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ADDITIVE MAIN EFFECT AND MULTIPLICATIVE INTERACTION ANALYSIS FOR PRODUCTION TRAITS IN RICE RECOMBINANT INBRED LINES USING AMMI BIPLOT TECHNIQUE

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ABSTRACT

The experiment was performed to assess the performance of 87 rice recombinant inbred lines (RILs), identify the productive environments and quantify genotype × environment interaction (GEI) effects on yield and yield related traits across four locations of the Khyber Pakhtunkhwa Province in Pakistan between 2021 and 2022. The pooled ANOVA showed significant differences of GEI for all traits. Across the studied environments, RIL AUP-3 took minimum days to heading (139) and produced the highest grain yield (4.1 t ha^{-1}). AUP-3 and AUP-30 displayed the highest kernel number in panicle of 214 and 226, respectively. Based on AMMI1 and AMMI2 biplots, RIL AUP-3 was unanimously declared as the most stable and the highest yielding genotype. AMMI biplot analysis cumulatively explained 55.3%, 46.3% and 52.1% of total variation due to GEI for days to maturity, grains panicle^{-1} and grain yield, respectively. The AMMI biplot analysis confirmed the differential response of genotypes across environments, suggesting environment-based expression of genes. The AMMI biplot also manifested AUP-3 and AUP-30 as ideal genotypes for grains panicle^{-1} and grain yield, respectively. The Peshawar (E-1 and E-5) and Mingora (E-2) were the most discriminating and representative environment for grains panicle^{-1} and grain yield. Application of various stability models in this study identified AUP-3 and AUP-30 as the most stable and widely adapted genotype for grain yield and its components. The AMMI analysis identified genotypes both for specific and wide adaptation. Based on stability and yield performance, said genotypes were identified with superior performance than check cultivars. Therefore, recommended for commercialization. Also environments were clustered regardless of their geographical location, which revealed unpredictable nature of agro-climatic conditions across four tested locations.

Key Words: Biplot technique, genotype by environment interaction, multi-environments, rice inbreed lines, yield related traits.

INTRODUCTION

Rice, (*Oryza sativa)* (2n = 24) is the second most important cereal crop and staple food for more than one third of the world's population (Ajmeera et al., 2017). Rice has assumed significant position as a source of food providing over 75% of Asian's staple food and more than three billion of world population's meal which represents 50-80% of their daily calorie intake (Amirjani, 2011). Varietal adaptability to environmental fluctuations is important for the stabilization of crop production over both the regions and years. An information on genotype × environment interaction leads to successful evaluation of stable genotype, which could be used for general cultivation (Ajmera et al., 2017). Also, GEI is important for disease resistant studies (Akcura et al., 2017; Unan, 2022). Development of rice varieties with high yield and desirable grain quality for different environments is one of the exciting research areas in rice breeding for successful identification of rice stable genotypes, which could be used for general and wider cultivation.

Several advancements have been made in the recent past for analyzing the varietal performance over diverse environments. The regression approach (Eberhart and Russell, 1966; Tai, 1971), variance components method (Shukla, 1972), additive main effects and multiplicative interaction (AMMI) analysis (Gauch, 1992), yield stability statistic approach (Kang, 1993) and biplot analysis (Yan, 2001) are major techniques for analyzing multi environmental trials. The AMMI analysis was designed to address the "which-won-where" pattern. It uses analysis of variance and singular value decomposition for additive parameters and multiplicative parameters, respectively and utilizes graphical method to identify the promising genotype. However, the “which won where” patterns are not usually easy for visualization with the larger number of genotype and the environments. If more than one interaction principal component is required, it will be complex in AMMI analysis (Yan et al., 2007).

A multivariate statistical methodology called principal components analysis (PCA) uses ordination techniques in multivariate methods to find data patterns as well as similarities and differences among variables. The scores of Principal Components can be drawn into useful biplots for visual inspection of GEI. The angle between genotypes and environmental vectors shows the degree of association between environments or genotypes. The interaction of genotypes with environments would be positive if the angle is less than 90° or larger than 270°. Similarly, the association would be negative when the angle is between 90° and 270°. The genotypes which lie close to the origin are considered stable and widely adapted, whereas genotypes lying far away from the origin are considered as sensitive and specifically adapted.

In the current study, 87 rice recombinant inbred lines (RILs) along with three check cultivars were field-tested across eight environments for yield and yield related traits to: i) interpret GEI obtained by AMMI analysis of yield and associated traits, (ii) assess yield performance of genotypes across environments based on the AMMI biplots, and (iii) identify high yielding and relatively stable genotypes based on AMMI model for further extensive testing before commercialization.

MATERIALS AND METHODS

This research was conducted at four locations of the Khyber Pakhtunkhwa province-Pakistan namely The University of Agriculture (UoA)-Peshawar (34.0206° N, 71.4814° E), Agriculture Research Institute (ARI) Mingora-Swat (34.7834° N, 72.3347° E), Agriculture Research Station (ARS) Baffa-Mansehra (34.3013° N, 73.1524° E) and Bacha Khan University (BKU)-Charsadda (34.1369° N, 71.8382° E) during 2021 and 2022 rice crop growing seasons. In summarized form the overall the eight environments (four locations across two years) were Peshawar-2021 (E-1), Mingora-2021 (E-2), Manshera-2021 (E-3), Charsadda-2021 (E-4), Peshawar-2022 (E-5), Mingora-2022 (E-6), Manshera-2022 (E-7) and Charsadda-2022 (E-8). The genetic material comprised F_5 derived rice recombinant inbred lines (RILs) along with standard check cultivars Pakhal, Kashmir-Basmati (K-Bas) and Fakhr-e-Malakand (F-MLD). The rice RILs have been developed by Rice Breeding Program, Department of Plant Breeding and Genetics, The University of Agriculture Peshawar. Rice hybridization program was initiated in 2010 through crossing of diverse elite rice cultivars of Pakistan. The segregating populations were advanced in bulk till F_4. In F_5, single plants were selected from the bulk populations of different cross combinations on the basis of superior yield and yield related traits. In F_6, the seeds of each selected plant were grown in two-row plots. The lines showing uniformity were selected and undesirable lines were discarded. The selected lines were tested during 2021 and 2022 rice growing seasons across four locations using alpha lattice design with three replications. Each replication consisted of six blocks with each block comprising 15 RILs. Each genotype was planted in four-row plots with row length of 3 meter and row to row distance of 30 cm.

Additive main effect and multiplicative interaction (AMMI) analysis

Based on the performance and relevance to adaptation three traits namely days to maturity, grains panicle^{-1} and grain yield were selected for the detailed stability analysis. Additive Main effect and Multiplicative Interaction (AMMI) analysis was carried out using GEA-R version 4.0 (GEA-R, 2015) computer software. Data for the mentioned four traits were subjected to AMMI analysis. AMMI biplots were constructed on the basis of PC1, PC2 scores and mean yield. Each location over years was considered as independent environment.

The AMMI model for genotypes and environments is given as;

$$Yij = \mu + Gi + Ej + \sum_{k=1}^{n} \lambda_k \, \alpha_{ik} \gamma_{jk} + \varepsilon ij$$

AMMI stability value

The ranking of genotypes based on their stability was computed following Purchase et al. (2000).

$$ASV = \sqrt{[\frac{SS_{IPCA1}}{SS_{IPCA2}}(IPCA1\;Score)]^2 + (IPCA2\;Score)^2}$$

Where SS_{IPCA1}/SS_{IPCA2} is the weight given to the IPCA1 (interaction principal component analysis) value by dividing the IPCA1 sum of squares by the IPCA2 sum of squares.

RESULTS

Days to maturity

The AMMI analysis of variance revealed significant differences among genotypes, environments and GEI for days to maturity (Table 1). The mean squares for environments (89%) were greater than genotype and GEI percentage. Genotypes accounted for only 1.9% of the total variation. Genotype by environment interaction was subdivided into seven principal components. The first four principal components were highly significant and collectively explained 84% of the total variation due to GEI. Similarly, first two principal components (PC1=31.7% and PC2=23.6%) explained 55.3% of GEI mean squares, indicating that first two principal components were sufficient to clarify the complex structures of GE interaction (Table 1).

The AMMI1 biplot depicted that the most conductive environment for early maturity was E-1, followed by E-8 and E-7, whereas, E-6 and E-4 were the late maturity environments. The most responsive environment for the evaluation of rice genotypes was E-5 lying away from the x-axis. In contrast, E-1, E-2, E-4, E-5, and E-8 were the most stable environments lying in the vicinity of x-axis and had nominal effects on genotypes performance in terms of days to maturity (Figure 1).

Among genotypes, AUP-3 lying at the extreme left y-axis matured the earliest, followed by AUP-62, AUP-63, AUP-61 and AUP-29. Similarly, AUP-19, AUP-75 and AUP-38 were found as late mature genotypes, due to their position at extreme right y-axis. In terms of stability, genotypes AUP-66 and AUP-10 were very prolific and highly stable lying on the left near y-axis (Figure 1).

Table 1. AMMI analysis of variance for different traits in rice genotype

SoV		Days to maturity		Grains panicle^{-1}		Grain yield (t ha^{-1})	
	Df	MS	Variance %	MS	Variance %	MS	Variance %
Environment	7	35310.8**	88.9	104338**	38.6	72.5**	77.4
Genotype	89	59.3**	1.9	4824**	22.7	0.8**	10.2
G×E	623	41.0**	9.2	1174**	38.7	0.1**	12.4
PC1	95	85.9**	31.7	1879**	24.4	0.2**	28.5
PC2	93	65.3**	23.6	1726**	21.9	0.2**	23.6
PC3	91	42.1**	14.8	1243**	15.5	0.2**	22.2
PC4	89	40.3**	13.9	1212**	14.7	0.1	9.0
PC5	87	24.0	8.1	968.9**	11.5	0.1	7.9
PC6	85	15.9	5.2	655	7.6	0.0	4.9
PC7	83	8.4	2.7	384	4.4	0.0	3.8
Residuals	1440	25.6	0.0	774	0	0.1	0.0

Double ** represent highly significant ($p < 0.01$), SoV mean source of variation and MS mean sum of square

The AMMI2 biplot showed that genotypes AUP-82, AUP-68 and AUP-28 lying near the origin could be considered widely adapted. Similarly, genotypes AUP-9, AUP-7 and AUP-24 (right lower quadrant), AUP-3, AUP-36, and AUP-48 (right upper quadrant), AUP-72 and AUP-47 (left lower quadrant) and AUP-39, AUP-46, AUP-52, AUP-15, and AUP-54 (left upper quadrant) positioning away from the origin inferred that these genotypes had site specific adaptability in terms of days to maturity. Widespread distribution of genotypes in the biplot implied that the performance of genotypes was generally environment specific. Environments E-03 and E-05 had high discriminating ability for genotypes due to their long vector's length, whereas E-04 and E-06 had short vector length and low discriminating ability for genotypes (Figure 2).

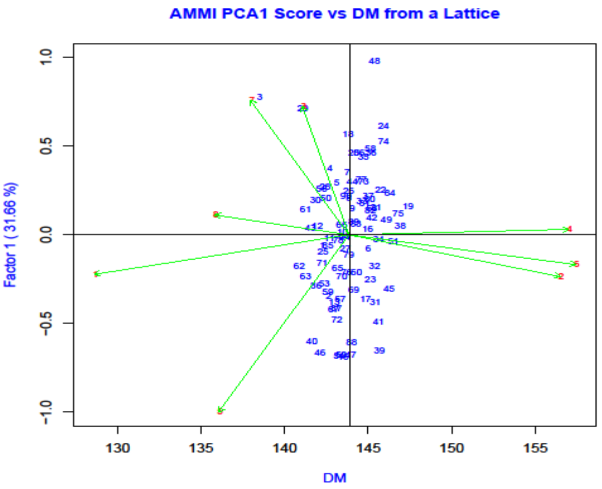

Figure 1. AMMI1 for days to maturity of 90 rice genotypes across eight environments

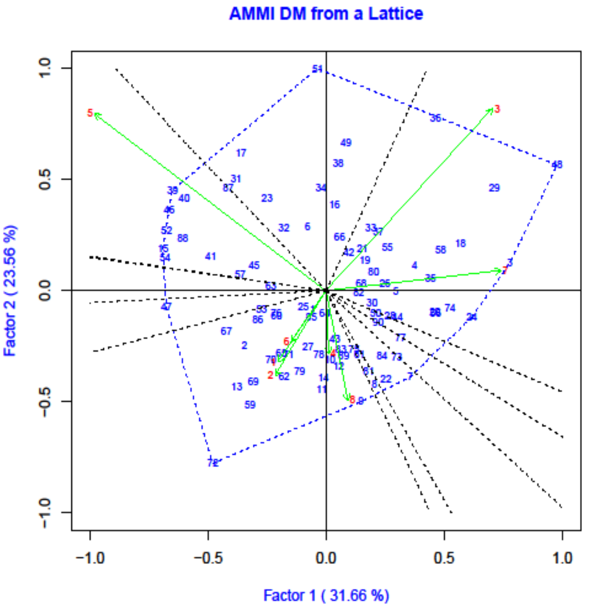

Figure 2. AMMI2 for days to maturity of 90 rice genotypes across eight environments

AMMI stability value (ASV) and ranking of genotypes based on ASV are given in Table 2. Genotypes AUP-3, AUP-24, AUP-74, and AUP-20 had lower ASV and thus were widely adapted. Contrary, AUP-15, AUP-54, and AUP-47 were the most unstable genotypes as evident from their higher ASV. Genotype AUP-3 had early maturity mean (139 days) and relatively low ASV (0.15) and thus could be considered as the early maturing and stable genotype. Likewise, late maturing and high ASV for AUP-19, AUP-38 and AUP-75 exhibited that these genotypes performed poorly across tested environments (Table 2)

Table 2. Ranking of rice genotypes based on mean performance and AMMI Stability Value (AMV) for days to maturity across eight environments during 2021 and 2022 rice growing seasons.

Days to maturity														
Genotypes	**Mean**	**Rank**	**ASV**	**Rank**	**Genotypes**	**Mean**	**Rank**	**ASV**	**Rank**	**Genotypes**	**Mean**	**Rank**	**ASV**	**Rank**
AUP-1	142	13	1.2	53	AUP-31	145	76	3.4	78	AUP-61	141	4	0.7	34
AUP-2	143	21	3.0	74	AUP-32	145	74	1.8	61	AUP-62	141	2	1.8	62
AUP-3	139	1	0.1	1	AUP-33	145	59	0.6	28	AUP-63	141	5	2.1	66
AUP-4	143	23	0.3	9	AUP-34	146	78	1.2	52	AUP-64	144	38	1.0	47
AUP-5	143	27	0.4	10	AUP-35	145	60	0.3	6	AUP-65	143	29	1.8	63
AUP-6	145	65	1.3	56	AUP-36	145	71	0.8	38	AUP-66	143	34	0.9	41
AUP-7	144	43	0.5	18	AUP-37	145	66	0.6	24	AUP-67	143	24	3.8	80
AUP-8	144	45	0.7	32	AUP-38	147	89	1.0	48	AUP-68	145	73	0.6	29
AUP-9	144	50	0.8	37	AUP-39	146	80	7.8	85	AUP-69	144	53	2.7	72
AUP-10	143	36	1.0	45	AUP-40	142	7	6.7	83	AUP-70	143	35	2.1	67
AUP-11	143	22	1.2	51	AUP-41	146	79	4.7	82	AUP-71	142	14	1.7	60
AUP-12	142	10	0.9	42	AUP-42	145	72	0.8	36	AUP-72	143	28	4.6	81
AUP-13	143	25	3.3	77	AUP-43	142	6	0.9	43	AUP-73	145	61	0.5	17
AUP-14	144	39	1.1	49	AUP-44	144	51	0.4	11	AUP-74	146	83	0.2	3
AUP-15	144	37	8.9	90	AUP-45	146	85	2.6	71	AUP-75	147	88	0.7	35
AUP-16	145	64	1.0	44	AUP-46	142	11	8.2	86	AUP-76	144	42	2.0	65
AUP-17	145	63	3.2	76	AUP-47	144	48	8.5	88	AUP-77	145	58	0.4	12
AUP-18	144	44	0.3	7	AUP-48	145	75	0.6	25	AUP-78	143	30	1.1	50
AUP-19	147	90	0.6	27	AUP-49	146	84	1.0	46	AUP-79	144	47	1.5	58
AUP-20	144	52	0.3	4	AUP-50	142	18	0.5	20	AUP-80	145	67	0.5	21
AUP-21	145	77	0.6	30	AUP-51	147	87	1.5	59	AUP-81	145	62	0.7	33
AUP-22	146	81	0.6	26	AUP-52	143	33	8.5	87	AUP-82	145	70	0.6	31
AUP-23	145	68	2.2	68	AUP-53	142	16	2.4	69	AUP-83	144	55	0.9	40
AUP-24	146	82	0.2	2	AUP-54	143	31	8.6	89	AUP-84	146	86	0.6	23
AUP-25	142	15	1.4	57	AUP-55	142	12	0.5	16	AUP-85	143	20	1.2	54
AUP-26	144	46	0.5	14	AUP-56	144	57	0.3	5	AUP-86	142	9	2.5	70
AUP-27	144	40	1.3	55	AUP-57	143	32	3.2	75	AUP-87	143	26	3.7	79
AUP-28	142	17	0.4	13	AUP-58	145	69	0.3	8	Pakhal	144	49	6.8	84
AUP-29	141	3	0.5	15	AUP-59	143	19	2.8	73	K-Bas	144	54	0.8	39
AUP-30	142	8	0.5	22	AUP-60	144	56	1.9	64	F-MLD	144	41	0.5	19

Grains panicle^{-1}

The AMMI analysis showed significant differences among genotypes, environments and GEI for grains panicle^{-1} (Table 1). Analysis of variance based on AMMI model revealed that genotypes explained 22.7% of the total phenotypic variation while environments captured only 38.6% of the mean squares, indicating that environments were relatively stable for grains panicle^{-1}. The GEI explained a major portion (38.6%) of the total variation for grains panicle^{-1}, indicating that the performance and ranking of genotypes mainly varied due to GEI. Small mean squares due to genotypes revealed that genotypes were not very distinct, although greater environmental sum of squares suggested unstable performance, which might lead to cross over interaction in terms of grains panicle^{-1}. Genotype by environment interaction was subdivided into seven principal components. The first five principal components were highly significant and collectively explained 88% of the total variation due to GEI. Similarly, first two principal components (PC1=24.4% and PC2=21.9%) explained 46.3% of GEI mean squares, indicating that first two principal components were sufficient to clarify the complex structures of GE interaction (Table 1).

The AMMI1 biplot depicted that the most productive environment was E-6 followed by E-5 and E-6, whereas, E-4 and E-8 were the least productive environments. The most responsive environment for the evaluation of rice genotypes was E-2, lying away from the x-axis. In contrast, E-5 and E-6 were the most stable environments lying in the vicinity of x-axis and had nominal effects on genotypes performance in terms of grains panicle^{-1} (Figure 3).

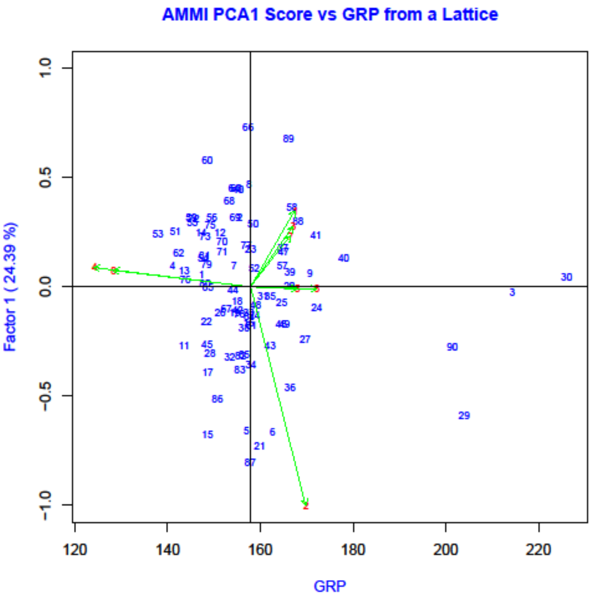

Figure 3. AMMI1 for grains panicle^{-1} of 90 rice genotypes across eight environments

Among genotypes, AUP-30 lying at the extreme right x-axis produced maximum grains panicle^{-1}, followed by

AUP-3, AUP-29, and AUP-90. Similarly, AUP-53, AUP-4, and AUP-51 were considered as poor performing genotypes, due to their position at extreme left x-axis. In terms of stability, genotypes AUP-30 and AUP-3 were very prolific and highly stable lying on the right near x-axis. On the other hand, genotypes AUP-53 and AUP-4 repeatedly failed to produce higher grains panicle^{-1} as indicated by their vicinity to extreme left x-axis. Likewise, AUP-30 was most productive and stable for grains panicle^{-1} lying near to x-axis in the right, whereas AUP-53 and AUP-4 were least productive and least stable being placed away from x-axis in the left corner (Figure 3).

The AMMI2 model was better than AMMI1 because the first two principal components (IPCA1 and IPCA2) explained 46.3% of the GEI. The AMMI2 biplot showed that genotypes AUP-80, AUP-76, and AUP-47 lying near the origin were considered widely adapted. Similarly, genotypes AUP-8 and AUP-89 (right lower quadrant), AUP-66 and AUP-58 (right upper quadrant), AUP-87, AUP-24, and AUP-3 (left lower quadrant) and AUP-5, AUP-15, and AUP-21 (left upper quadrant) positioning away from the origin inferred that these genotypes had site specific adaptability in terms of grains panicle^{-1} (Fig. 4). Widespread distribution of genotypes in the biplot implied that the performance of genotypes was generally environment specific. Environments E-2 and E-5 had high discriminating ability for genotypes due to their long vector's length, whereas E-6 and E-4 had short vector length and low discriminating ability for genotypes based on grains panicle^{-1} (Figure 4).

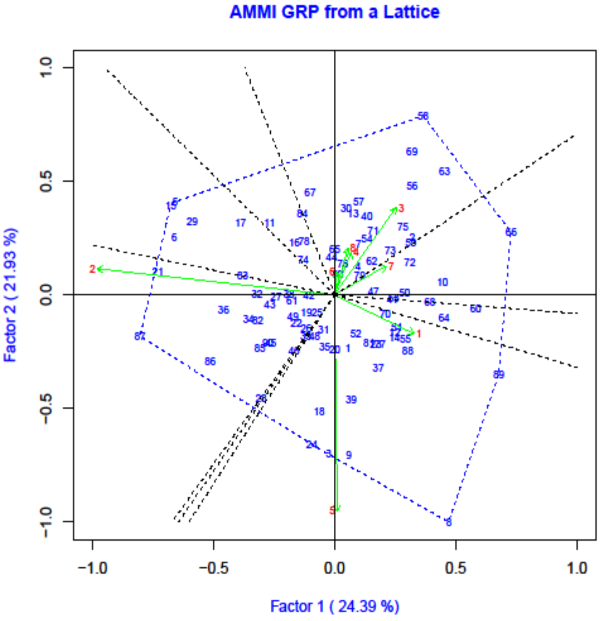

Figure 4. AMMI2 for grains panicle^{-1} of 90 rice genotypes across eight environments

AMMI stability value (ASV) and ranking of genotypes based on ASV are given in Table 3. Genotypes AUP-1, AUP-77, AUP-31, and AUP-3 had lower ASV and thus were widely adapted. Contrary, AUP-40, AUP-64, and AUP-29 were the most unstable genotypes as evident from their higher ASV. Genotype AUP-3 and AUP-30 had higher mean grains panicle^{-1} of 214 and 226, respectively and relatively low ASV of 0.08 and 0.12, respectively and thus could be declared as high yielding and stable genotype. For these traits likewise, lower values for grains panicle^{-1} and ASV for AUP-40, AUP-64, and AUP-29 exhibited that these genotypes performed poorly across tested environments for grains panicle^{-1} (Table 3).

Grain yield

The combined AMMI analysis of variance exhibited significant differences among genotypes, environments and GEI for grain yield (Table 4). Genotypes accounted for only 10.2% of the total variation. Genotype by environment interaction was subdivided into seven principal components. The first three principal components were highly significant and collectively explained 74.1% of the total variation due to GEI. Similarly, first two principal components (PC1= 28.5% and PC2= 23.6%) explained 52.1% of GEI sum of squares, indicating that first two principal components were sufficient to clarify the complex structures of GE interaction (Table 4).

Mean yield of eight environments were plotted against the scores of first principal component (PC1) to examine visually the genotypic response to varying environments. It is clear from the Figure 5 that E-6 was the most productive environment in terms of grain yield followed by E-3, E-2, and E-5. Environments E-1 and E-5 appeared as most stable causing least fluctuations in the yield performance of the tested genotypes due to their close proximity to x-axis. Environments E-4 and E-8 were the most discriminating as specified by their long distances from the x-axis. Among genotypes, AUP-30 was the most stable and produced maximum grain yield (Figure 5).

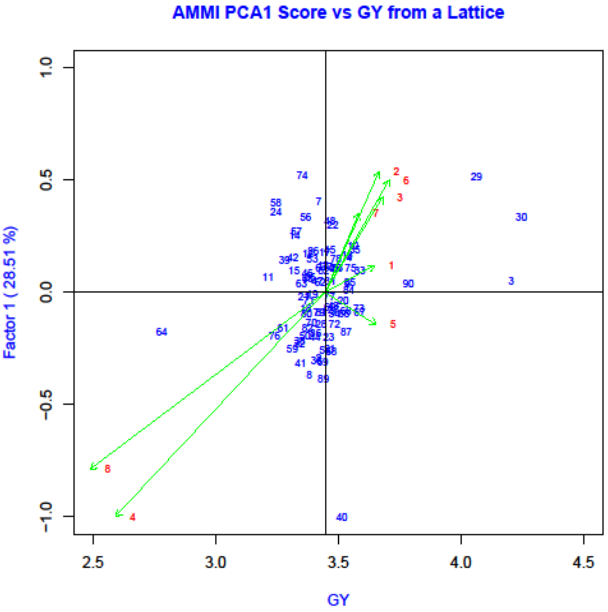

Figure 5. AMMI1 for grain yield of 90 rice genotypes across eight environments

Table 3. Ranking of rice genotypes based on mean performance and AMMI Stability Value (ASV) for grains panicle^{-1} across eight environments during 2021 and 2022 rice growing seasons.

Grains panicle^{-1}														
Genotypes	Mean	Rank	ASV	Rank	Genotypes	Mean	Rank	ASV	Rank	Genotypes	Mean	Rank	ASV	Rank
AUP-1	147.3	79	0.02	1	AUP-31	160.5	25	0.06	3	AUP-61	148.5	71	0.18	28
AUP-2	155.6	45	0.34	65	AUP-32	153.4	57	0.36	67	AUP-62	158.0	31	0.1	7
AUP-3	214.3	2	0.08	4	AUP-33	157.5	38	0.22	38	AUP-63	142.4	87	0.53	86
AUP4	141.0	89	0.23	40	AUP-34	157.9	32	0.17	21	AUP-64	154.8	51	0.75	89
AUP-5	157.0	40	0.15	17	AUP-35	162.1	23	0.19	30	AUP-65	154.3	55	0.52	85
AUP-6	162.6	22	0.12	14	AUP-36	166.4	12	0.47	80	AUP-66	148.7	68	0.32	59
AUP-7	154.3	54	0.50	84	AUP-37	164.8	18	0.30	55	AUP-67	157.3	39	0.37	71
AUP-8	157.5	37	0.50	83	AUP-38	156.5	43	0.40	76	AUP-68	152.6	59	0.29	53
AUP-9	170.6	8	0.12	13	AUP-39	166.3	13	0.34	64	AUP-69	153.3	58	0.37	69
AUP-10	155.3	48	0.34	62	AUP-40	178.0	5	1.10	90	AUP-70	154.5	52	0.25	46
AUP-11	143.5	85	0.24	45	AUP-41	172.0	7	0.35	66	AUP-71	151.7	61	0.24	43
AUP-12	151.3	63	0.27	49	AUP-42	155.1	49	0.19	31	AUP-72	151.8	60	0.17	20
AUP-13	143.5	86	0.16	18	AUP-43	162.1	24	0.37	72	AUP-73	145.6	81	0.48	82
AUP-14	147.2	80	0.28	52	AUP-44	154.1	56	0.27	50	AUP-74	148.0	75	0.57	87
AUP-15	148.6	70	0.44	78	AUP-45	147.3	79	0.22	39	AUP-75	158.7	28	0.2	36
AUP-16	157.5	36	0.38	73	AUP-46	148.5	72	0.24	86	AUP-76	149.2	66	0.29	54
AUP-17	148.6	69	0.20	32	AUP-47	164.5	21	0.25	88	AUP-77	143.8	84	0.03	2
AUP-18	155.0	50	0.18	24	AUP-48	165.0	17	0.38	25	AUP-78	156.9	41	0.2	34
AUP-19	154.4	53	0.18	27	AUP-49	159.0	27	0.15	46	AUP-79	155.5	47	0.34	63
AUP-20	166.2	14	0.19	29	AUP-50	165.2	16	0.23	20	AUP-80	148.4	74	0.15	15
AUP-21	159.8	26	0.12	12	AUP-51	158.4	30	0.31	59	AUP-81	148.0	76	0.1	6
AUP-22	148.4	73	0.33	61	AUP-52	141.7	88	0.16	87	AUP-82	148.0	77	0.18	26
AUP-23	157.9	33	0.28	51	AUP-53	158.6	29	0.17	69	AUP-83	155.7	44	0.18	25
AUP-24	172.1	6	0.40	75	AUP-54	137.9	90	0.37	89	AUP-84	155.5	46	0.09	5
AUP-25	164.6	20	0.12	11	AUP-55	147.7	78	0.23	16	AUP-85	157.6	35	0.17	23
AUP-26	151.3	62	0.20	33	AUP-56	145.3	82	0.37	5	AUP-86	156.5	42	0.44	79
AUP-27	169.6	9	0.33	60	AUP-57	149.5	65	0.30	75	AUP-87	150.7	64	0.27	48
AUP-28	149.1	67	0.22	37	AUP-58	164.7	19	0.47	8	Pakhal	157.8	34	0.12	9
AUP-29	203.9	3	0.69	88	AUP-59	166.8	11	0.32	73	K-Bas	168.1	10	0.43	77
AUP-30	226.0	1	0.12	10	AUP-60	145.1	83	0.10	64	F-MLD	166.1	15	0.2	35

The AMMI2 model was better than AMMI1 because the first two principal components (IPCA1 and IPCA2) explained 52.1% of the GEI. Seven vectors representing eight environments were spread over four quadrants. Vectors sharing the same quadrant indicated similar response of genotypes towards that particular environment(s). Likewise, the widespread of genotypes in all quadrants showed the overall inconsistency of genotypes across the tested environments. The long vector of E-4 and E-5 showed its high discriminating power. In contrast, environments E-3 and E-7 have shortest vectors indicating their low discriminating power. In other words, these environments exerted less force on genotypes to deviate from mean yield. Genotypes AUP-30 lying in proximity of Mansehra (E-3 and E-7), respectively, showed that these genotypes were specially adapted to these environments (Figure 6).

AMMI stability value (ASV) and ranking of genotypes based on ASV. Genotypes AUP-1 (0.02), AUP-77 (0.03), AUP-3 (0.06), and AUP-73 (0.08) had the lower ASV and thus were relatively stable. In contrary, AUP-40 (1.1), AUP-64 (0.8), and AUP-29 (0.7) were the most unstable genotypes as evident from their larger ASV. Genotype AUP-3 and AUP-30 had high mean grain yield (4.2 t ha^{-1}) with relatively low ASV (0.06 and 0.1) and hence could be declared as high yielding and stable genotype. Likewise, lower values for grain yield and ASV for AUP-64 (2.8 t ha^{-1} and 0.8), AUP-58 (3.2 t ha^{-1} and 0.5) and AUP-24 (3.2 t ha^{-1} and 0.4) implied that these genotypes repeatedly produced low grain yield in all the tested environments (Table 4).

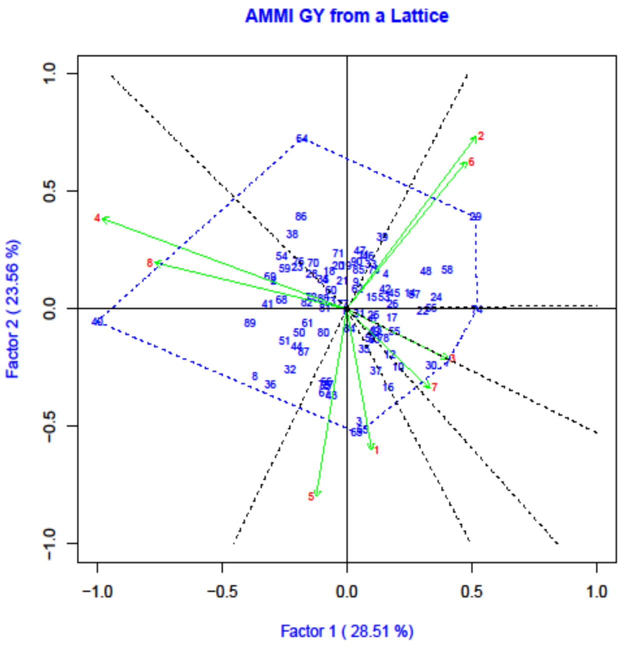

Figure 6. AMMI2 for grain yield of 90 rice genotypes across eight environments

Table 4. Ranking of rice genotypes based on mean performance and AMMI Stability Value (ASV) for grain yield across eight environments during 2021 and 2022 rice growing seasons.

Grain yield														
Genotypes	**Mean**	**Rank**	**ASV**	**Rank**	**Genotypes**	**Mean**	**Rank**	**ASV**	**Rank**	**Genotypes**	**Mean**	**Rank**	**ASV**	**Rank**
AUP-1	3.4	51	0.02	1	AUP-31	3.5	3	0.48	82	AUP-61	3.3	85	0.18	28
AUP-2	3.4	50	0.34	65	AUP-32	3.3	78	0.36	67	AUP-62	3.4	48	0.10	7
AUP-3	4.2	2	0.06	3	AUP-33	3.6	5	0.22	38	AUP-63	3.3	75	0.53	86
AUP-4	3.5	12	0.23	40	AUP-34	3.5	25	0.17	21	AUP-64	2.8	90	0.75	89
AUP-5	3.5	30	0.15	17	AUP-35	3.4	61	0.19	30	AUP-65	3.4	65	0.52	85
AUP-6	3.4	52	0.12	14	AUP-36	3.4	54	0.47	80	AUP-66	3.5	17	0.32	59
AUP-7	3.4	51	0.50	84	AUP-37	3.5	39	0.30	55	AUP-67	3.6	6	0.37	71
AUP-8	3.4	62	0.50	83	AUP-38	3.3	77	0.40	76	AUP-68	3.5	31	0.29	53
AUP-9	3.5	14	0.12	13	AUP-39	3.3	84	0.34	64	AUP-69	3.4	45	0.37	69
AUP-10	3.6	9	0.34	62	AUP-40	3.5	20	1.10	90	AUP-70	3.4	60	0.25	46
AUP-11	3.2	89	0.24	45	AUP-41	3.3	76	0.35	66	AUP-71	3.4	63	0.24	43
AUP-12	3.4	64	0.27	49	AUP-42	3.3	82	0.19	31	AUP-72	3.5	26	0.17	20
AUP-13	3.4	44	0.16	18	AUP-43	3.5	27	0.37	72	AUP-73	3.6	7	0.08	4
AUP-14	3.3	80	0.28	52	AUP-44	3.4	56	0.27	50	AUP-74	3.4	74	0.57	87
AUP-15	3.3	81	0.12	10	AUP-45	3.5	34	0.22	39	AUP-75	3.5	10	0.20	36
AUP-16	3.5	15	0.38	73	AUP-46	3.4	68	0.24	44	AUP-76	3.2	88	0.29	54
AUP-17	3.4	41	0.20	32	AUP-47	3.4	53	0.25	47	AUP-77	3.5	2	0.03	2
AUP-18	3.4	71	0.18	24	AUP-48	3.5	33	0.38	74	AUP-78	3.5	22	0.20	34
AUP-19	3.4	58	0.18	27	AUP-49	3.5	24	0.15	16	AUP-79	3.4	49	0.34	63
AUP-20	3.5	19	0.19	29	AUP-50	3.4	72	0.23	42	AUP-80	3.4	69	0.15	15
AUP-21	3.4	73	0.12	12	AUP-51	3.5	36	0.31	57	AUP-81	3.4	47	0.10	6
AUP-22	3.5	29	0.33	61	AUP-52	3.4	42	0.16	19	AUP-82	3.4	67	0.18	26
AUP-23	3.5	38	0.28	51	AUP-53	3.4	59	0.17	22	AUP-83	3.5	21	0.18	25
AUP-24	3.2	86	0.40	75	AUP-54	3.4	40	0.37	68	AUP-84	3.5	13	0.09	5
AUP-25	3.5	23	0.12	11	AUP-55	3.6	8	0.23	41	AUP-85	3.5	11	0.17	23
AUP-26	3.4	57	0.20	33	AUP-56	3.4	70	0.37	70	AUP-86	3.4	55	0.44	79
AUP-27	3.5	28	0.33	60	AUP-57	3.3	79	0.30	56	AUP-87	3.5	16	0.27	48
AUP-28	3.4	46	0.22	37	AUP-58	3.2	87	0.47	81	Pakhal	3.5	18	0.12	9
AUP-29	4.1	3	0.69	88	AUP-59	3.3	83	0.32	58	K-Bas	3.4	43	0.43	77
AUP-30	4.2	1	0.10	8	AUP-60	3.5	35	0.44	78	F-MLD	3.8	4	0.20	35

DISCUSSION

The ANOVA based on AMMI analysis revealed major role of GEI in total phenotypic expression of grain yield and its production traits. This indicated that the performance and change in ranking of genotypes were mainly due to their interaction with the environments. Crossa et al. (1990) believed that AMMI with two, three, or four IPCA were the best predictive models, however Misra et al. (2009) stated that only the first bilinear interaction term of the AMMI analysis was significant. The larger mean squares of environment indicated the significant response of environments (Kulsum et al., 2012). The large contribution of environment indicated that the environments were diverse, with large differences among environment means causing most of the variation in the grain yield. The AMMI model confirmed the intricate pattern of GEI and partitioned them into as many as even IPCAs. However, the first two principal components explained 88.2% the complex nature of GEI sum of squares (Luguterh et al., 2016). For each genotype, the magnitude of principal component scores indicates the stability of that genotype over environments. Genotypes which have higher score of IPCA indicate inconsistency and hence, such genotypes are specifically adapted to a particular environment (Islam et al., 2014). E-6 was the most productive environment in terms of grain yield followed by E-3, E-2, and E-5. Environments E-1 and E-5 appeared as most stable causing least fluctuations in the yield performance of the tested genotypes due to their close proximity to x-axis. Environments E-4 and E-8 were the most discriminating as specified by their long distances from the x-axis. Among genotypes, AUP-30 was the most stable and produced maximum grain yield (Fig. 6).

The AMMI2 biplot is better in both fitness and accuracy for exploring the complex pattern of GEI. Principal component (PC) scores acquired through AMMI analysis for each genotype identify the stability of that genotype over environments. Genotypes having higher score of PC indicate their inconsistent performance and might have specific adaptation to certain environment. In the current experiment the first two principal components (IPCA1 and IPCA2) explained 52.1% of the GEI. Genotypes AUP-3, AUP-30, AUP-29, AUP-77 and AUP-84 appeared as widely adaptable to diverse environments due to their position in the proximity of origin in the proximity of x-axis in AMMI1 biplot. The AMMI2 model constructed based on IPCA1 and IPCA2 scores was observed better than AMMI1 because the first two principal components explained more variation of the total sum of squares of the GEI. Several researchers reported AMMI2 as better model than AMMI1 and AMMI3 to explore GEI (Zobel et al., 1988; Crossa et al., 1990 and Gauch et al., 2008). Purchase et al. (2000) elucidated the inadequacy of AMMI3 biplot by plotting IPCA2 and IPCA3 scores, because higher axes are dominated by noise and have little projecting value.

Seven vectors representing eight environments were spread over four quadrants. Vectors sharing the same quadrant indicated similar response of genotypes towards that particular environment(s). Likewise, the widespread of genotypes in all quadrants showed the overall inconsistency of genotypes across the tested environments. The long vector of E-3 and E-5 showed its high discriminating power. In contrast, environments E-4, E-8 and E-7 have shortest vectors indicating their low discriminating power. In other words, these environments exerted less force on genotypes to deviate from mean yield (Satoto et al., 2016**)**. Genotypes AUP-30 lying in proximity of Charsadda (E-3 and E-7) respectively, showed that these genotypes were specially adapted to these environments. Genotypes exhibited superior performance in particular environment hampers their use in other environments and hence, could be considered as specifically adapted (Islam et al., 2014).

AMMI stability value (ASV) was proposed by Purchase et al. (2000) to quantify and rank genotypes according to their yield stability. The ASV is the distance from zero in a two-dimensional scattergram of IPCA1 (interaction principal component analysis axis 1) scores against IPCA2 scores. Since the IPCA1 score contributes more to GEI mean squares, it has to be weighted by the proportional difference between IPCA1 and IPCA2 scores to compensate for the relative contribution of IPCA1 and IPCA2 to the total GEI mean squares. The AMMI stability values (ASVs) were calculated for genotypes to identify stable genotypes for various traits. Genotype AUP-3 and AUP-30 had high mean grain yield (4.2 t ha^{-1}) with relatively low ASV (0.06 and 0.1) could be considered as high yielding and stable genotypes. Various researchers have earlier reported stability of the rice genotypes for grain yield across various environments using ASV. Luguterh et al. (2016) and Bose et al. (2014) have reported the efficiency of ASV to rank genotypes for the yield stability across environments.

The AMMI analysis identified genotypes both for specific and wide adaptation. Based on stability and yield performance, several genotypes were identified with superior performance than check cultivars. The wide spread distribution of environmental vectors showed lack of association among these environments. However, environments were clustered regardless of their geographical location, which revealed unpredictable nature of agro-climatic conditions across four tested locations i.e., Peshawar, Charsadda, Swat and Mansehra.

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