

## **G×E analysis to identify the stable high-yielding rice lines among a set of selected germplasm panel**

### **Abstract**

Rice lines need to be grown and evaluated for yield under different agro-ecological locations to identify stable and high-yielding lines for deployment in breeding programs. With this aim, a set of rice germplasm was evaluated for G×E in four different environments (E1-Dadesuguru-*Wet* 2020, E2-ICAR-IIRR-*Dry* 2019, E3-ICAR-IIRR-*Wet* 2020, E4-ICAR-IIRR-*Dry* 2020). The experimental trial was laid out in a randomized complete block (RCB) design with three replications at each location for 118 rice lines. Data on yield per plant was analyzed using the Additive Main Effect and Multiplicative Interaction (AMMI) and Genotype, and Genotype × Environment Interaction (GGE) models. The combined analysis of variance (ANOVA) manifested significant variations for tested genotypes, locations, years, genotype × year, and genotype × location interactions revealing the influence of environmental factors on yield traits. All four environments showed discrimination power, whereas E2 and E3 were found as the representative environment as they fall near the Average-Environment axis (AEA). The AMMI biplot PC1 contributed 79.20% variability and PC2 contributed 15.18% variability. From the GGE biplot analysis, the rice lines Phouren, JBB-631-1, and JBB-1325 were found to be the best and most stable. The rice lines Phouren, PUP-229, and TI-112 were stable in the first sub-group Dhadesugur-*Wet* 2020 (E1). The rice lines Langphou, and NPK-45 were stable in the second sub-group ICAR-IIRR-*Wet* 2020 (E3). Environment ICAR-IIRR-*Dry* 2019 (E2) was the third subgroup and the rice lines Moirangphou-Yenthik and TI-3 topped for the same. The ICAR IIRR-*Dry* 2020 (E4) environment formed the fourth subgroup where Phouren-Amubi, TI-128 and JBB-1325 topped the season. In conclusion, this study revealed that G × E interactions are significant for yield variation, and its AMMI and biplots analysis are efficient tools for visualizing the response of genotypes to different locations.

**Keywords:** Rice, AMMI, G × E interaction, stability

## 1. INTRODUCTION

Grain yield is a complex quantitative trait, with high environmental interaction. The selection of lines for breeding needs to be made based on the performance under multiple environments, especially for rice which is grown under a wide range of ecosystems. It is essential to carry out selection based on yield stability evaluation rather than average performance in multiple environment conditions (Islam *et al.*, 2015) [1]. Selection of genotypes for stability and adaptability is required prior to the recommendation. Stability is the suitability of a variety over a wide range of environments while adaptability is the better survival of a genotype over any specific environment (Balakrishnan *et al.* 2016) [2]. There are several methods to study stability and genotype  $\times$  environment interactions of traits through conventional analysis. Different models were proposed on stability variance, covalence, regression coefficient analysis or principal component analysis (PCA) (Finlay and Wilkinson, 1963; [3]. Eberhart and Russell, 1966; [4]. Perkins and Jinks, 1968; [5]. Freeman and Perkins, 1971; [6]. Shukla, 1972; [7]. Kang, 1993 [8]). However, the additive main effects and multiplicative interaction (AMMI) model and the genotype main effects and genotype  $\times$  environment interaction effects (GGE) model are more popular methods. This method is followed to quantify the genotype-environment interaction through PCA and graphical representation and has been widely applied in multi-environment cultivar trials (Kempton, 1984; [9] Crossa *et al.*, 1997; [10] Gauch and Zobel, 1997 [11]). The breeding protocol must quantify genotype, environment, and their interaction factors to obtain successful breeding results of yield and related traits in rice (Balakrishnan *et al.*, 2016 [2]).

An evaluation of phenotypic traits (P) assessed upon multiple environments (E) will be different from an assessment of genotypic traits (G), so  $P = G + E + (G \times E)$ . Due to the huge impact that G $\times$ E interactions have on phenotype, it is imperative to conduct stability analyses to assess genotype performance in various environments and make the process easier for plant breeders. Therefore, the estimation of the G $\times$ E interaction, on the other hand, has continuously an intriguing factor in plant breeding. Biplots are presently broadly utilized to evaluate genotype-environment interaction (GEI) since the G $\times$ E impacts can be envisioned in a single chart, making genotypes and their intelligence with situations less demanding to compare (Gauch *et al.*, 1988) [12]. Yan *et al.* (2000) [13] proposed a modern GEI examination procedure based on biplots,

comparative to the AMMI method, that has the advantage of dissecting down the combined impact of genotype (G) and  $G \times E (G + GE)$  by central component examination, as restricted to the initial AMMI investigation.

The essential ANOVA depicts fundamental impacts and determines whether genotype  $\times$  environment may be a critical source of variability, but it does not give knowledge into the variation caused by genotypes or environment. Besides, PCA contains no sources of variations for genotype or environment and does not viably dissect interactions. AMMI analysis (Gauch and Zobel, 1997) [11] improves the likelihood of effective selection and has been used to assess genotype  $\times$  environment interaction with greater precision in various crops (Balakrishnan *et al.*, 2016) [2]. The GGE biplot is regularly utilized to discover the GEI variation generated in the experimental design. It clearly simplifies the testing locations for large environments. The goal of this study was to figure out how studied four environments affect yield in specific genotypes and to find sites that are best suited for higher production. As a result, it offers the optimum genotype for rice growers in the region, as well as for the country's familiar agro-ecologies.

## 2. MATERIAL AND METHODS

The experimental material consists of 118 rice lines including North-Eastern landraces, aromatic genotypes, advanced breeding lines, soft rice lines, mutants of BPT-5204 and Nagina 22 (N22), wild introgression lines, *tropical japonica* accessions, *Oryza glaberrima* accessions and popular varieties (Table 1).

### 2.1 Field Experiments

The experiments were conducted for four seasons at two different locations to evaluate the rice lines (E1-Dadesuguru-wet 2020, E2-ICAR-IIRR-Dry 2019, E3-ICAR -IIRR-wet 2020, E4-ICAR -IIRR-Dry 2020). The experimental trial was laid out in a randomized complete block (RCB) design with three replications at each location for 118 rice lines. At each replication, 25-30 days-old seedlings were transplanted into 13 rows with a spacing of 20 x15cm, and the recommended package of practices for rice production in the region was followed. Data on yield traits were analyzed using the Additive Main Effect and Multiplicative Interaction (AMMI), Genotype and Genotype  $\times$  Environment Interaction (GGE) as mentioned by Balakrishnan *et al.*, 2016) [2].

## 2.2 Additive Main and Multiplicative Interaction (AMMI) Analysis

Using the statistical program R studio, the G×E interaction of 118 lines in four environments was assessed using the AMMI model proposed by Gauch and Zobel in 1997 [11]. After fitting an ANOVA model with the main effects of genotype and environment (without interaction), the standardized residuals were used to fit a principal component analysis (PCA). The experimental error as well as the influence of the G×E interaction is included in these residuals. The equation was: 1.  $Y_{ij} = \mu + G_i + E_j + \sum \lambda_k \alpha_{ik} \gamma_{jk} + e_{ij}$  where  $Y_{ij}$  is the observed mean yield of the  $i^{\text{th}}$  genotype in the  $j^{\text{th}}$  environment,  $\mu$  is the general mean,  $G_i$  represents the effects of genotypes and environments for the  $k^{\text{th}}$  axis,  $\alpha_{ik}$  is the eigenvector of the  $i^{\text{th}}$  genotype for the  $k^{\text{th}}$  axis,  $\gamma_{jk}$  represents the eigenvector of the  $j^{\text{th}}$  environment for the  $k^{\text{th}}$  axis,  $n$  is the number of principal components in the model,  $e_{ij}$  is the average of the corresponding random errors. The contribution of IPCA1 and IPCA2 sums of squares to the interaction sum of squares was used to compute it for each genotype (Purchase *et al.*, 2000). The formula for calculating the AMMI stability value is as follows: 2.  $ASV = \sqrt{\left( \frac{SS_{pc1}}{SS_{pc2}} \times PC1_i \right)^2 + (PC2_i)^2}$  where,  $SS_{pc1}$  and  $SS_{pc2}$  are the sums of squares of **pc1** and **pc2** respectively, and the score and **pc2** score are the scores of the genotype in those particular PCAs.

## 2.3 GGE bi-plot Analysis

In order to interpret GEI patterns, we used the GGE bi-plot methodology, which is a combination of AMMI bi-plot and GGE concepts. An average-environment coordination (AEC) view of biplots based on environment-focused scaling was used to interpret mean genotype performance vs their adaptability patterns from the polygon view of genotype-environment interaction biplots of symmetrical scaling (Babu *et al.*, 2020) [15].

## 3. RESULTS AND DISCUSSION

The yield per plant exhibited a considerable contribution from main factors (genotypes and environments) and interaction effects, according to the AMMI model. A significant mean sum of squares attributable to lines suggested that there were genotypic differences, and the relevance of

the environment explains why environmental effects change across different sites and test locations. Furthermore, genotype-environment interaction results indicate that lines behave differently in different seasons (Table 1). Based on the mean yield performance and stability of the rice lines, three North-Eastern landraces Phouren, Longphou, Phouren-Amubi and Moirangphou-Yenthink, two advanced breeding lines derived from *indica /tropical japonica* crosses JBB-631-1 and JBB-1325, a Near isogenic line, PUP 229, two mutants of BPT-5204 TI-112 and TI-3 and wild introgression line NPK-45 were stable.

The AMMI plot demonstrated that the rice lines Phouren, JBB-631-1, and JBB-1325 were stable for grain yield per plant, which is in agreement with the study of Sharifi *et al.* 2017 [16] that reported seven stable rice lines for grain yield stability in three consecutive years. Similarly, Ashwini *et al.* (2019) [17] used the AMMI plot to analyze conventional and enhanced rice varieties in five districts of Karnataka. In the case of yield, it was observed that genotypic mean fluctuations were far higher than environmental mean variations. Dewi *et al.* (2014) [18] also found that when rice genotypes were examined in different growing seasons, the mean sum of squares due to the genotype's main effect was high for grain yield.

The multiplicative variance of the treatment sum of squares due to the GE interaction was significant and was further partitioned into the interaction principal component axis (IPCA). The IPCA I and IPCA II scores, explained 79.20 *per cent* and 15.18 *per cent* of the interaction. The total GEI for the trait grain yield per hectare was captured by these two PCA axes, which accounted for 94.38% of the total GEI. Sharifi *et al.* (2017) [16] conducted a G×E interaction study in which the proportion of IPC1 (49%) to the interaction sum of squares was far greater than that of IPC2 (24%).

### 3.1 Stability parameters

The rice lines Phouren (26.18 g/plant) had the lowest AMMI stability value (0.68), followed by JBB-631-1 (24.70 g/plant) and JBB-1325 (23.90 g/plant) with 0.75 and 0.89 ASV, respectively. Similarly, according to the Genotypic Selection Index (GSI), Phouren was ranked as the best line as it had a lower GSI value (Table 1).

### 3.2 GGE Biplots

GGE biplot represents the polygon view of the GGE biplot and it revealed the best-performing genotypes for traits in a single group location (Yan *et al.*, 2000) [13]. As explained by Oladosu *et al.* (2017) [19] the genotypes lying on the vertex of a polygon with no environmental indicator nearby are poorly performed genotypes, and the genotypes that are present on the vertex of a polygon where one or more environmental indicators are present are the best-performing genotypes in the relevant environments. From 'Which won where' pattern of GGE biplots for grain yield of chosen varieties revealed that rice lines Phouren, JBB-631-1, and JBB-1325 were found to be best most and stable for grain yield per plant because they were placed at edge of the polygon (Figure 1). The radiating lines from the biplot origin intersected each of the polygon sides at right angles, dividing the four environments into four sub-groups. The rice lines Phouren, and PUP-229, TI-112 fall in the first sub-group Dhadesugur-*Wet* 2020 (E1). The rice lines Langphou, NPK-45 the second sub-group in ICAR-IIRR-*Wet* 2020 (E3). Environment ICAR-IIRR-*Dry* 2019 (E2) was the third subgroup consisting of the rice lines Moirangphou-Yenthik and TI-3. The ICAR IIRR-*Dry* 2020 (E4) environment formed the fourth subgroup consisting of Phouren-Amubi, TI-128 and JBB-1325 were found to be stable. This result confirms the presence of distinct interaction between genotype and environment for all the traits evaluated. Babu *et al.*, 2020 [15] identified genotypes G22 (Edavankudi Pokkali), G17 (Taraori Basmati), G27 (Chittimuthyalu) and G26 (Kalanamak) stable for zinc in polished rice (ZPR) and G8 (Savitri) stable for single plant yield (SPY) across three environments. The findings of our study are the agreement with the report stated by Khan *et al.* (2021) [20] and Mwiinga *et al.*, (2020) [21].

The GGE biplot for grain yield per plant, that is descriptiveness vs representativeness (Figure 2) revealed that the environment Dhadesugur (E1) had the shortest vector, indicating that this environment was unable to discriminate lines, whereas the environments ICAR-IIRR-*Dry* 2019 (E2), ICAR-IIRR-*Wet* 2020 (E3), and ICAR-IIRR-*Dry* 2020 (E4) had longer vectors than Dhadesugur-*Wet* 2020 (E1), indicating that environments were able to discriminate lines. The location, Dhadesugur- *Wet* 2020 (E1) has a limited ability to discriminate, which could be due to environmental or other error factors (Babu *et al.* 2020) [15].

The stability pattern across four locations was analyzed using the mean vs stability pattern of the GGE biplot (Figure 3). The GGE plot facilitates line evaluation based on mean performance and

stability across four environments. The biplot graph is formed by the intersection of a vertical AEC abscissa and a horizontal AEC ordinate line. Each line has a single arrowhead that points towards a higher mean performance for the studied trait. In our investigation, the mean vs. stability analysis recorded Phouren, Chakhao, Moirangphou-Yenthik, and Langphou-Chakao a high mean yield performance, whereas Phouren, JBB-1325 and Swarna were found to be the most stable lines

The GGE biplot for grain yield per hectare for ranking environments (Figure 4) indicated that the environment ICAR-IIRR-Dry 2019 (E2) and ICAR-IIRR-Wet 2020 (E3) formed smaller angle with AEA and contemplated the best representative environments for grain yield per plant than other environments, therefore these environments are more informative. In terms of line discrimination, ICAR-IIRR-Dry 2020 (E4) had the longest vector and formed the smallest angle with AEA, followed by ICAR-IIRR-Dry 2019 (E2) and ICAR-IIRR-Wet 2020 (E3), Dhadesugar-Wet 2020 (E1) has the shortest vector forms the biggest angle with AEA, and thus this environment is not suitable for line discrimination but can be used after culling unstable lines. The present findings of significant sources of variation have been previously noted in rice (Sharif *et al.*, 2017 [21] and Shrestha *et al.*, 2020 [22]) and other cereal crops (Shojaei *et al.*, 2021 [23]). Although in the present study, both the AMMI model and GGE biplots have been found to be useful tools for understanding GE interactions, however, GGE biplots may provide more meaningful information with regard to genotype-environment relationships.

#### 4. CONCLUSION AND RECOMMENDATIONS

A significant Genotype  $\times$  Environment interaction was detected for yield by evaluating 118 lines across four environments using AMMI analysis. The combined analysis of variance (ANOVA) manifested significant variations for the tested rice lines, locations, years, genotype  $\times$  year, and genotype  $\times$  location interactions revealing the influence of environmental factors on yield per plant. All Four environments showed discrimination power, whereas E2 and E3 were found as the representative environment. The AMMI biplot showed that PC1 contributed 79.20% variability and PC2 contributed 15.18% variability (Table 2). From the GGE biplot analysis, the rice lines Phouren, JBB-631-1 and JBB-1325, PUP 229, TI-112, Longphou, NPK-45, Moirangphou-Yenthik, TI-3, and Phouren-Amubi have top-ranked rice lines based on ASV-AMMI stability value. The rice lines Phouren, PUP-229, and TI-112 own the first sub-group

which is Dhadesugur-Wet 2020 (E1). The rice lines Langphou, NPK-45 won the second subgroup which was produced by ICAR-IIRR-Wet 2020 (E3). Environment ICAR-IIRR-Dry 2019 (E2) was the third subgroup the rice lines Moirangphou-Yenthik and TI-3 were the winner. The ICAR IIRR-Dry 2020 (E4) environment formed the fourth subgroup where Phouren-Amubi, TI-128 and JBB-1325 were the winners. The high-yielding stable lines can be recommended for release after evaluation at multiple locations and can also be deployed in breeding programs for enhancing yield per plant under irrigated ecosystems.

## REFERENCES

1. Islam MR, Sarker MR, Sharma N, Rahman MA, Collard BC, Gregorio GB, Ismail AM. Assessment of adaptability of recently released salt tolerant rice varieties in coastal regions of South Bangladesh. *Field Crops Res.* 2016;1:190:34-43.
2. Balakrishnan D, Subrahmanyam D, Badri J, Raju AK, Rao YV, Beerelli K, Mesapogu S, Surapaneni M, Ponnuswamy R, Padmavathi G, Babu VR. Genotype× environment interactions of yield traits in backcross introgression lines derived from *Oryza sativa* cv. Swarna/*Oryza nivara*. *Front. plant sci.* 2016;19:7:1530.
3. Finlay KW & Wilkinson GN. The analysis of adaptation in a plant-breeding programme. *Aust. J. Agric. Res.* 1963;14(6):742-54.
4. Eberhart ST & Russell WA. Stability parameters for comparing varieties 1. *Crop sci.* 1966;6(1):36-40.
5. Perkins J & Jinks. Environmental and genotype-environmental components of variability. VI. Diallel sets of crosses. *Heredity.* 1968;25:29-40.
6. Freeman GH & Perkins JM. Environmental and genotype-environmental components of variability VIII. Relations between genotypes grown in different environments and measures of these environments. *Heredity.* 1971;27(1):15-23.
7. Shukla GK. Some statistical aspects of partitioning genotype environmental components of variability. *Heredity.* 1972;29(2):237-45.

8. Kang MS. Simultaneous selection for yield and stability and yield-statistic. J. Agron. 1993;85(3):754-7.
9. Kempton RA. Adjustment for competition between varieties in plant breeding trials. The J. Agril. Sci. 1984;98(3):599-611.
10. Crossa J, Cornelius PL. Sites regression and shifted multiplicative model clustering of cultivar trial sites under heterogeneity of error variances. Crop Sci. 1997;37(2):406-15.
11. Gauch Jr HG & Zobel RW. Identifying mega-environments and targeting genotypes. Crop sci. 1997;37(2):311-26.
12. Gauch Jr HG. Model selection and validation for yield trials with interaction. Biometrics. 1988;1:705-15.
13. Yan W, Hunt LA, Sheng Q, Szlavnics Z. Cultivar evaluation and mega-environment investigation based on the GGE biplot. Crop sci. 2000;40(3):597-605.
14. Purchase JL, Hatting H, Van Deventer CS. Genotype× environment interaction of winter wheat (*Triticum aestivum* L.) in South Africa: II. Stability analysis of yield performance. S. Afr. J. Plant Soil. 2000;1:17(3):101-7.
15. Babu PM, Neeraja CN, Rathod S, Suman K, Uttam GA, Chakravartty N, Lachagari VR, Chaitanya U, Rao LV, Voleti SR. Stable SNP allele associations with high grain zinc content in polished rice (*Oryza sativa* L.) identified based on ddRAD sequencing. Front. Genet. 2020;11:11:763.
16. Sharifi P, Aminpanah H, Erfani R, Mohaddesi A, Abbasian A. Evaluation of genotype× environment interaction in rice based on AMMI model in Iran. Rice sci. 2017 May 1;24(3):173-80.
17. Ashwini GL, Rajanna MP, Deepak CA, Chethana BS, Shobha D, Gouda TH, Dushyanthkumar BM, Hanamaratti NG, Ramesh S, Nagaraj MS, Mahantashivayogayya KH. Stability analysis for grain yield and quality traits in

- selected traditional and improved varieties of rice over different Zones of Karnataka. *Oryza*- 2019;56(2):193-203.
18. Dewi AK, Chozin MA, Triwidodo H, Aswidinnor H. Genotype× environment interaction, and stability analysis in lowland rice promising genotypes. *Int. J. Agron. Agril. Res.* 2014;5(5):74-84.
19. Oladosu Y, Rafii MY, Abdullah N, Magaji U, Miah G, Hussin G, Ramli A. Genotype× Environment interaction and stability analyses of yield and yield components of established and mutant rice genotypes tested in multiple locations in Malaysia. *Acta Agriculturae Scandinavica, Section B—Soil & Plant Sci.* 2017;3:67(7):590-606.
20. Khan MM, Rafii MY, Ramlee SI, Jusoh M, Al Mamun M. AMMI and GGE biplot analysis for yield performance and stability assessment of selected Bambara groundnut (*Vigna subterranea* L. Verdc.) genotypes under the multi-environmental trials (METs). *Sci. Rep.* 2021;23:11(1):22791.
21. Mwiinga B, Sibiya J, Kondwakwenda A, Musvosvi C, Chigeza G. Genotype x environment interaction analysis of soybean (*Glycine max* (L.) Merrill) grain yield across production environments in Southern Africa. *Field crops Res.* 2020;1:256:107922.
22. Shrestha S, Asch F, Dusserre J, Ramanantsoanirina A, Brueck H. Climate effects on yield components as affected by genotypic responses to variable environmental conditions in upland rice systems at different altitudes. *Field Crops Res.* 2020;12:134:216-28.
23. Shojaei SH, Mostafavi K, Omrani A, Omrani S, Nasir Mousavi SM, Illes A, Bojtor C, Nagy J. Yield stability analysis of maize (*Zea mays* L.) hybrids using parametric and AMMI methods. *Scientifica.* 2021;25:1-9.

**Table 1. AMMI stability parameters for grain yield/ plant**

Sl. No.	Rice lines	Special Characters	IPCA1	IPCA2	ASV	Rank ASV	Mean Yield/plant	Rank of mean	GSI	Rank of GSI
G1	KJ-214	Tropical <i>japonica</i> accessions	2.41	-1.99	2.95	45	17.86	46	91	46
G2	KJ-216		-0.62	0.51	5.91	111	17.00	111	222	111
G3	KJ-219		-1.53	-1.42	4.42	73	16.05	73	146	73
G4	KJ-221		-1.84	1.74	3.49	57	17.40	57	114	57
G5	KJ-222		1.41	-1.19	4.68	81	15.23	81	162	81
G6	KJ-226		-1.72	-1.71	4.17	67	16.45	67	134	67
G7	WB-3 (Wangoo-Phou)	North-Eastern Landraces	2.39	-1.97	2.98	47	17.70	47	94	47
G8	WB-5 (Phouren)		-3.24	1.62	0.68	1	26.18	1	2	1
G9	WB-6 (Chakhao)		-1.44	-1.28	4.64	79	15.35	79	158	79
G10	WB-8 (Moirangphou-Yenthik)		-3.14	-2.76	1.19	8	22.10	8	16	8
G11	WB-10 (Langphou)		3.16	-2.98	1.05	6	22.84	6	12	6
G12	WB-12 (Langphou-Chakao)		-0.82	0.64	5.82	106	10.52	106	212	106
G13	WB-14 (Ayangleima)		-0.29	-0.39	6.86	118	10.00	118	236	118
G14	WB-15		-1.46	-1.29	4.57	78	15.53	78	156	78

	(Heimang-Phou)									
G15	WB-16 (Phouoibi)		-1.38	1.18	4.72	82	15.23	82	164	82
G16	WB-22 (Moirang-Phou- Khokngangbi)		-0.91	0.76	5.79	104	11.28	104	208	104
G17	WB-23 (Kakcheng-Phou)		-1.15	0.93	5.35	95	13.24	95	190	95
G18	WB-24 (Pat-Phou)		-2.91	-2.58	2.02	22	20.10	22	44	22
G19	WB-26 (Taothabi)		2.63	-2.47	2.14	26	19.73	26	52	26
G20	WB-27 (Langmanbi)		-3.12	-2.66	1.56	14	20.79	14	28	14
G21	WB-29 (Akut-Phou)		-2.54	-2.27	2.45	34	19.16	34	68	34
G22	WB-30 (MoirangPhou-Angouba)		3.13	-2.72	1.46	13	20.81	13	26	13
G23	WB-32 (Keibi-Phou)		-3.12	-2.7	1.67	15	20.58	15	30	15
G24	WB-39 (Phouren-Amubi)		-3.14	2.82	1.41	10	21.66	10	20	10
G25	GNV-1109	Advanced breeding line	-0.43	-0.46	6.32	116	12.00	116	232	116
G26	GNV-1089	Advanced breeding line	-0.61	0.58	5.96	112	17.00	112	224	112
G27	RNR-15048	Popular mega variety	-1.71	1.55	4.19	68	16.43	68	136	68
G28	Pokkali	Cultivated variety	-2.92	-2.59	1.95	20	20.25	20	40	20
G29	Siri-1253	Cultivated variety	-1.19	-0.97	5.03	92	13.77	92	184	92
G30	GNV-14-96-1	Advanced breeding lines	-2.5	2.18	2.6	38	18.90	38	76	38
G31	RP-Bio-226	Cultivated variety	2.55	2.31	2.42	33	19.20	33	66	33

G32	Tellahamsa	Popular mega variety	-2.57	2.35	2.38	31	19.48	31	62	31
G33	FL-478	Cultivated variety	2.53	2.23	2.53	36	18.96	36	72	36
G34	Ratnamudi	Karnataka landrace	-0.78	0.64	5.88	109	19.00	109	218	109
G35	Ratnachudi		2.54	-2.25	2.53	35	19.10	35	70	35
G36	Tanu	Popular mega varieties	0.81	-0.61	5.84	107	10.34	107	214	107
G37	Rasi		2.37	-1.91	3.16	49	17.61	49	98	49
G38	Swarna Sub-1		1.77	-1.64	3.62	63	16.90	63	126	63
G39	MTU-1010		-1.01	0.77	5.78	103	11.34	103	206	103
G40	BPT-5204		1.3	1.15	4.81	85	14.76	85	170	85
G41	Jaya		-3.11	2.69	1.78	16	20.55	16	32	16
G42	MTU-1001		2.44	-2.06	2.81	43	17.99	43	86	43
G43	TI-3	Mutants of BPT-5204	-3.14	2.74	1.36	9	21.89	9	18	9
G44	TI-4		-0.51	0.49	6.14	114	14.00	114	228	114
G45	TI-8		1.13	-0.89	5.4	97	13.09	97	194	97
G46	TI-11		-1.09	0.83	5.51	100	12.65	100	200	100
G47	TI-12		1.11	-0.84	5.49	99	12.69	99	198	99
G48	TI-15		-1.81	1.73	3.54	60	17.13	60	120	60
G49	TI-16		1.54	-1.44	4.36	72	16.18	72	144	72
G50	TI-17		-1.12	0.88	5.48	98	13.08	98	196	98
G51	TI-18		1.86	-1.76	3.43	56	17.43	56	112	56
G52	TI-19		-1.37	1.16	4.76	83	14.89	83	166	83
G53	TI-23		-0.49	-0.47	6.32	115	13.00	115	230	115
G54	TI 24		1.79	-1.72	3.58	61	17.02	61	122	61
G55	TI-25		-2.49	2.17	2.63	39	18.47	39	78	39
G56	TI 35		-1.36	1.17	4.79	84	14.78	84	168	84
G57	TI 36		3.13	-2.71	1.42	12	20.87	12	24	12
G58	TI-37		-1.27	1.13	4.88	87	14.72	87	174	87
G59	TI-44		-1.76	-1.62	3.67	64	16.65	64	128	64
G60	TI-87		1.42	-1.21	4.66	80	15.25	80	160	80
G61	TI-112		3.17	2.18	1	5	23.10	5	10	5

G62	TI-128		-3.13	-2.78	1.42	11	21.54	11	22	11
G63	TI-166		-1.21	1.04	5	91	13.86	91	182	91
G64	TI-124		-1.69	1.54	4.24	69	16.38	69	138	69
G65	Swarna	Cultivated variety	-1.51	-1.37	4.47	75	15.71	75	150	75
G66	Vandana	Cultivated variety	-1.82	-1.72	3.54	59	17.18	59	118	59
G67	Wazuhophek	Landrace	-1.52	-1.43	4.43	74	15.99	74	148	74
G68	Improved Samba Mahsuri (ISM)	Cultivated variety	-2.38	-1.96	3.15	48	17.69	48	96	48
G69	PUP-225 (ISM × VANDANA)	Near isogenic lines	-1.22	1.07	4.97	90	14.31	90	180	90
G70	PUP-229 (MTU1010 × Vandana)		-3.2	-3.12	0.96	4	23.50	4	8	4
G71	PUP-230 (MTU1010 × Vandana)		-1.9	-1.8	3.38	54	17.47	54	108	54
G72	KR-209 (ISM × Wazuhophek)	Recombinant inbred lines	-2.56	2.32	2.4	32	19.36	32	64	32
G73	KR-262 (ISM × Wazuhophek)		-2.59	-2.41	2.25	28	19.56	28	56	28
G74	CR Dhan-202	Aerobic adapted cultivar	2.96	-2.61	1.92	19	20.30	19	38	19
G75	SR-50	Short rice, landrace from Nagaon, Assam	-0.52	-0.53	5.99	113	15.00	113	226	113
G76	MAS 946-1	Aerobic adapted cultivar	-2.43	-2.04	2.88	44	17.96	44	88	44
G77	PB-3	Pusa basmati	-1.83	-1.77	3.51	58	17.26	58	116	58
G78	CR Dhan-201	Aerobic adapted cultivar	-1.14	0.91	5.35	96	13.11	96	192	96
G79	DRR Dhan-42	First Drought tolerant MAS derived variety	-2.46	2.11	2.78	42	18.14	42	84	42
G80	DRR Dhan-44	Aerobic adapted cultivar	-1.47	1.31	4.55	77	15.56	77	154	77
G81	NPS-24	Wild introgression lines  (Swarna × <i>Oryza nivara</i> )	-1.26	-1.12	4.92	88	14.50	88	176	88
G82	NPS-53		-2.47	-2.08	2.75	41	18.14	41	82	41
G83	NPS-25		-2.48	-2.16	2.72	40	18.40	40	80	40
G84	DB-5		-1.91	-1.82	3.34	53	17.49	53	106	53

G85	DB-6		-1.08	0.81	5.57	101	12.48	101	202	101
G86	DB-7		-0.77	0.59	5.9	110	18.00	110	220	110
G87	DB-9		2.81	-2.49	2.11	25	19.91	25	50	25
G88	NPK-13		-2.32	-1.87	3.23	51	17.55	51	102	51
G89	NPK-27		-1.67	-1.49	4.34	71	16.21	71	142	71
G90	NPK-40		-1.88	-1.79	3.41	55	17.46	55	110	55
G91	NPK-41		2.31	-1.86	3.26	52	17.50	52	104	52
G92	NPK-43		-1.17	-0.94	5.3	94	13.65	94	188	94
G93	NPK-45		3.15	2.84	1.13	7	22.12	7	14	7
G94	SM-363	Mutants of N22	2.91	-2.57	2	21	20.24	21	42	21
G95	SM-669		1.75	-1.59	3.7	65	16.59	65	130	65
G96	SM-686		-2.58	2.39	2.33	30	19.53	30	60	30
G97	PB-4	Pusa basmati	2.86	-2.54	2.05	23	20.09	23	46	23
G98	PB-5	Pusa basmati	2.61	-2.42	2.16	27	19.67	27	54	27
G99	Sahbhagidhan	Drought tolerant variety	-1.48	1.33	4.5	76	15.68	76	152	76
G100	Sabita	<i>Oryza sativa</i> cultivar	-0.79	-0.62	5.85	108	10.04	108	216	108
G101	DRR Dhan-41	Drought tolerant variety	-1.07	-0.79	5.6	102	11.48	102	204	102
G102	KMR-3	Variety	-0.86	-0.7	5.8	105	11.12	105	210	105
G103	IR-64	Cultivated Mega variety	1.28	-1.14	4.86	86	14.73	86	172	86
G104	ATR-486	Introgression line (Azucena × Dular)	-1.18	0.96	5.1	93	13.70	93	186	93
G105	ASG-73	Landrace from West Bengal	3.11	2.68	1.86	17	20.46	17	34	17
G106	ASG-126	Landrace collected from Uttar Pradesh	-1.73	1.42	3.73	66	16.45	66	132	66
G107	Saali	<i>Oryza glaberrima</i> accessions	1.68	-1.53	4.28	70	16.25	70	140	70
G108	Dissi		1.24	-1.09	4.95	89	14.40	89	178	89
G109	Mow		-2.34	-1.9	3.23	50	17.59	50	100	50
G110	Mouli		2.52	-2.2	2.56	37	18.90	37	74	37
G111	Basmathi-370	Traditional Bamati cultivar	-2.58	2.37	2.29	29	19.54	29	58	29

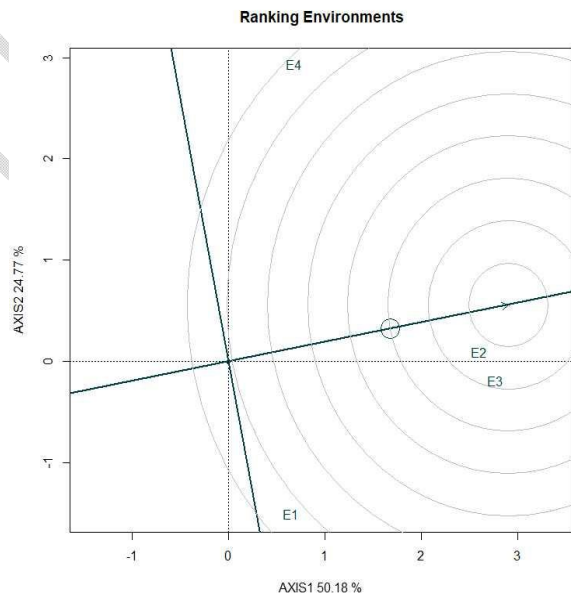
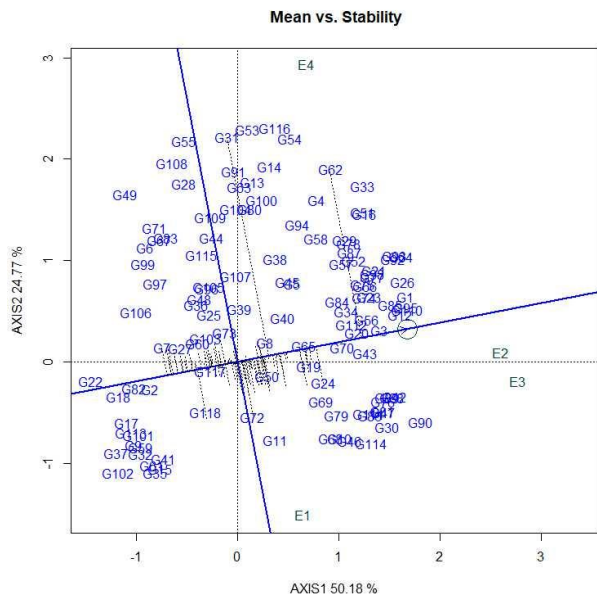
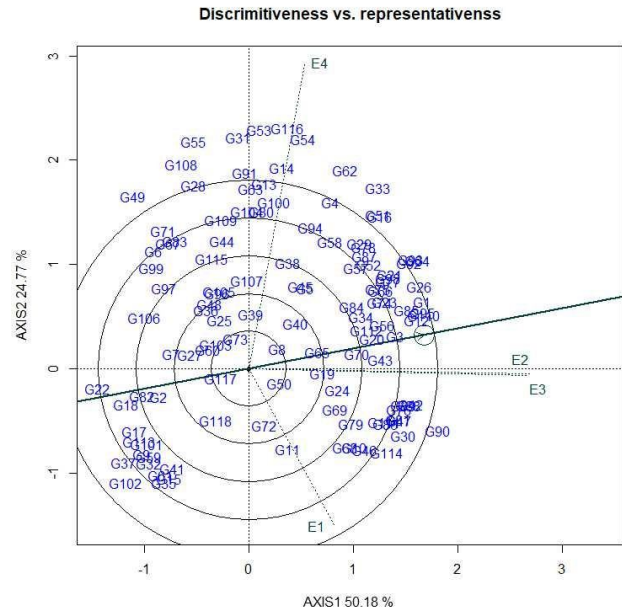
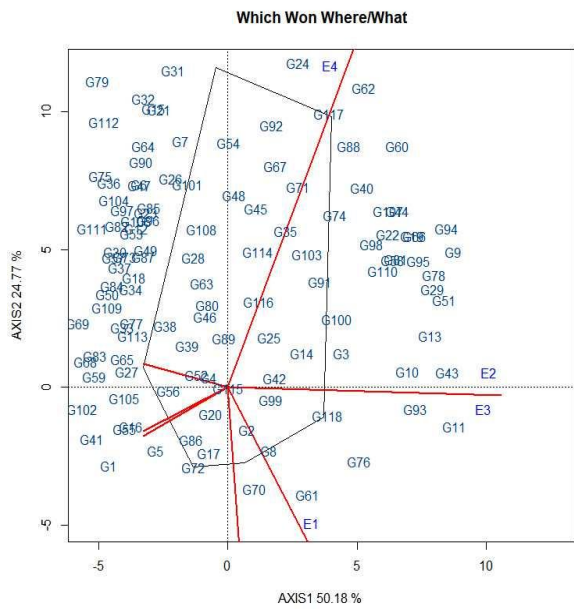
G112	Thurur Bhog	Landrace	-0.31	0.44	6.354	117	11.00	117	234	117
G113	D-92	North-Eastern Landrace	2.98	-2.62	1.89	18	20.42	18	36	18
G114	JBB-661	<i>Tropical japonica</i> × <i>indica</i> introgressed lines	-2.84	2.51	2.08	24	19.92	24	48	24
G115	JBB-610		1.78	-1.71	3.6	62	16.91	62	124	62
G116	JBB-684		2.42	-2.01	2.95	46	17.90	46	92	46
G117	JBB-1325		3.21	-0.98	0.89	3	23.90	3	6	3
G118	JBB-631-1		-3.21	-2.14	0.75	2	24.70	2	4	2

ASV-AMMI stability value, GSI- Genotypic selection index, IPCA- interaction principal component axes

**Table 2. AMMI ANOVA for Grain yield**

Source	d.f.	Sum of squares	Mean squares	F ratio	%TSS	G*E%
<b>ENV</b>	3.00	79528.20	26509.40**	3.18	1.96	
<b>GEN</b>	117.00	1010908.98	8640.24**	1.03	25.02	
<b>ENV*GEN</b>	351.00	2948569.95	8400.48**	1.00	73.00	
<b>PC1</b>	119.00	2942036.09	24722.99**	2.96	99.77	79.20
<b>PC2</b>	117.00	6128.92	52.38	0.006	0.20	15.18
<b>Residuals</b>	944.00	7855141.49	8321.12	NA	0	
<b>Mean</b>	17.100					
<b>SD</b>	3.327					
<b>Variance</b>	11.070					
<b>CV (%)</b>	19.457					
<b>CD (%)</b>	12.527					

\*\*Significance @ p=0.001, %TSS= % of total sum of squares, IPCA= interaction principle component Axes, %G\*E= % of genotype and environment interactions, SD= standard deviation, CV=coefficient of variation, CD= critical difference



**Figure 1.** ‘which won-where’ pattern of genotypes and locations for grain yield, **Figure 2.** ‘Discriminateness vs representativeness’ pattern of genotypes and locations for grain yield, **Figure 3.** ‘Mean vs Stability’ pattern of genotypes and locations for grain yield, **Figure 4.** ‘Ranking of Environments’ for grain yield.