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

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). 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). There are several methods to study stability and genotype × 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; Eberhart and Russell, 1966; Perkins and Jinks, 1968; Freeman and Perkins, 1971; Shukla, 1972; Kang, 1993). However, the additive main effects and multiplicative interaction (AMMI) model and the genotype main effects and genotype × 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; Crossa et al., 1997; Gauch and Zobel, 1997). 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).

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×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×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×E impacts can be envisioned in a single chart, making genotypes and their intelligence with situations less demanding to compare (Gauch et al., 1988). Yan et al. (2000) 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

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genotype (G) and G×E (G + GE) by central component examination, as restricted to the initial AMMI investigation.

The essential ANOVA depicts fundamental impacts and determines whether genotype × 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) improves the likelihood of effective selection and has been used to assess genotype × environment interaction with greater precision in various crops (Balakrishnan et al., 2016). 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.

MATERIAL AND METHODS

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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).

Field Experiments

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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 20x15cm, 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 × Environment Interaction (GGE) as mentioned by Balakrishnan et al., 2016).

Additive Main and Multiplicative Interaction (AMMI) Analysis

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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. 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: $\boldsymbol{Y_{ij} = \mu + G_i + E_j + \Sigma\lambda_k \alpha_{ik} \gamma_{jk} + e_{ij}}$ where Y_{ij} is the observed mean yield of the i^{th} genotype in the j^{th} environment, m is the general mean, G_i represents the effects of genotypes and environments for the k^{th} axis, a_{ik} is the eigenvector of the i^{th} genotype for the k^{th} axis, g_{jk} represents the eigenvector of the j^{th} environment for the k^{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: ASV = sqrt ((SSpc1/SSpc2 * PC1i)^2+(PC2i)^2). where, SSIPCA1 and SSIPCA2 are the sum of squares of IPCA1 and IPCA2 respectively. The IPCA1 score and IPCA2 score are the scores of the genotype in those particular PCAs.

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GGE bi-plot Analysis

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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).

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RESULTS AND DISCUSSION

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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 that reported seven stable rice lines for grain yield stability in three consecutive years. Similarly, Ashwini et al. (2019) 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), 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.

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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) 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%).

Stability parameters

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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).

GGE Biplots

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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). As explained by Oladosu et al. (2017) the genotypes lying on the vertex of a polygon with no environmental indicator nearby

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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 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) and Mwiingaa et al., (2020).

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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).

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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), Dhadesugur -*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 and Shrestha et al., 2020) and other cereal crops (Shojaei et al., 2021). 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.

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CONCLUSION

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A significant Genotype × 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 × year, and genotype × 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-Yenthink, 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 sub-group 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.

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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 *japonica* 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 (Heimang-Phou)		-1.46	-1.29	4.57	78	15.53	78	156	78
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× *Oryza nivara)*	-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	*Oryza sativa* 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	*Oryza glaberrima* 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	*Tropical japonica* × *indica* 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

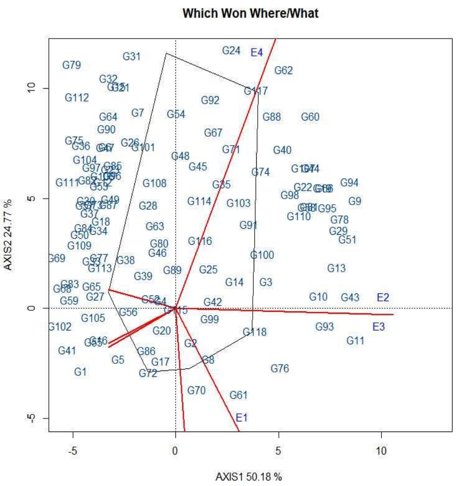
G117	JBB-1325		3.21	-0.98	0.89	3	23.90	3	6	3
G118	JBB-631-1		-3.21	-2.14	0.75	2	24.70	2	4	2

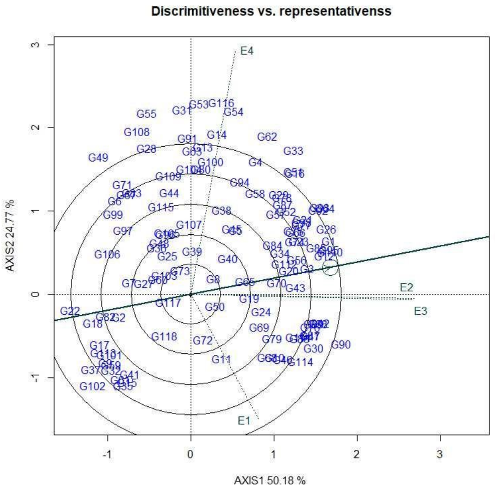
ASV-AMMI stability value, GSI- Genotypic selection index, IPCA- interaction principal component axes

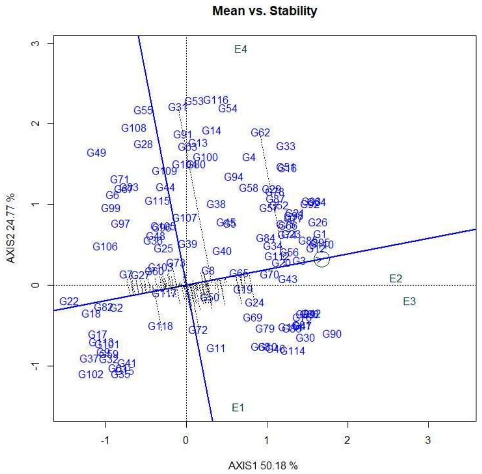
Table 2. AMMI ANOVA for Grain yield

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







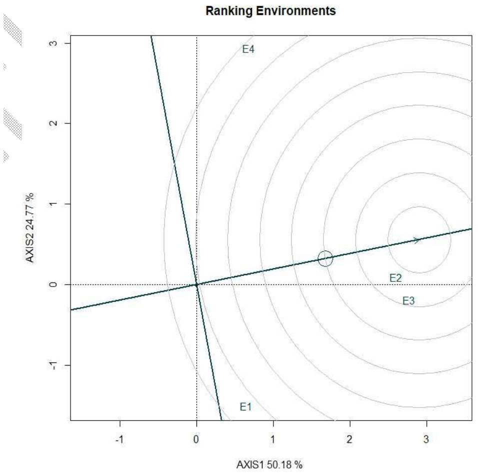


Figure 1. ‘which won-where’ pattern of genotypes and locations for grain yield, **Figure 2.** ‘Discrimitiveness vs representativeness’ pattern of genotypes and locations for grain yield, **Figure 3.** ‘Mean vs Stability’ pattern of genotypes and locations for grain yield, **Figure 4.** **‘**Ranking of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