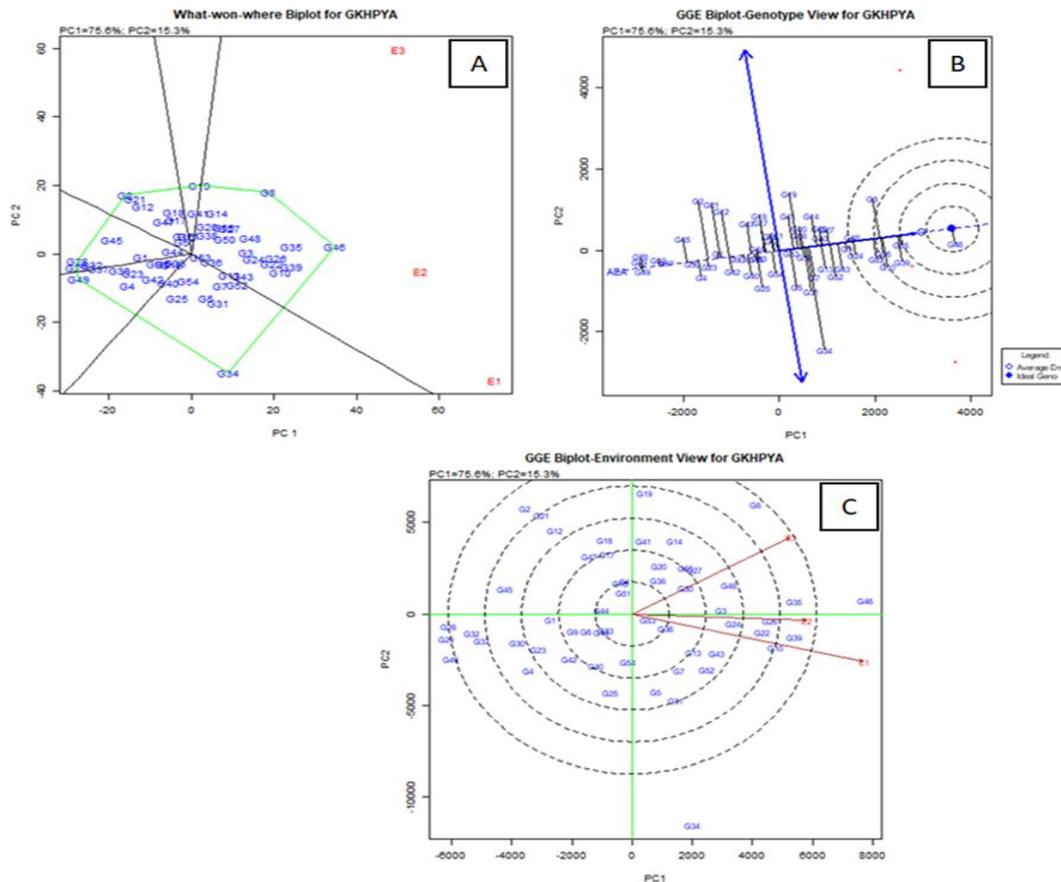

Figure 3. (A) Polygon view of genotype- environment interaction across three test environments (B) GGE biplot – Genotype view to rank genotypes relative to ideal genotype (C) The environment view of GGE biplot to show the discriminating ability and representativeness the test environments

Chandramohan et al. [31] reported locations E4, E2, and E5 were relatively deemed ideal for achieving good yield, whereas E1, E3, and E6 were identified as poor and highly discriminating. These findings can be applied to design and deploy targeted interventions specific to different locations, select niche areas for high-quality seed production, agronomic zoning of genotypes, and selectively breed elite genotypes with stable yields. These applications are crucial in addressing the impacts of climate change and have the potential to significantly increase rice production in the future [28].

Conclusion

AMMI analysis revealed a significant genotype-environment interaction amongst 55 genotypes tested over 3 different locations. The most stable genotypes were discovered to be HL19WS-33B-171, HL19WS-33B-317, and HL19WS-33B-77 across three distinct locations. GGE biplots revealed three locations were part of a single mega-environment, with genotypes HL19WS-33B-359 and HL19WS-33A-51 performing best. Among all other screened genotypes HL19WS-33B-359 produced the best grain yield and stable across three locations. Although both the AMMI model and GGE biplots

are useful in this study for understanding GE interactions, GGE biplots may provide more insightful information about genotype-environment relationships. The high-yielding stable genotypes shall be suggested for advanced testing to release or utilized in breeding programs to enhance rice yield and grain quality attributes.

Acknowledgment

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