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## Study of yield stability for rice (*Oryza sativa* L.) genotypes using AMMI model

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### Abstract

The twenty two midlate rice genotypes having fine type were evaluated at four different locations of Gujrat in the years of 2021-22 in RCBD with three replications. The data on grain yield were subjected to statistical analysis with a view to fulfill the objective: (1) To study the G×E interaction using the multivariate technique (AMMI model) (2) To find the stable genotypes using AMMI model and AMMI based stability measures. The grain yield data were subjected to analysis of variance and pooled over locations. G×E interaction was found significant indicating genotypes performed differently in different locations. The results of the AMMI model indicated that GEI was further divided into two PCA axes IPCAI (65.22%) and IPCAII (22.49%) which together contributed 87.71 percent of the GEI. E1 (Nawagam) and E3 (Navsari) were found high yielding environments whereas E2 (Dabhoi) and E4 (Vyara) were found low yielding environments. Mean vs. IPCAI biplot found that genotypes G7, G19, G14 and G11 had general adaptability to the environments. Genotypes G3, G8, G17 and G18 were higher yielder and adapted to favorable environments. Where, genotypes G10, G12, G16 and G22 were lower yielders and adapted to poor environments. According to IPCA scores genotypes G3, G5, G7, G8, G11, G13, G17, G18 and G19 had positive GEI with environments E1 and E3. Which-won-where biplot indicated that genotypes G3 and G8 were vertex genotypes and they gave higher grain yield in environments E1 and E3. Genotypes G2 and G4 were vertex genotypes and high yielding in the E4 and E2 respectively. Genotypes G11, G7, G14 and G19 were the most stable genotypes as had low values of  $W_i$  (AMMI), ASV,  $ASTAB_i$  and simultaneous selection indices. Genotypes G15, G4, G21 and G18 were found unstable across the environments.

**Keywords:** Rice, yield stability, AMMI Model, IPCA, genotypes, environments

### Introduction

Rice (*Oryza sativa* L.) is a grass species that is the most widely consumed staple food crop for over 60% of the world's population. It is a member of the genus *Oryza*, which also includes wild rice and other species of cultivated rice. Rice is a versatile crop that can be grown in a variety of environments, from flooded fields to upland areas. It is also a low-input crop, requiring less water and fertilizer than other cereal crops. Rice is a major source of carbohydrates, fiber, vitamins and minerals. It is also a low-fat food, making it a healthy choice for people trying to lose or maintain a healthy weight. Rice is a common ingredient in many different meals around the world as well as ready-to-eat foods including popped and puffed rice, instant rice, and canned rice. In the cottage industry, rice straw is made into hats, mats, ropes, sound absorbing boards also used as litter material and as animal feed. In the current situation in 2020, China is the leading producer of paddy followed by India. The productivity of India is 2705 kg/ha (Anon., 2020a) [3]. In Gujarat, the area of rice cultivation is about 0.91 million hectares with a production of 2.14 million tons with 2367 kg/ha productivity (Anon., 2020b) [4]. As the world's population continues to grow the rice demand will likely increase. This will require the development of new stable varieties of rice that are more productive, resistant to pest and adapted to wide environments.

The study of genotype × environment interaction (GEI) can be approached using three different methods: parametric, non-parametric, and multivariate. Parametric methods, such as the Eberhart and Russell model, use analysis of variance (ANOVA) to identify and test sources of variability in GEI. However, these methods do not provide insight into the underlying pattern of interaction. On the other hand, non-parametric techniques can be used to spot interaction patterns because they do not rely on any presumption about the distribution of data.

The AMMI model is a powerful multivariate technique for study GEI that fuses ANOVA and principal component analysis (PCA) to identify and interpret GEI. ANOVA is used to identify the main additive effects, while PCA is used to identify the non-additive interaction effects. The AMMI model provides a more comprehensive understanding of GEI than either parametric or non-parametric methods alone. The advantage of the AMMI model is, it can identify both additive and non-additive effects of GEI, it can be used to identify patterns of interaction and it is easy to interpret. This study investigated the genotype x environment interaction (GEI) for rice yield, with the aim of selecting stable genotypes and to compare the stability measures *viz.*,  $W_{i(AMMI)}$  (Raju, 2002) [17], ASV (Purchase, J. L., 1997) [16]. and  $ASTA B_i$  (Rao, *et al.*, 2004) [18] were calculated based on AMMI analysis for stability of rice genotypes.

### Materials and Methods

A set of twenty-two rice genotypes was evaluated for their yield stability at four different locations *viz.*, Nawagam (E1), Dabhoi (E2), Navsari (E3) and Vyara (E4) Gujarat, India during *khariif* 2021-2022. The rice genotypes were grown in a randomized complete block design with three replications at each location. The yield data of multi-location were subjected to stability analysis using a multivariate method (AMMI).

### Statistical model

ANOVA:  $Y_{ij} = \mu + \alpha_g + \beta_e + \alpha\beta_{ge} + \rho_{ij} + \varepsilon_{ijk}$

PCA:  $Y_{ij} = \mu + \sum_n \lambda_n \gamma_{gn} \delta_{en} + \rho_{ij} + \varepsilon_{ijk}$

AMMI:  $Y_{ij} = \mu + \alpha_g + \beta_e + \sum_n \lambda_n \gamma_{gn} \delta_{en} + \varepsilon_{ijk}$

Where,

$\mu$ : grand mean

$\alpha_g$ : deviation of genotype g from grand mean

$\beta_e$ : deviation from environment e

$\lambda_n$ : Singular value for Interaction Principal Component

Analysis Axis n (IPCA)

$\gamma_{gn}$ : genotype eigenvector for axis 'n'

$\delta_{en}$ : environment eigenvector for axis 'n'

$\rho_{ij}$ : Residual

$\varepsilon_{ijk}$ : error term

The result of AMMI analysis is graphically represented by the biplot. It is a useful tool to comprehend more intricate and specific patterns of genotypes and GEI or both genotypes and environments. The concept of biplot was first developed by Gabriel (1971) [8]. It is a scatter plot that visually illustrates the genotype and environments of two-way data and enables the visualisation of the relationships between genotypes, environments and GEI. The biplot is a useful tool for identifying genotypes that are well-adapted to particular environments. It can also be used to identify genotypes that have high GEI, which means that they perform well in some environments but not others. The biplot can be used to visualize the overall pattern of GEI in a data set. This can help researchers to understand how genotypes and environments interact to produce different phenotypes (Yan *et al.*, 2000) [22].

### $W_{i(AMMI)}$

$W_{i(AMMI)}$  a measure of stability which is good as wrick's ecovalence ( $W_i^2$ ) was estimated as under (Raju, 2002) [17]. Lower values of the  $W_{i(AMMI)}$  score indicated the stable genotypes across the different environments.

$$W_{i(AMMI)} = \sum_{m=1}^M \lambda_m^2 \gamma_{mi}^2$$

$\lambda_m$  = singular value for interaction Principal Components Axis m(IPCA)

$\gamma_{mi}$  = genotype eigenvector for axis m

### AMMI stability value (ASV)

The AMMI model does not provide a quantitative measure of stability, which is required for quantifying and ranking genotypes based on their yield stability, the following measure proposed by Purchase (1997) [16]. The ASV score is a measure of the genotypic stability of a genotypes. A higher ASV score implies that the genotype is specifically adapted to certain environments, while a lower ASV score indicates that the genotype is more genetically stable across different environments. It can be calculated by the following formula.

$$ASV = \sqrt{\left[\left(\frac{IPCA1 SS}{IPCA2 SS}\right) \times (IPCA score)\right]^2 + (IPCA2 score)^2}$$

### AMMI based selection indices

A new stability measure and incorporated as a stability component (Rao, *et al.*, 2004) [18] When more than two axes are retained in AMMI model, the biplot formulation of interaction is failed. When n' of N axis are retained in the AMMI model to explain GEI, then the stability measure of  $i^{th}$  variety can be determined as the end point of its vector  $\alpha_{1i}^*$ ,  $\alpha_{2i}^*$ , ...,  $\alpha_{n'i}^*$  from the origin  $0'_{n' \times 1}$ . This can also be taken as the squared Euclidean distance between the vector  $\gamma = (\alpha_{1i}^*, \alpha_{2i}^*, \dots, \alpha_{n'i}^*)$  from the origin, in the n'- Dimensional and was calculated as under.

$$ASTAB_i = d_i(\gamma, 0) = \alpha_{1i}^{2*} + \alpha_{2i}^{2*} + \dots + \alpha_{n'i}^{2*} = \sum_{n=1}^{n'} \alpha_{ni}^{2*} = \sum_{n=1}^{n'} \lambda_n \alpha_{ni}^2$$

A genotype is considered as highly stable when the values of  $ASTAB_i$  is small or near to zero.

### Results and Discussion

Table 1 shows the combined analysis of variance (ANOVA) of twenty two genotypes over 4 locations using AMMI model. The table clearly demonstrated that mean squares for genotype and location (environment) were found significant. This implied that there was a wide range of variability among genotypes and locations and that genotype performance varied depending on the location as the G×E interaction was significant. The largest portion of the total treatment variation (trial SS) was attributable to in location (42.12%) followed by genotype-related variance (39.03%) and G × E interaction related variance (18.86%). Mostafavi *et al.* (2011) [11], Farshadfar *et al.* (2012) [7], Pande *et al.* (2013) [13], Das *et al.* (2018) [6].

A significant portion of the GEI was further divided into two PCA axes (IPCAI and IPCAII) which together contributed 87.71 percent of the GEI. The variance of total GEI was made up of 65.22 and 22.49 percent by the first two PCAs, respectively. Abeytilkaratna (2010) [1], Kesh *et al.* (2022) [10], Yan (2002) [21] and Gauch and Zobel (1997) [9]. found similar kind of result in rice.

**Table 1:** Analysis of Variance (ANOVA) for AMMI analysis of rice genotypes over environments

Source of Variations	df	Sum of Squares	Mean Squares	F Ratio	% SS
Trials	87	16.2494	0.1867	3.84*	--
Genotypes	21	6.3419	0.3020	6.21*	39.03
Env	3	6.8434	2.2811	46.90*	42.12
G*E	63	3.0639	0.0486	2.53*	18.86
PCA I	23	1.9982	0.0868	4.38*	65.22
PCA II	21	0.6891	0.0328	1.65	22.49
Residual	19	0.3765	0.0198		12.29
P. error	168	3.2052	0.0191		

\*Significant at 0.05 percent level of probability

The result of AMMI analysis can also be easily comprehended using the AMMI 1 biplot as shown in Fig. 1. The biplot was constructed using the mean performance and IPCA I score for both the genotypes and environments, as presented in Table 2. The effects (genotypes and environments means) were shown on the abscissa (X-axis) and ordinate (Y-axis) represents the first IPCA score. The conventional interpretation of such biplot assay is that if genotype or an environment has a PCA score close to '0', it has very small interaction effects and when the genotypes and environment have the same sign on the PCA axis their interaction is positive but if different then their interaction is negative. The AMMI model considers genotypes with a mean

higher than the grand mean and IPCAI scores nearly zero to be as generally adapted to all environments. However, the genotypes with high mean performance and with large values of IPCA scores considered to have certain adaptability to the environments. Biplot assay shown in Fig. 1 identify five high yielding genotypes viz., G7, G19, G14, G11 and G2 having general adaptability as they were situated at right hand side of grand mean level (2.298 kg/plot) and close to IPCA I = 0 line. Genotypes G3, G8, G17, G18, G15 and G1 were higher yielding and specially adapted to favorable environments. Genotypes G10, G12, G16 and G22 had low mean yield indicated that they were adapted to poor environments Padmavathi *et al.* (2020)<sup>[12]</sup> and Kesh *et al.* (2022)<sup>[10]</sup>.

**Table 2:** Mean grain yield, IPCA1 and IPCA2 scores of different rice genotypes and environments

Genotypes	Mean Yield (kg/plot)	Rank	PC1	PC2
G1	2.475	6	-0.288	-0.2452
G2	2.723	1	-0.0191	0.4549
G3	2.573	2	0.2804	-0.0988
G4	1.943	20	-0.4266	-0.0436
G5	2.325	14	0.2406	0.1104
G6	2.270	15	0.3552	0.031
G7	2.371	13	0.02202	-0.1547
G8	2.500	4	0.2921	-0.1177
G9	1.664	22	-0.2889	-0.207
G10	2.263	16	0.1316	0.1412
G11	2.443	8	0.05942	-0.1022
G12	2.225	17	-0.2336	0.01969
G13	2.443	9	0.1564	-0.2307
G14	2.415	10	0.00468	-0.2169
G15	2.373	12	-0.4197	0.1666
G16	1.961	19	-0.2176	-0.1599
G17	2.475	5	0.2697	0.249
G18	2.475	7	0.3515	0.1033
G19	2.389	11	0.07197	0.1916
G20	2.505	3	-0.1765	0.1635
G21	1.697	21	-0.3535	0.2332
G22	2.041	18	0.188	-0.2876
Average	2.298			
<b>Environments</b>				
E1	2.554	1	0.5336	-0.3025
E2	1.882	4	-0.9729	-0.2563
E3	2.550	2	0.4269	-0.2289
E4	2.204	3	0.01240	0.7877

IPCA scores of genotypes G3, G5, G7, G8, G11, G13, G17, G18 and G19 and IPCA scores of Nawagam (E1) and Navsari (E3) locations were positive, which revealed that these genotypes were associated with higher yield at these locations with positive GEI. E4 had a relatively small IPCA1 score, indicating that E4 had little interaction with genotypes (Anandan *et al.*, 2009)<sup>[2]</sup>.

Environments were widely spread over scatter diagram. It

showed that there was a high degree of variability among the locations. Environment E1 (Nawagam) and E3 (Navsari) were highly yielding potential locations, whereas, E4 and E2 were found low yielding environments (Fig. 1) (Campbell and Jones, 2005)<sup>[5]</sup>.

The Visualization of the polygon ("Which-won-where") pattern of MLT data is crucial for studying the presence of different mega-environments. The GGE biplot view Fig. 2

made up of an irregular polygon and a set of lines drawn from the biplot origin to intersect the sides of the polygon at right angles. The vertices of the polygon were the genotype markers away from the biplot origin in various directions in such a manner to accommodate all genotype markers. The biplot is divided into sectors by perpendicular lines to the polygon sides, each having its own winning cultivar, (Yan and Tinker, 2006) [20]. The vertex cultivar at the intersection of the two polygon side was the winning cultivar for a sector and it is positioned usually within its wining sector. The ten rays divide the biplot into ten sectors. Out of four locations, two locations E1 and E3 were fall in the third sector. Whereas, environments E4 and E2 occupy in seventh and tenth sectors, respectively.

The third sector had locations E1 (Nawagam) and E3 (Navsari) with higher yielding genotypes G3 and G8 while seventh sector showed E4 (Vyara) with higher yielding genotypes G2 and G19. The sector ten with environment E2 (Dabhoi) showed advantage for genotype G4. The other genotypes G1, G22, G6, G18, G17, G21 and G15 lying on vertices did not respond at any locations. The first principal component (PC1) in this graphic presentation shows cultivar productivity and the second principal component (PC2) represents cultivar stability. A genotype with high PC1 value (high productivity) and a low PC2 value near to zero (more stable) would be considered an ideal genotype. The present study indicated that Genotypes G6 and G18 had largest PC1 scores and had the higher grain yield than overall mean grain yield. In contrast, genotype G12 yielded poorly at all sites but was relatively stable, as indicated by its small PC1 scores (low yielding) and relatively small PC2 score (stable). Genotypes with PC1 scores more than zero were identified as higher yielding, while those with PC1 scores < 0 were identified as lower yielders. Accordingly, the average yield of G15 and G21 were below average and highly unstable (largest absolute PC2 scores), genotype G2 had highest yield across four environments but also had largest PC2 scores which indicate that G2 is highly unstable genotype. In contrast, genotypes G3, G6, G5, G8, G13, G17, G18 and G22 had positive PC1 scores and were identified as high yielder genotypes. Genotypes located near the plot of origin were less

responsive than vertex genotypes. In this study, genotypes G11 and G10 were close to the origin and hence, they were non-responsive to environmental interactive forces therefore they have general adaptation with different mean grain yield, meaning that they were able to produce a similar yield in variety of environments. Similarly, the environment close together i.e., E1 and E3 were found to have similar interaction pattern in genotypes (Kesh *et al.*, 2022) [10].

#### W<sub>i</sub>(AMMI) measure

The various W<sub>i</sub>(AMMI) values were calculated and are shown in Table 3 The W<sub>i</sub>(AMMI) results showed that W<sub>i</sub>(AMMI) ranks were superimposed on ASV measures. The genotypes G11, G7, G14, and G19 were the most stable as W<sub>i</sub>(AMMI) values were found small while G15, G4, G21, and G18 were the most unstable as W<sub>i</sub>(AMMI) values were found large (Parmar, 2009) [14].

#### AMMI stability value (ASV)

In the AMMI model the ASV is distance between the coordinate point and the origin in the dimension of IPCA 1 scores and IPCA 2 scores. The genotype G11 was most stable genotype followed by genotypes G7, G14, and G19 while genotypes G15, G4, G21 and genotype G18 were unfavorable in terms of stability (Table 3). The mean grain yield of all stable genotypes were higher than the overall mean grain yield. Among unstable genotypes G18, G15, and G4 has higher grain yield while G21 had lower grain yield than mean grain yield (Singh *et al.*, 2019) [19].

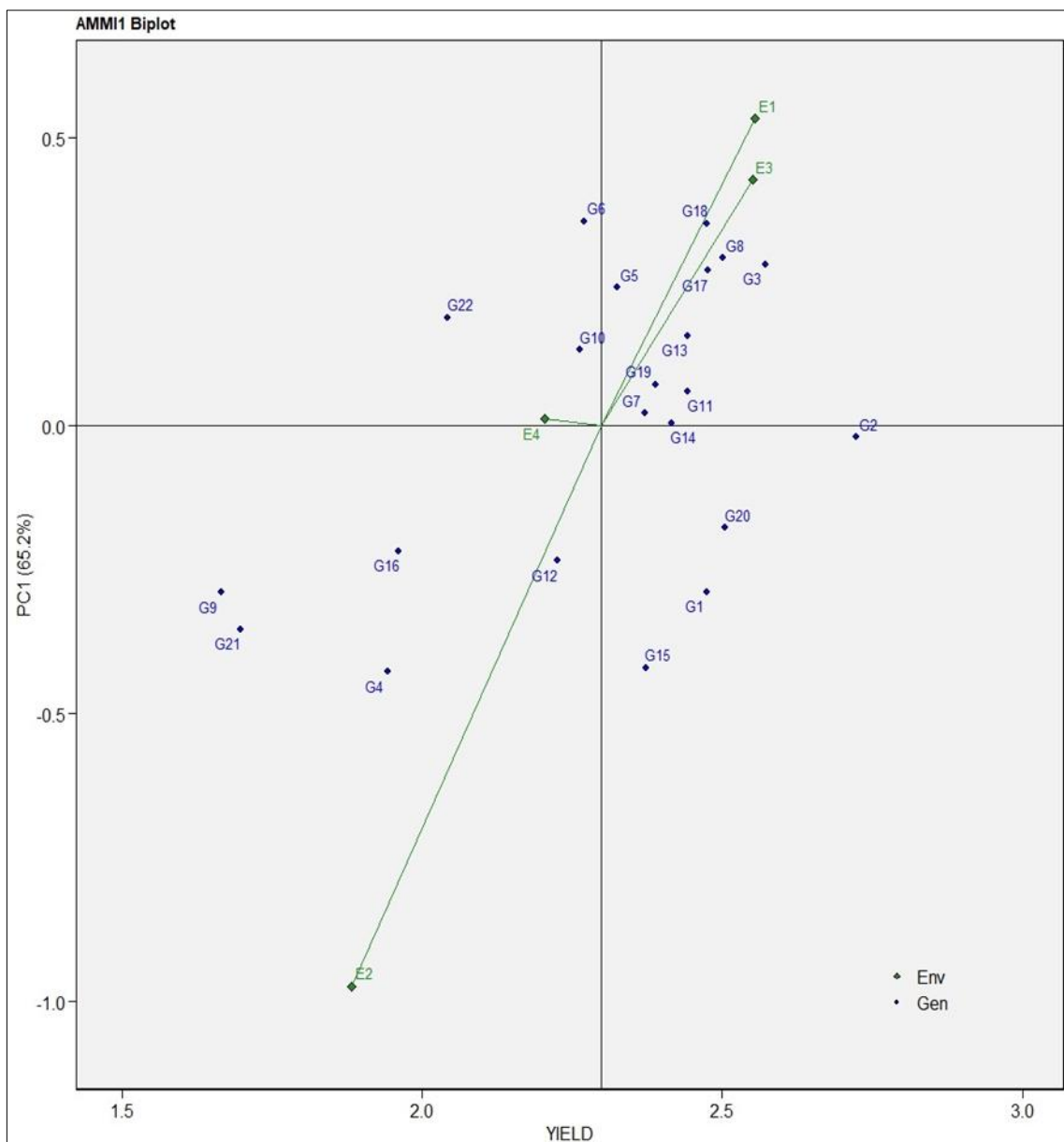
#### AMMI based selection index (ASTABi)

Stability measures for ASTABi (squared Euclidean distance) were computed and shown in Table 3. When ASTABi is close to zero or has a small value, a variety is considered highly stable. The ASTABi value for the genotype G11 was the lowest followed by genotypes G7, G14 and G19. All the four genotypes had higher mean grain yield than overall mean. Genotypes G15, G4, G21, and G18 had highest value of ASATB<sub>i</sub> indicating their environmental instability. (Rao *et al.*, 2004 and Parmar *et al.*, 2022) [18, 15].

**Table 3:** Selection of genotypes based on different indices based on AMMI model for rice genotypes

Genotypes	Mean Yield	Rank	W <sub>i</sub> (AMMI)	Rank	ASV	Rank	ASTABi	Rank
G1	2.475	6	0.2071	17	0.5483	17	0.2071	17
G2	2.723	1	0.1433	12	0.4561	12	0.1433	12
G3	2.573	2	0.1638	13	0.4876	13	0.1638	13
G4	1.943	20	0.3649	21	0.7277	21	0.3649	21
G5	2.325	14	0.1240	10	0.4243	10	0.1240	10
G6	2.270	15	0.2527	18	0.6056	18	0.2527	18
G7	2.371	13	0.0174	2	0.1592	2	0.0174	2
G8	2.500	4	0.1800	14	0.5111	14	0.1800	14
G9	1.664	22	0.1962	16	0.5337	16	0.1962	16
G10	2.263	16	0.0483	5	0.2649	5	0.0483	5
G11	2.443	8	0.0142	1	0.1438	1	0.0142	1
G12	2.225	17	0.1093	8	0.3983	8	0.1093	8
G13	2.443	9	0.0855	7	0.3523	7	0.0855	7
G14	2.415	10	0.0324	3	0.2170	3	0.0324	3
G15	2.373	12	0.3710	22	0.7338	22	0.3710	22
G16	1.961	19	0.1122	9	0.4036	9	0.1122	9
G17	2.475	5	0.1880	15	0.5224	15	0.1880	15
G18	2.475	7	0.2542	19	0.6074	19	0.2542	19

G19	2.389	11	0.0356	4	0.2274	4	0.0356	4
G20	2.505	3	0.0806	6	0.3421	6	0.0806	6
G21	1.697	21	0.2871	20	0.6455	20	0.2871	20
G22	2.041	18	0.1276	11	0.4303	11	0.1276	11
Mean	2.298							



**Fig 1:** AMMI 1 biplot for rice genotypes (yield) and environments





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