



AMMI Biplot Analysis for Genotype X Environment Interaction and Stability for Yield in Hybrid Rice (*Oryza sativa* L.) Under Different Production Seasons

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Authors' contributions

This work was carried out in collaboration among all authors. Author KR D designed the study, performed the statistical analysis, wrote the protocol and wrote the first draft of the manuscript. Authors VV, NL, KRP, BSC and YH managed the analyses of the study. Author PJMR managed the literature searches. All authors read and approved the final manuscript.

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ABSTRACT

The aim of the study was to determine the genotype x environment interaction and stability performance of fifteen rice hybrids in three different production seasons during 2016, 2017 at Regional Agricultural Research Station, Warangal, Telangana. Data was subjected to the additive mean effects and multiplicative interaction (AMMI) analysis, results indicated that significant genotype x environmental interaction (GEI) influenced the relative ranking of the hybrids across the seasons. It was evident from AMMI analysis that first two principal components accounted for

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94.09%, which is enough to explain the variability among the hybrids. The hybrids, G9 (WGRH 18), G8 (WGRH-17) and G12 (WGRH-22) and G3 (WGRH-10), exhibited high grain yield. The AMMI 2 biplot revealed that the rice genotype, G15 (WGL-14), close to the origin indicated non sensitive nature of this genotype with the seasons and highly stable genotype across the environments with low yield potential when compared to hybrids. Whereas the rice hybrids, G9 (WGRH-18), G8 (WGRH-17), G3 (WGRH-10) and G5 (WGRH-14), were also close proximity to origin and have limited interaction with the seasons. The rice hybrid, G9 (WGRH-18), has high mean yield with stable performance over three environments being the overall best can be considered for the release after through conformation.

Keywords: Rice; G x E interaction; AMMI biplot; what-won-where biplot.

1. INTRODUCTION

Rice has a special significance as a source of food crop providing over 75% of Asian population and more than three billion of world population's meal which represents 50 to 80 % of their daily calorie intake [1]. This population will increase to over 4.6 billion by 2050 [2]. Yields of improved rice varieties in favourable conditions have reached to a plateau or even subsequently declined. A large number of high yielding stable hybrids with high adaptation capability to diverse environments are required to accomplish specific socio economic and agricultural needs. It is obviously proved that hybrids show better performance under adverse conditions like drought and saline conditions. Developing high yielding stable hybrids adapted to diverse environments is the need of hour to meet increasing demands of world population. But grain yield depends upon genotype, environment and management practices and their interaction with each other [3]. Genotypes tested in different years or different locations have significant fluctuations in yield due to the response of genotypes to environmental factors such as soil fertility or the presence of biotic and abiotic environmental stresses [4]. Information on genotype and environmental interaction provides a better strategy to successful evaluation and identification of stable genotype, which could be used for general cultivation. A genotype may be considered to be stable if its environmental variance is small. The level of performance of a character is a result of the genotype of cultivar, the environment in which it is grown and interaction of G and E. Interaction between these two explanatory variables gives insight for identifying genotypes suitable for specific environments. The environmental effect is typically a large contribution to total variation [5]. Moreover G x E interaction greatly affect the phenotype of a variety and inform us to perform stability analysis to know the performance of

varieties and hybrids in different environments to help the plant breeders in selecting desirable genotypes. Various statistical procedures have been proposed to find out the stability of new cultivars, many of them are based on a regression model [6]. The additive main effect and multiplicative interaction (AMMI) model has found more use recently since it incorporates both the additive main effects model for G x E interaction and the multiplicative components as integrated least square analysis and thus became more effective in selection of stable genotypes [7]. Difference in genotype stability and adaptability to environments can be quantitatively assessed using the biplot graphical representation that scatters the genotypes accordingly to their principal component values [8].

2. MATERIALS AND METHODS

The experiments were conducted at Regional Agricultural Research Station, Warangal, Telangana State, India during *Kharif*, 2016, *Rabi* 2016-17 and *Kharif* 2017. The experimental material comprised of fifteen rice genotypes (twelve hybrids and three checks) and experiment was laid out in Randomised block design with three replications. Each experimental unit consists of 3 rows of 4 mtrs length. Twenty five days old seedlings were transplanted at a spacing of 20 cm between rows and 15 cm between the plants at 20 plants per row and plant density was maintained at 33 plants/m². Fertilizer (N:P:K) was applied at 120:60:40 Kg/ha. The entire phosphorous and half quantity of murate of potash and 1/3 of nitrogen was applied as basal and the rest of nitrogen was applied in two equal splits one at maximum tillering and another at panicle initiation stage along with half quantity of murate of potash. Standard agronomic practices were under taken to raise a healthy crop. The grain yield

data were collected following standard method [9].

The grain yield data were subjected to pooled analysis of variance indicated the significant variation among the genotypes, seasons and genotype x environment interaction. This confirms the usefulness of AMMI analysis. The AMMI model which combines standard analysis of variance with principal component analysis [10] was used to investigate G x E interaction. In AMMI model the contribution of each genotype and each environment to the GEI is assessed by using biplot graph display in which yield means are plotted against the scores of the PCA [10]. ANOVA and Stability analysis for yield traits was carried out by using the AMMI model R-package 1.5 PB Tools 1.4 version of IRRI.

3. RESULTS AND DISCUSSION

3.1 AMMI Analysis of Variance

The details of the rice hybrids and testing seasons presented in Table 1. The combined analysis of variance for genotype, environments and genotype x environment interactions of fifteen hybrids in three production seasons were highly significant for grain yield indicating the use of AMMI analysis. Further, it indicated that 56.0% of the total sum of squares was attributed to environmental effects, 22.89% to genotypic effects and 14.43% to genotype x environment interaction effects (Table 2). The presence of genotype x environment interaction (GEI) was clearly demonstrated by the AMMI model and variance of G x E was partitioned into two significant principal components. This implied that the first two principal components are enough to explain the interaction effects of fifteen rice hybrids in three production seasons. These findings were in conformity with the findings of [11]. Biplots are graphs where both genotypes and environments are plotted on the same axes that interrelationships can be visualized [12].

The mean grain yield value of genotypes averaged over environments indicated that the genotypes, G9 and G7, had the highest 7380 Kg/ha and the lowest (5537 kg/ha) yield, respectively. Different genotypes showed inconsistent performance across all the environments. The environmental mean grain yield ranged from 7740 Kg/ha for E1 to 5683 Kg/ha for E2 and averaged grain yield over environment and genotype was 6473 kg/ha.

3.2 AMMI I Biplot

In the AMMI 1 biplot, the usual interpretation of biplot is that the displacements along the axis indicate difference in mean (additive) effects, whereas displacements along the ordinate indicate differences in interaction effects. Genotypes that group together have similar adaptation while environments which group together influence the genotype in the same way [13]. If a genotype has an IPCA score of nearly zero it has small interaction effect with environment and considered as stable. Rice hybrids grain mean yields and IPCA1, IPCA2 values were presented in Table 3. Genotypes and environments on the same parallel line relate or ordinate have similar yields and a genotype or environment on the right side of the midpoint of this axis has higher yield than those of left hand side. In the present study, the hybrids, G9 (WGRH-18), G8 (WGRH-17) and G12 (WGRH-22), exhibited high grain mean yield with high additive effects showing positive IPCA1 score and the hybrid, G 9, recorded the overall best in terms of yield. The rice hybrid G9 (WGRH-18) can perform better in the environment E1. A similar outcome was reported by [14].

The rice hybrids, G7 (WGRH-16), G4 (WGRH-13) and G13 (PA 6444), performed better in environment E2 while the environment E3 was suitable for the rice genotypes, G14 (MTU-1010) and G 15(WGL-14). These findings are in tune with the [15].

3.3 AMMI II Biplot

In AMMI II biplot (Fig. 2), the environmental scores are joined to the origin by sidelines. Sites with short spokes do not exert strong interactive forces, those with long spokes exert strong interaction. The IPCA 1 versus IPCA 2 biplot explains the magnitude of interaction of each genotype with the environment. The points representing E1, E2 and E3 are connected to the origin.

The genotypes falling in the circle or near to origin will tend to have similar yields in all the environments. Hence, the genotypes which are near to the origin, G15 (WGL-14), G9 (WGRH-18), G10 (WGRH-19), G3 (WGRH-10) and G8 (WGRH-17), are not sensitive or had little interaction with environment and considered as more stable genotypes over all environments. Among the rice hybrids, G15 (WGL-14), was considered as more stable genotype. Genotypes

distant from the origin are sensitive and have large interaction with the environments. In the present study, the rice hybrids, G7 (WGRH-16), G13 (6444) and G6 (WGRH-15) are more sensitive to environments. Similar results were reported by [16].

Table 1. The codes and names of rice hybrids

S.N.	Hybrids/ genotypes codes	Hybrids/ genotypes names	Environment code	Environment name
1	G1	WGRH-5	E1	Kharif, 2016
2	G2	WGRH-6	E2	Rabi, 2016-17
3	G3	WGRH-10	E3	Kharif, 2017
4	G4	WGRH-13		
5	G5	WGRH-14		
6	G6	WGRH-15		
7	G7	WGRH-16		
8	G8	WGRH-17		
9	G9	WGRH-18		
10	G10	WGRH-19		
11	G11	WGRH-21		
12	G12	WGRH-22		
13	G13	PA-6444		
14	G14	MTU-1010		
15	G15	WGL-14		

Table 2. AMMI analysis of variance for grain yield over three seasons

Source of variation	D.F	S.S	M.S	% S.S explained
Varieties	14	29708673.62	2122048.11**	22.89
Environments	2	73683812.42	36841906.21**	56.77
Varieties X Environments	28	18731691.24	668988.97**	14.43
PC1	15	13413016	894201.1**	
PC2	13	5318675	409128.9**	
Error	45	7652204.50	170048.98	
Total	89	129776381.78		

Table 3. Mean yield and IPCA1, IPCA2 values for fifteen rice hybrids over three seasons

S. No.	Hybrid/Genotype	E1 ()	E2 ()	E3 ()	Mean ()	PCA1	PCA2
1	WGRH-5	6993	5495	5386	5958	-0.18	0.01
2	WGRH-6	7550	5542	7427	6839	0.05	-0.23
3	WGRH-10	7730	6170	6852	6917	0.07	-0.10
4	WGRH-13	7150	5462	5121	5911	-0.19	0.06
5	WGRH-14	7287	5730	5784	6267	-0.10	-0.005
6	WGRH-15	8527	6663	5307	6832	-0.05	0.24
7	WGRH-16	7563	4101	4947	5537	-0.29	0.08
8	WGRH-17	8178	6619	7049	7282	-0.17	-0.06
9	WGRH-18	9069	6890	6183	7380	0.20	0.18
10	WGRH-19	8408	5915	5737	6686	0.01	0.13
11	WGRH-21	7978	5466	6122	6522	-0.03	0.007
12	WGRH-22	7810	6567	6964	7113	0.12	-0.09
13	PA-6444	8389	5109	5538	6345	-0.07	0.12
14	MTU-1010	6530	4474	6086	5697	-0.25	-0.19
15	WGL-14	6941	5051	5444	5812	-0.22	-0.02
Mean		7740	5683	5996	6473		

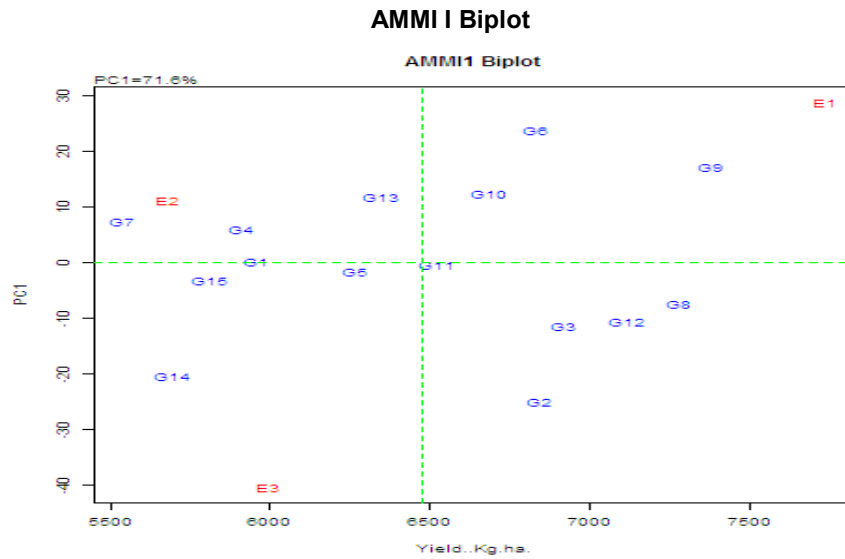


Fig. 1. Biplot of the first interaction principal component axis (IPCA1) versus mean yields

3.4 What-won-where Biplot

The striking feature of what-won-where GGE biplot is its ability to show the what-won-where pattern of a genotype by environment. A polygon is first drawn on genotypes that are furthest from the biplot origin so that all other genotypes are contained within the polygon. Then perpendicular lines to each side of the polygon are drawn, starting from the biplot origin [17]. These perpendiculars divide the biplot into

several sectors. There are six sectors and the environments fall into the two of them. The environment group within each sector and the genotypes at the polygon's extremity characterized the mega environment [18]. The polygon view of GGE biplot (Fig. 3) is the best way for the identification of winning genotypes with visualizing the interaction patterns between genotypes and environments. There are two mega environments one with E3 and second consisting of E1 and E2.

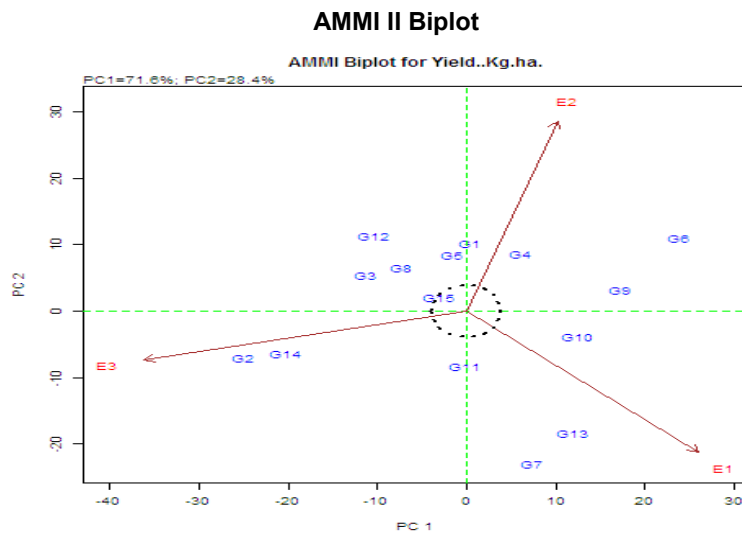


Fig. 2. Biplot of the first interaction principal component axis (IPCA1) versus the second interaction principal component axis (IPCA2) in rice

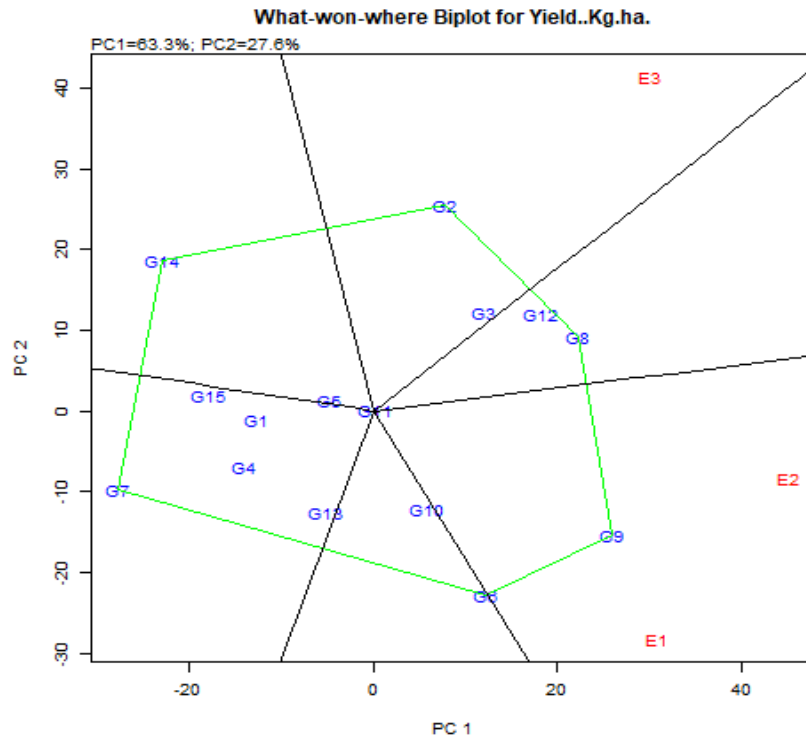


Fig. 3. The what-won-where view of the GGE biplot to show which genotype performed best in which environment in rice

4. CONCLUSION

The AMMI 1 biplot revealed that the rice hybrids, G9 (WGRH-18), G8 (WGRH-17) and G12 (WGRH-22), were the best yielders in terms of mean yield. AMMI 2 biplot indicated that the rice genotype, G15, was hardly affected by the genotype x environment interaction and considered as more stable genotype among all tested entries. The hybrids, G9 (WGRH-18), G10 (WGRH-19), G3 (WGRH-10) and G8 (WGRH-17), were close to origin indicating their stability ver seasons and little interaction with the environments. Overall, the rice hybrid, G9 (WGRH-18), performed better with higher grain mean yield and little environmental interaction considered as most promising hybrid. The rice genotypes, G2 (WGRH-6) and G3 (WGRH-10), had better performance in mega environment E3. Similarly, the rice genotype, G9 (WGRH-18), exhibited better performance in the second mega environment consisting of E1 and E2. When two environments (E1 and E2) fall in single mega environment provides information that testing of genotypes in one environment is enough in order to reduce the cost of testing and increase breeding efficiency.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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