

## GGE BI-PLOT ANALYSIS OF HIGH-ZINC RICE (*ORYZA SATIVA* L.) GENOTYPES UNDER MULTIPLE ENVIRONMENTS FOR GRAIN YIELD

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**Abstract.** Bi-plot analysis has been a popular method for determining the magnitude of the genotype-environment (G × E) interaction in plant breeding and agricultural research. The 21 high-zinc rice genotypes for grain yield per plant (GYP) and grain zinc content (GZC) were evaluated in a complete randomized block design with three replications in Uttar Pradesh, India to identify the winning genotype through multi environmental trials (MET) using GGE bi-plot analysis. The first principal component (PC1) and the second principal component (PC2) each showed 61.56% and 17.25% of the variance, respectively, and together they explained 78.81% of the overall variance. Using GGE bi-plot polygon views, GYP and GZC might each have two feasible mega-environments. In E1 and E2, the genetic information for GYP and GZC was highly correlated and comparable. The genotype V13 (BRRI dhan 72) had the greatest mean GYP and was the most stable, while V8 (IR 96248-16-3-3-2-B) was highly unstable and V17 (IR 64) yielded the least. The greatest GZC and most stable genotypes were found in V1 (IR 95044:8-B-5-22-19-GBS), whereas the highest GZC and most unstable genotypes were found in V19 (Sambamahsuri). For GYP, V20 (Swarna) won only in E3, while V13 (BRRI dhan 72) won in the other environments; for GZC, V3 (IR 99704-24-2-1) won only in E3, while V1 (IR 95044:8-B-5-22-19-GBS) won in the other environments. As

a conclusion, in future breeding programmes, the V13 (BRRI dhan 72) for GYP and V1 (IR 95044:8-B-5-22-19-GBS) for GZC might be suggested for cultivar selection and zinc bio-fortification.

**Keywords:** *genotype-environment (G × E) interaction, grain Zinc content, multi environmental trial, stable genotypes, winner genotypes*

## Introduction

Rice (*Oryza sativa* L.) is considered an essential food for humans and it is cultivated all over the world. Rice is consumed by about half of the world's population (Suman et al., 2021). Asia produces about 80% of the world's rice. Despite having the world's largest rice crop area (44.1 million hectares) and a production of 165.3 million tonnes, India's productivity per hectare (3.78 tonnes) is low (Kesh et al., 2021). Zinc concentration in rice is also important. More than 30% of the world's soils are Zinc (Zn) deficient. Legumes are more vulnerable to Zn deficiency, affecting grain production and nutritional quality (Impa et al., 2013). Rice grown on soils lacking in Zn leads to lower yields and nutritional quality. For example, poor plant-accessible Zn soils reduced grain Zn concentration by 80%. Reduced human bioavailability owing to decreasing Zn concentration in grain has increased Zn deficiency in vulnerable areas (Cakmak, 2008a). Agronomic Zn bio-fortification of rice grains is a promising and cost-effective strategy (Zaman et al., 2018). As a result, in the present day, sufficient sustainable production of healthy, safe foods production is challenging task. Demands for higher productivity with micronutrients availability have become a serious concern all over the world.

As a consequence, producing enough nutritious, safe meals in a sustainable manner is a challenging job in today's world. Micronutrient availability has become a key issue globally as productivity demands grow. Rice production has been hampered by a lack of better varieties (early maturing, biotic and abiotic stress resistant and high-yielding genotypes), inadequate soil fertility, and genotype-environment interactions (GEI) that hinder the selection process for several crops, including rice. GEIs for quantitative characteristics like seed yield may lead genotypes to behave differently in different situations (Gurmu et al., 2009). For this purpose, plant breeders use multi-environment trials (MET) to evaluate genotype performance and assess genotype adaptability and stability. Stable genotypes must be able to perform well in ideal conditions and yield well in less favourable environments. Rice cultivars need to be bred in order to measure how well they can adapt and stay stable. While MET collects data on several variables, it generally focuses on only one (usually yield), ignoring data on other features. Even though the observed yield is a result of the influence of genotype (G), environment (E), and genotype environment interaction (GEI), only G and GE matter (GE). Bi-plot analysis is a vital statistical tool in plant breeding and agricultural research. Genotype-by-environment data, defined as noise or a confounding factor, is frequently confined to genotype evaluation based on genotype main effect (G). Some practitioners, such as breeders, biometricians, and quantitative geneticists, still disagree on how GE should be judged. The term "GGE bi-plot" was recently coined, and numerous bi-plot visualisation methodologies were developed to address specific GGE data difficulties (Kaplan et al., 2017).

Diverse studies have validated and then used the GGE bi-plot methodology to analyse data from multi-environment trials, showing the method's effectiveness for selecting optimum stable genotypes. The first two symmetrically scaled principal components, PC1 and PC2, are formed through the singular value decomposition of environment-centered multi-environment trial (MET) data. The GGE biplot graphically displays a MET's G plus

GE for easy visual cultivar evaluation and mega-environment identification. In addition, GGE biplot analysis can visually answer most inquiries given to a genotype by an environment table (Yan and Tinker, 2005, 2006). It enables accurate genotype evaluation as well as a full understanding of the target and test environments. An understanding of the target environment as a whole, i.e., whether it is made up of one or several mega-environments, may help determine if GE can be used or avoided. Bi-plot analysis may help evaluate if test conditions within a single mega-environment are informative, representative, and genotype discriminative. Simultaneously, bi-plot analysis may examine genotypes' mean performance as well as their environmental stability. Short-and long-term difficulties may be addressed using GGE biplot analysis of genotype by environment data. The GGE biplot has been used to analyse durum (Kendal and Sener, 2015), maize (Oyekunle et al., 2017), barley (Solonechnyi et al., 2018), sorghum (Gasura et al., 2016), lentil (Karimizadeh et al., 2013), sweet-potato (Mustamu et al., 2018) and Bambara groundnut (Tena et al., 2019; Olanrewaju et al., 2021). So, GGE Bi-plot analysis was used in this study to find the best genotypes and environments based on both average performance and stability for both grain yield per plant and grain zinc content.

## Materials and methods

### Plant materials

Twenty-one genotypes used in the present study were mentioned in *Table 1*. These genotypes were locally collected from IRRI South Asia Hub, Hyderabad, India and the experiment was conducted at five different locations (*Table 2*) in Uttar Pradesh, India during *Kharif-2017*.

**Table 1.** List of high zinc rice genotypes used for the experiment (Source: IRRI South Asia Hub, Hyderabad, India)

Entry No.	Entry Name	Grain Zinc Content (ppm)	Entry No.	Entry Name	Grain Zinc Content (ppm)
1	IR 95044:8-B-5-22-19-GBS	20.6	12	BRRRI dhan 64	24.97
2	IR 84847-RIL 195-1-1-1-1	21.8	13	BRRRI dhan 72	20.7
3	IR 99704-24-2-1	14.67	14	DRR Dhan 45	18.13
4	IR 99647-109-1-1	23.7	15	DRR Dhan 48	19.2
5	IR 97443-11-2-1-1-1-1 -B	14.45	16	DRR Dhan 49	17.63
6	IR 97443-11-2-1-1-1-3 -B	23.47	17	IR 64	23.57
7	IR 82475-110-2-2-1-2	24.73	18	MTU1010	21.70
8	IR 96248-16-3-3-2-B	27.18	19	Samba Mahsuri	24.47
9	R-RHZ-7	26.61	20	Swarna	18.89
10	CGZR-1	24.43	21	Local check (HUR3022)	16.9
11	BRRRI dhan 62	23.33			

### Experimental design

The experiment was laid out in a completely randomized block design with three replications. The weather conditions during the evaluations period from June 2017 to November 2017 were almost normal and favorable for crop growth. All the experiments

of five different locations were carried out at irrigated ecosystem and medium upland with transplanted nursery establishment.

**Table 2.** Five different environments used for the experiment

Environment Code	Location Name	Latitude	Longitude	Altitude	Land Type	Avg. Temp. (°C)	Avg. Rainfall (mm)
E1	BHU Agriculture Research farm –I	25.18° N	80.30° E	81M	Up land	27.51	181.4
E2	BHU Agriculture Research farm –II	25.18° N	80.30° E	81M	Low land	27.5	181.5
E3	Bhikaripur	25.26° N	82.83° E	87M	Low land	28.32	187.4
E4	Karsada	25.22° N	82.90° E	85M	Up land	28.88	167.2
E5	Rampur	25.23°N	82.89°E	80M	Up land	29.39	155.8

### Cultural practices

The single seedling was transplanted at a 15 cm × 20 cm distance. All the standard recommended cultural practices were followed. Fertilizers were applied as 120 kg N, 60 kg P<sub>2</sub>O<sub>5</sub> and 60 kg K<sub>2</sub>O per hectare.

### Quantitative and qualitative traits data observations

For all yield and yield attribution variables except days to first flowering, 50% flowering, and maturity, five competing plants were randomly chosen from each row of each genotype in each replication. The performance of the cultivars was assessed using the parameters listed (Grain yield per plant and Grain zinc content) in Table 3 and Table 4. The quantitative features were shown and evaluated as indicated by Biodiversity International (IPGRI and WARDA, 2007).

**Table 3.** Mean Grain Yield per Plant (gm) of 21 high zinc rice genotypes in five different environments

Genotypes	Name of the genotype	E1	E2	E3	E4	E5	Mean
V1	IR 95044:8-B-5-22-19-GBS	10.86	12.92	13.05	7.68	6.01	10.11
V2	IR 84847-RIL 195-1-1-1-1	11.50	13.66	13.74	7.99	6.57	10.69
V3	IR 99704-24-2-1	13.12	15.58	14.33	9.96	8.39	12.27
V4	IR 99647-109-1-1	10.79	12.77	15.28	5.35	5.12	9.86
V5	IR 97443-11-2-1-1-1-1 -B	14.90	17.62	18.01	9.10	9.31	13.79
V6	IR 97443-11-2-1-1-1-3 -B	15.39	18.15	20.30	7.59	9.10	14.11
V7	IR 82475-110-2-2-1-2	12.91	15.30	15.61	8.35	7.66	11.97
V8	IR 96248-16-3-3-2-B	12.22	14.42	17.81	5.09	6.01	11.11
V9	R-RHZ-7	11.25	13.33	15.49	5.88	5.63	10.31
V10	CGZR-1	10.96	13.03	13.57	7.33	5.96	10.17
V11	BRRRI dhan 62	10.76	12.76	14.95	5.65	5.21	9.86
V12	BRRRI dhan 64	12.73	15.01	18.73	4.98	6.32	11.56
V13	BRRRI dhan 72	15.92	18.78	20.36	8.38	9.75	14.64
V14	DRR Dhan 45	12.99	15.33	18.31	5.81	6.80	11.85
V15	DRR Dhan 48	11.52	13.69	13.69	8.07	6.61	10.72
V16	DRR Dhan 49	14.34	16.95	18.11	8.13	8.58	13.22
V17	IR 64	9.63	11.46	12.84	5.96	4.54	8.89
V18	MTU1010	13.67	16.14	18.63	6.56	7.54	12.51
V19	Samba Mahsuri	11.91	14.12	15.11	7.28	6.59	11.00
V20	Swarna	13.85	16.29	21.02	4.47	6.91	12.51
V21	Local check(HUR3022)	13.95	16.49	18.11	7.52	8.09	12.83

**Table 4.** Mean Grain Zinc content (ppm) of 21 high zinc rice genotypes in five different environments

Genotypes	Name of the genotype	E1	E2	E3	E4	E5	Mean
V1	IR 95044:8-B-5-22-19-GBS	29.63	27.25	29.00	15.61	32.54	26.81
V2	IR 84847-RIL 195-1-1-1-1	27.63	25.67	28.67	17.62	29.66	25.85
V3	IR 99704-24-2-1	25.23	23.66	27.28	18.43	26.64	24.25
V4	IR 99647-109-1-1	28.79	26.41	27.47	14.22	31.93	25.76
V5	IR 97443-11-2-1-1-1-1-B	19.61	18.12	17.47	9.84	22.43	17.49
V6	IR 97443-11-2-1-1-1-3-B	19.88	18.73	20.66	14.60	21.46	19.07
V7	IR 82475-110-2-2-1-2	29.14	26.68	27.40	13.65	32.50	25.87
V8	IR 96248-16-3-3-2-B	27.34	25.16	26.32	14.22	30.25	24.66
V9	R-RHZ-7	25.92	23.95	25.35	14.45	28.54	23.64
V10	CGZR-1	26.57	24.77	27.93	17.77	28.39	25.09
V11	BRR1 dhan 62	24.67	22.99	25.32	15.99	26.66	23.13
V12	BRR1 dhan 64	26.26	24.24	25.56	14.36	28.96	23.88
V13	BRR1 dhan 72	18.26	17.14	17.91	12.26	20.21	17.16
V14	DRR Dhan 45	24.05	22.24	23.20	13.38	26.65	21.90
V15	DRR Dhan 48	21.88	20.48	22.40	14.86	23.72	20.67
V16	DRR Dhan 49	22.13	20.37	20.04	10.76	25.12	19.68
V17	IR 64	24.22	22.40	23.38	13.45	26.82	22.05
V18	MTU1010	22.97	21.24	21.78	12.49	25.63	20.82
V19	Samba Mahsuri	20.07	19.13	22.71	17.63	20.86	20.08
V20	Swarna	17.32	16.37	17.55	12.87	18.94	16.61
V21	Local check(HUR3022)	23.53	21.61	21.36	11.11	26.65	20.85

### Nutritional traits data estimation

Grain Zinc content of samples was estimated by Atomic Absorption Spectrophotometer (Thermo Scientific, Model: iCE 3500, Double beam optics, Acetylene flame) in Indian Institute of Rice Research (IIRR), Hyderabad as followed the protocol suggested by the Sahrawat et al. (2002).

### Statistical analysis

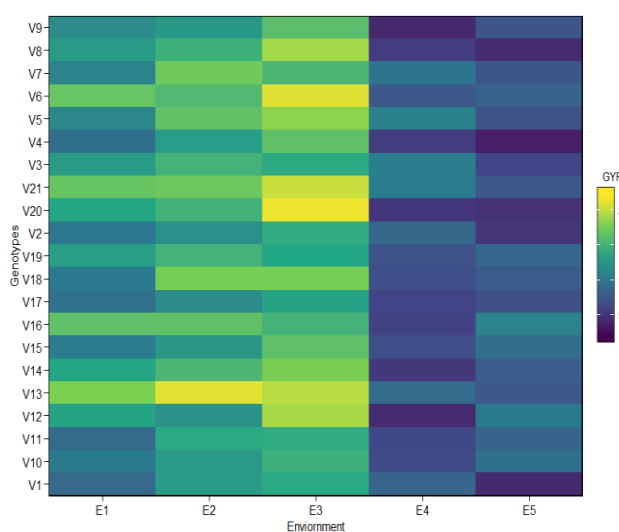
Multivariate Analysis was carried out in using R (4.0.5) software packages and R studio (Team R, 2019). Multi-trait multi-environment analysis including GGE bi-plot analysis for grain yield per plant (GYP) and grain zinc content (GZC) were analyzed using METAN packages (Olivoto and Lúcio, 2020). The ggplot2 packages were used to create the GGE bi-plot display (Wickham et al., 2016). A mixed ANOVA was performed using genotypes and environmental factors as fixed and random factors, respectively. Based on the singular value decomposition (SVD) of the first two main components, a GGE biplot (Yan et al., 2000) model is:

$$Y_{ij} = \mu + \beta_i + \sum_{n=1}^K \lambda_n \xi_{in} \gamma_{jn} + \varepsilon_{ij} \quad (\text{Eq.1})$$

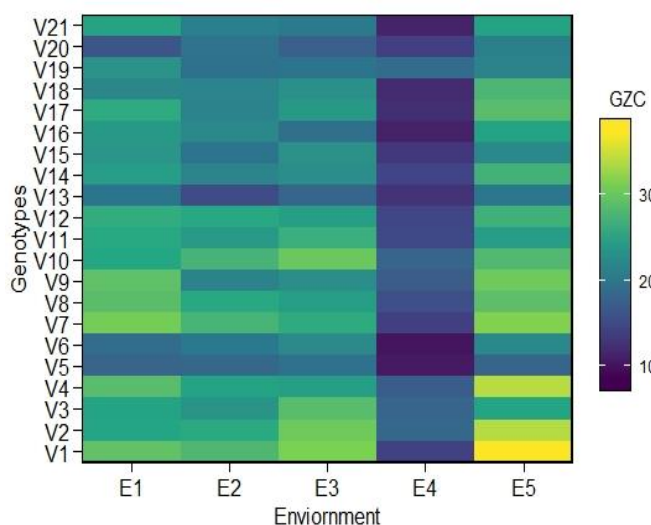
$$Y_{ij} = \mu + \beta_j + \sum_{n=1}^k \lambda_n \xi_m \eta_m + \varepsilon_{ij} \quad (\text{Eq.2})$$

where  $Y_{ij}$  is the mean of genotype  $i$  in environment  $j$ ;  $\mu$  is the grand mean;  $\beta_j$  is the environment  $j$  main effect;  $n$  is the singular value;  $\lambda_n$ ,  $\xi_{in}$  and are, respectively, singular value, genotype eigenvectors, and environment eigenvectors for  $n^{\text{th}}$  interaction principal component; and  $\varepsilon_{ij}$  is the residual effect.

Grain yield and zinc content were modelled using a mixed linear model (site). The GGE bi-plot study used mean grain yield and zinc content as two-way table data. For ATC, polygon, and vector views, GGE bi-plots employed the first two symmetrically scaled PCs (to visualise the correlations among environments or genotypes). The GGE bi-plots utilised the mean GYP and GZC performances of 21 high zinc rice genotypes (Table 3, Table 4, Figure 1 and Figure 2). We compared genotypes to ideal environments and environments to ideal genotypes. The “which-won-where” option identified mega-environments and winning genotypes.



**Figure 1.** Heat map showing which genotype win in which environment based on GYP mean performance



**Figure 2.** Heat map showing which genotype win in which environment based on GZC mean performance

## Results and discussion

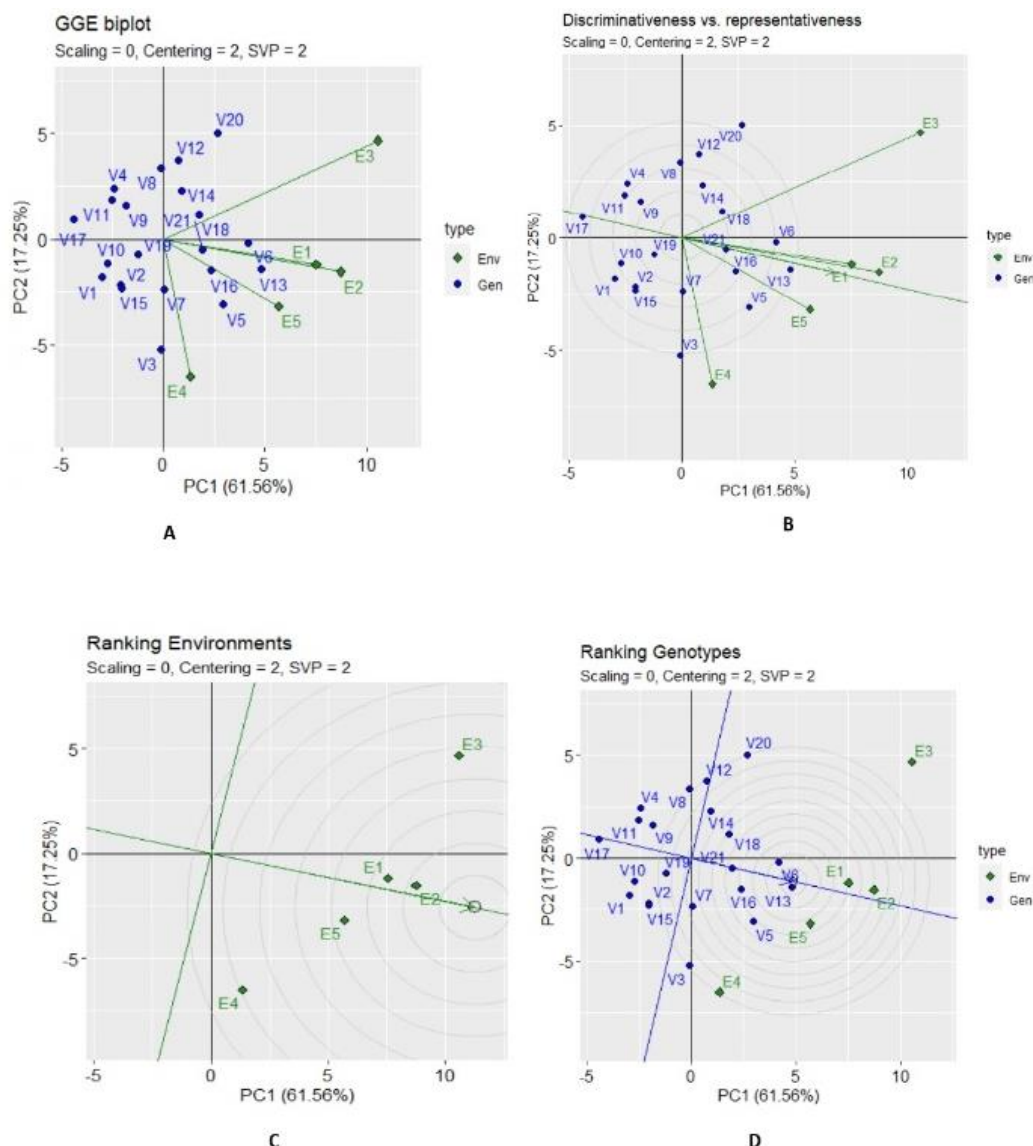
### *Evaluation of environments using GGE bi-plots for GYP and GZC*

#### *Relationships among test environments*

The GGE bi-vector plot's view summarises the environment. Variability in the bi-plot between two environments is a good indicator. The length of an environmental vector may be used to assess its discriminating power (Yan et al., 2007). This study revealed that the first and second principal components (PC1) explained 61.56 and 17.25% of the variation, respectively (*Figure 3*). It can detect environmental correlations. This is seen in *Figure 3A* and *Table 3*, while *Figure 4A* and *Table 4* exhibit GZC data. An environment-centered (centering = 2) G by E bi-plot with no scaling (scaling = 0). This bi-plot explained 78% of the environmental G by E variation. These lines can be thought of as environment vectors in the GGE bi-plot shown in *Figure 3A*. In GYP, the acute angle between E1, E2, E3, and E5 suggests a good connection between the environments. When E3 and E4 form an obtuse angle, the two have a negative correlation. The absence of a straight angle between the two environments indicates no relationship. Large negative correlations (obtuse angles) suggest a substantial crossover GE. The greatest angle between E3 and E4 is more than 90°, indicating a larger GE here. The distance between two habitats reveals their genetic similarities (Yan and Tinker, 2006). The cosine of the angle between two environments indicates their resemblance (covariance). Fewer testing contexts (E1 and E2) provide the same genetic information, cutting testing expenses. One of two test conditions may be eliminated without impacting genetic information. For GZC, all environments form an acute angle. E1 and E2 have similar GZC genetic information, but E5 and E4 are considerably distinct.

#### *Discriminativeness and representativeness of test environments*

An ideal environment is one that is descriptive and has the greatest ability to discriminate (Yan and Tinker, 2006). The ideal environment is positioned in the first concentric circle of the GGE bi-plot, and the desirable environments are those that are close to the ideal environment. In the bi-plot, each environment's standard deviation shows its discriminating ability. E3 was the most discriminating (informative) environment for GYP, whereas E5 was the least (*Fig. 3A*). Non-discriminating (non-informative) test environments provide minimum genetic information and should not be used. GZC found E5 to be the most discriminatory, whereas E2 was the least (*Fig. 4A*). *Figure 3B* depicts the average-environment axis (AEA). AEA connects the average coordinates of all test environments to the bi-plot origin. As in *Figure 3B*, the AEA for GYP represents numerous test situations. So E2 represents the most and E4 the least. Good test environments for choosing generic genotypes are discriminating and representative (e.g. E2). Discriminating but non-representative test environments (E4 and E3) may be used to select genotypes that are perfectly matched to target environments through removing the unstable genotypes. Non-discriminating test environments E1 (with short vectors) is less beneficial since it gives minimal genotype discrimination in GZC, E1 is the most representative, while E4 is the least representative (*Figure 4B*). Similar kinds of results were reported in hybrid rice by Akter et al. (2015) and high zinc rice by Inabangan-Asilo et al. (2021).

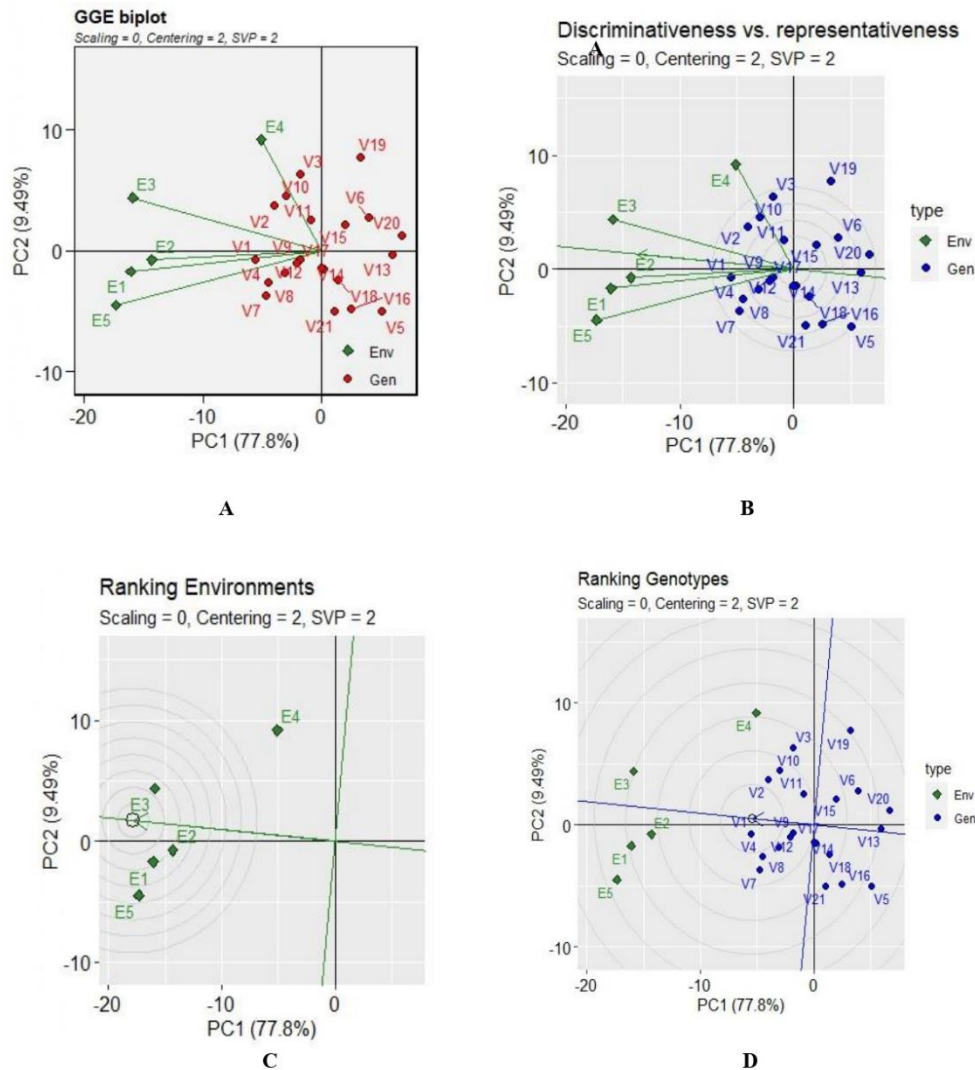


**Figure 3.** GGE Biplots of GYP A) Relationship among test environments in discriminating the genotypes B) Discriminativness vs. representativeness of test environments C) Ranking environments relative to an ideal test environment based on both discriminating ability and representativeness D) Ranking genotypes based on performance of each genotype in each environment

### Ideal test environments for selecting generally adapted genotypes

The ideal test environment inside a mega-environment is discriminating (informative) and reflective of the intended environment. The concentric rings in *Figure 3C* and *Figure 4C* constitute an "ideal test environment". It is a positive point on the AEA ("most representative") with a distance from the bi-plot origin equal to the longest vector of all environments ("most informative"). For GYP, E2 is the best, while E4 and E3 were worse for choosing cultivars suitable for the whole area (*Fig. 3C*). Regarding GZC, E3 was the best choice for picking cultivars suited to the whole area, whereas E4 and E5 were the worst (*Fig. 4C*). A similar kind of experiment was conducted by Sincik et al. (2021) in canola, where she used E8 and E6 as the target environments in canola.





**Figure 4.** GGE Biplots of GZC A) Relationship among test environments in discriminating the genotypes B) Discriminateness vs. representativeness of test environments C) Ranking environments relative to an ideal test environment based on both discriminating ability and representativeness D) Ranking genotypes based on performance of each genotype in each environment

### Evaluation of genotypes using GGE bi-plots for GYP and GZC

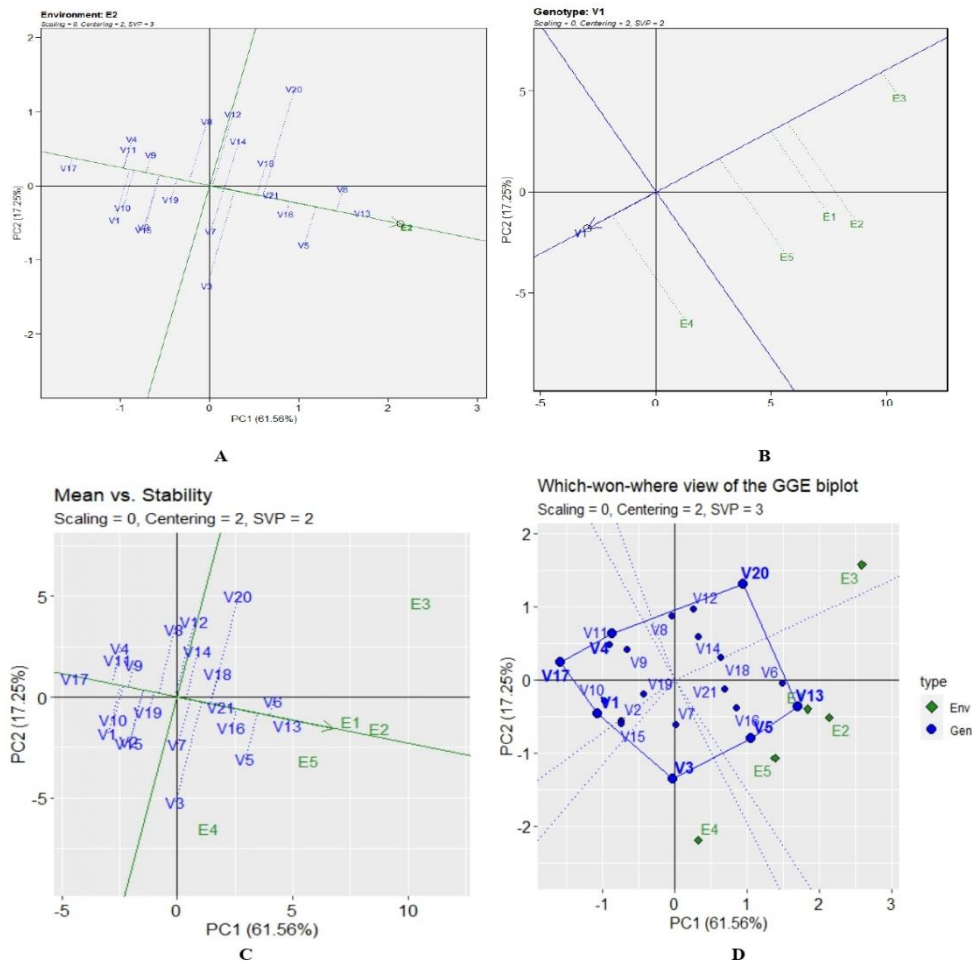
#### Performance of the genotypes in specific environments

Figure 3D depicts the relationships between genotypes and environments (i.e., genotype performance in each environment). A genotype's performance in an environment is better than average if the angle between its vector and the environment's vector is less than  $90^\circ$  (Yan and Tinker, 2006). While, V4, V9, V11, and V17 were below average in all environments (obtuse angles) in the current experiment for GYP, V21, V6, V13, V16, and V5 were above average in all contexts (acute angles). In all environments, V5, V13, and V20 were below average, but V1, V4, V9, and V2 were above average. In E2, V14 is the same as the average GZC, while V21 is closer to the average (right angle). The interaction's amplitude is determined by the cosine (angle) and length (vector length)

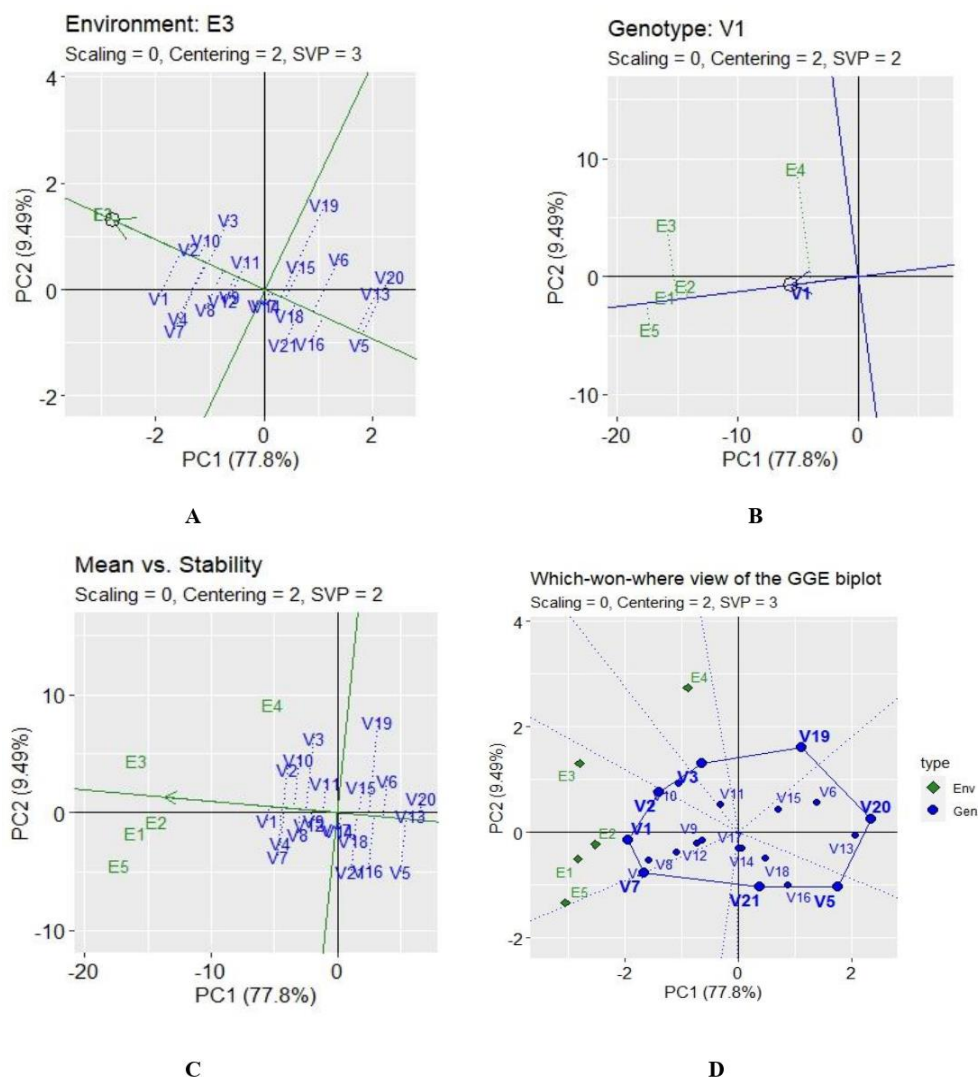
of the interaction. The performance of a genotype in different situations can be used to figure out where it ranks, as can the performance of the places where it lives.

*Ranking genotypes based on performance in best environment*

A line is formed between the bi-plot origin and the environment to rank the genotypes in the best environment (E2). This is the axis for this environment, and it ranks the genotypes (Yan and Tinker, 2006). The genotypes are ranked in *Figure 5. A* based on their performance in E2 for GYP. V17, V4, V11, V1, V10, V9, V2, V15, V19, and V8 yielded less than average, while V12, V7, and V14 yielded near-average and the others yielded more than average. V13 had the greatest yield in E2, followed by V6 and V17, which had the lowest output. *Figure 6A* ranks the genotypes in GZC depending on their performance in E2. GZC was lower than normal in the V5, V20, V13, V16, V6, V21, V18, and V15 genotypes, but near average in the V19 genotype. In E2, the genotypes with the greatest GZC were V2 and V1, followed by V10, and the genotype with the lowest GZC was V5. Similar kinds of findings were reported by Khan et al. (2021) in Bambara groundnut.



**Figure 5.** GGE Biplots of GYP A) Ranking genotypes based on their performance in one environment E2 B) Ranking test environments in terms of the relative performance of a genotype V1 C) The average-environment coordination (AEC) view to rank genotypes based on both mean and stability D) The which-won-where polygon view of the GGE biplot to show which genotype performed best in which environment



**Figure 6.** GGE Biplots of GZC A) Ranking genotypes based on their performance in one environment E2 B) Ranking test environments in terms of the relative performance of a genotype V1 C) The average-environment coordination (AEC) view to rank genotypes based on both mean and stability D) The which-won-where polygon view of the GGE biplot to show which genotype performed best in which environment

### Ranking environments based on the performance of a genotype

A line is drawn from the bi-plot origin to the genotype to rate the genotype's relative performance in each environment. The axis of this genotype is a line that ranks the environments (Yan and Tinker, 2006). *Figure 5B* ranks the test environments based on the genotype V1's relative performance. Environment E4 had the highest average yield, whereas other environments yielded lower average yields. In *Figure 6B*, V1 had a greater GZC than the average in the environment E5, as seen in the figure.

### Mean performance and stability of the genotypes

All genotypes in a single mega-environment must be evaluated on mean performance and environmental stability. *Figure 5C* displays the GGE bi-plot from an AEC viewpoint.

The single-arrowed line is the (AEA), which leads to increased mean yield across environments (SVP =1) (Yan and Tinker, 2006). The highest mean yield was V13, followed by V6, V5, V16, and V21; the grand mean was V12; and the lowest, V17. The AEC ordinate is a double-red line that denotes poor stability. Due to the excellent stability of V13, it may be used as a genotype reference. Given that the bi-plot only addresses a small fraction of the entire variance, certain genotypes that seem stable may not be stable at all. Unlike other rice genotypes, V8 was very unstable, yielding less in E3 and E4, but more in E5, and was less appealing than other rice genotypes. Its E1 and E2 yields were precisely anticipated by its total yield. For example, in *Figure 6B*, V1 had the greatest GZC, followed by 4, 2, 7, 10, 8, and 11, with a mean close to the grand mean, and V20 the lowest. V19 was a very unstable genotype, while V1 was a stable one. In 2017, Haider et al. (2017) found similar findings.

#### *Ranking genotypes relative to the ideal genotype*

To maximize yield, genotypes should have a high PC1 (high yielding ability) and a low (absolute) PC2 score (high stability). However, an "ideal" genotype's vector length is equal to the longest genotype's vector ("highest mean performance"). Thus, closer genotypes to the "ideal genotype" are desired (Rakshit et al., 2012). In spite of the greater average yield, V16 beat V5 in the case of GYP. Of course, V17 was the worst, and V13 was the greatest. *Figure 3D* shows "Stability." The best stability is combined with ordinary performance. *1. D* shows V17 as "stable." Inconsistency in V17's performance does not make it good. V17 outperformed V20 and V3 in several situations. Similarly, for GZC, on average, V20 was the worst genotype in *Figure 4D*, whereas V1 was the best. Searching for "stability" genes might be deceptive. Only genotypes with high mean performances are considered "stable".

#### *Comparison among all genotypes*

The GGE bi-plot in *Fig. 3B* for GYP can also give clear cut differences among the genotypes. The distance between two genotypes approximates the Euclidean distance between them, which is a measure of their total dissimilarity. V20 and V3 are distinct genotypes, although V2 and V15 are extremely similar. For each setting, the bi-plot origin represents a "virtual" genotype. This "average" genotype contributes nothing to G or GE. A genotype's distance from the bi-plot origin assesses its contribution to G, GE, or both. Thus, genotypes near the bi-plot origin contribute little to both G and GE, whereas genotypes with longer vectors contribute much to either G or GE (Yan and Tinker, 2006). Thus, the best (V13), worst (V17), or most unstable (V3 and V20) genotypes have the longest vectors. The angle between a genotype's vector and the AEA divides its length into G and GE components. For example, an obtuse or acute angle suggests the contribution is mostly to G, resulting in lower-than-average mean performance; while a right angle means the contribution is mostly to GE, resulting in higher-than-average mean performance. The angle between two genotypes reveals their environmental similarity. For example, an acute angle (V11 vs. V4) suggests the two genotypes behaved similarly and the difference was proportionate in all settings. Obtuse angles (e.g., V20 vs. V3) indicate that the two genotypes behaved inversely, with the first genotype outperforming the second. For each genotype (for example, V6 and V12), the environments for GZC are in *Figure 4B*, V19, and V5 have quite distinct genotypes, although V2 and V10 are fairly close. An acute angle between V1 and V2 shows similarity in response to GZC contexts, but an obtuse angle between V7 and V19 implies the opposite response. Inabangan-Asilo

et al. (2019) found that by looking at genotype-environment interaction ( $G \times E$ ) and stable genotypes from multiple locations, they could help find lines that could be released as new varieties.

### ***Which-won-where***

In multi-location yield trials, the GGE-bi-plot analysis polygon perspective helps discover cross-over and non-crossover genotype-by-environment interactions and helps identify mega environments (Yan et al., 2007). A GGE bi-plot may display the which-won-where pattern of a genotype by environment dataset for GYP (*Figure 5D*). That it visually handles essential themes like crossover GE, mega-environment differentiation, particular adaptation, etc. The GGE bi-plot's "which-won-where" function extends the previous "pair-wise comparison" function. First, a polygon was created on the genotypes farthest from the bi-plot origin, including all other genotypes. The environments were in two sectors, whereas the genotypes were in all four. The genotypes in the sector's vertices are the most beneficial (Yan and Tinker, 2006). Then, starting from the bi-plot origin, draw perpendicular lines to each side of the polygon. The GGE bi-plot polygon views revealed one probable mega habitat for both GYP and GZC. The first mega environment for GYP was made up of four environments (E1, E2, E4 and E5), and the second mega environment was made up of one environment (E3), whereas the first mega environment for GZC was made up of four environments (E1, E2, E3 and E5), and the second mega environment was made up of one environment (E3) (E4). In one or more situations, the genotypes placed at the polygon's vertices (V17, V20, V13, and V3) fared best or worse. The perpendicular lines on the polygon are equality lines that allow for visual comparison of neighbouring genotypes. According to the equality line between V20 and V13, V20 was better in just E3, but V13 was better in all other environments, too. As shown by the equality line between the two, V20 was better than V11 in all situations. V12 and V8 are connected to V20 and V11 via a line. This indicates that in all environments, the order  $V20 > V12 > V4 > V11$  was true. In E1 and E2, V13 was the best, while in E5 and E4, V5 and V3 were the greatest. Only E3 saw V20 emerge victorious, while the other environments witnessed V13 succeed. In *Fig. 6D*, the same goes for GZC. In one or more situations, V1, V2, V3, V19, V20, V5, V21, and V7 were the best or worse. The equality line between V2 and V3 suggests that V3 was superior in just one environment, E4, while V2 was superior in all others. According to the equality line between V2 and V3, V2 was superior to V3 in all environments. In all contexts, the genotype hierarchy for GZC was  $V3 > V19 > V20$ . V1 had the greatest success in E2 and E1, while V7 had the greatest success in E5, and V2 had the greatest success in E3. Only E3 had a winner, whereas the other settings had V1 as the winner. The findings suggest that the environment and GEI have a role in yield trait expression (Gedif et al., 2014; Bhartiya et al., 2017).

### **Conclusion**

The results of the present study revealed that the first principal component (PC1) and the second (PC2) explained 61.66% and 17.25% of the variation separately, and combined they explained 78% of the variance. Bi-plot analysis has been a vital tool in the fields of crop improvement and agricultural research throughout the years. The GGE bi-plot analysis solves a long-standing problem of genotype by environment data analysis for plant breeders, geneticists, and agronomists. The GGE bi-plot's polygon views revealed two feasible mega environments for both GYP and GZC. The discriminativeness

vs. representativeness concept has proved useful in evaluating test environments. For GYP, there was a positive correlation among the environments (E1, E2, E3 and E5) and a negative correlation between E3 and E4 for GYP; whereas for GZC, all environments were positively correlated among themselves. There were close associations among the test environments (E1 and E2) having similar kinds of genotype information for GYP and GZC. For GYP, E5 was the most discriminating and E2 was the least discriminating of the tested high zinc rice genotypes. For GZC, E5 was the most discriminating and E2 was the least discriminating. E2 was the most representative and E3 the least representative, whereas for GZC, E1 was the most representative and E3 the least representative. The highest GYP and GZC test environments were E3 and E5, respectively. E2 was the best or ideal test environment for selecting generally adapted genotypes for GYP, whereas for GZC, E3 was the ideal test environment. The genotypes with codes V21, V6, V13, V16, and V5 for GYP and V1, V4, V9, and V2 for GZC were above average in all the environments. The genotype V13 had the highest mean grain yield and the most stable genotypes, while V8 was highly unstable and V17 was the lowest yielder. V1 had the highest GZC and the most stable genotypes, whereas, V19 was highly unstable. For GYP, V3 was the winner in only E3, whereas V13 was the winner in the other environments. For GZC, V3 was the winner in only E3, whereas V1 was the winner in the other environments. As a result, the V13 (BRRI dhan 72) for grain yield and the V1 (IR 95044:8-B-5-22-19-GBS) for grain zinc content could be recommended for future breeding programmes for cultivar selection and zinc bio-fortification.

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