

## GENOTYPE BY ENVIRONMENT INTERACTION AND STABILITY ANALYSIS FOR RICE GENOTYPES UNDER BORO CONDITION

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Genotype (G) × Environment (E) interaction of nine rice genotypes possessing cold tolerance at seedling stage tested over four environments was analyzed to identify stable high yielding genotypes suitable for boro environments. The genotypes were grown in a randomized complete block design with three replications. The genotype × environment (G×E) interaction was studied using different stability statistics viz. Additive Main effects and Multiplicative Interaction (AMMI), AMMI stability value (ASV), rank-sum (RS) and yield stability index (YSI). Combined analysis of variance shows that genotype, environment and G×E interaction are highly significant. This indicates possibility of selection of stable genotypes across the environments. The results of AMMI (additive main effect and multiplicative interaction) analysis indicated that the first two principal components (PC1–PC2) were highly significant ( $P < 0.05$ ). The partitioning of TSS (total sum of squares) exhibited that the genotype effect was a predominant source of variation followed by G×E interaction and environment. The genotype effect was nine times higher than that of the G×E interaction, suggesting the possible existence of different environment groups. The first two interaction principal component axes (IPCA) cumulatively explained 92 % of the total interaction effects. The study revealed that genotypes GEN6 and GEN4 were found to be stable based on all stability statistics. Grain yield (GY) is positively and significantly correlated with rank-sum (RS) and yield stability index (YSI). The above mentioned stability statistics could be useful for identification of stable high yielding genotypes and facilitates visual comparisons of high yielding genotype across the multi-environments.

*Key words:* boro rice, G×E interaction, stability

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## INTRODUCTION

The boro rice is commonly known as winter rice. Improved cultivars possessing cold tolerance at seedling stage along with high yield generally grown during boro season. Cold tolerance at seedling stage is the primary requirement of boro cultivars. Generally seedlings for boro cultivation are raised during the cold months of November and December. Farmers adopt boro cultivation in the area where water accumulates during the monsoons but cannot be drained, thus providing ideal settings for boro rice cultivation during winter season. Boro rice produces more yields than the kharif rice in the same ecology and reduces risk of natural calamities like flood during main season under flood prone areas through boro rice cultivation.

Genotype adaptability and stabilization of rice production under boro climate over to environmental fluctuations is vital. Thus, evaluation of rice genotypes for yield stability under varying environmental conditions has become an essential part of any breeding programme. Genotype by environment interaction has been studied by various researchers (ZUBAIR and GHAFOR, 2001; ANNICCHIARICO, 2002; RAMBURAN *et al.*, 2011; MUKHERJEE *et al.*, 2013, BOSE *et al.*, 2014).

Many statistical methods for quantifying genotypes (G) environment (E) and their  $G \times E$  interaction effects are available (GAUCH, 2013). However, a method called (AMMI) has been found particularly useful in visualizing  $G \times E$  effects graphically (NAYAK *et al.* 2008; BOSE *et al.*, 2014).

The AMMI model increases the probability of selecting high yielding genotypes. The other stability statistics like AMMI stability value (ASV) has been taken into consideration (PURCHASE *et al.*, 2000) because AMMI model does not make any provision for quantitative stability measure, which is essential to quantify and rank the genotypes for their stability. Apart from this another stability statistics i.e. Yield stability index (YSI) which incorporates both mean yield and stability in a single criterion (FARSHADFAR, 2011) has been used to measure the stability of tested genotypes. Hence, the objective of this study is to find out the stable genotypes across the environment using different stability statistics and to find out the interrelationship among these stability statistics.

## MATERIALS AND METHODS

The experiment was conducted with nine rice genotypes suited for boro in a completely randomized block design with three replications. The experiment was repeated in four consecutive years 2009-2013 at the CRRRI experimental farm. The genotypes were sown on 2nd week of December of each year. Seedlings were managed in the nursery bed by covering seedlings by plastic sheet in night and removing it in day. Twenty one days-old healthy seedlings were transplanted in the well puddle plots of 3m  $\times$  4m size. The plant population density was maintained at 33 plants  $m^2$  with spacing of 20 x 15 cm line to plant basis. Fertilizer was applied @ 100:40:30 of N: P: K  $ha^{-1}$ . In addition to this,  $ZnSO_4$  was applied @ 20kg  $ha^{-1}$ . The entire dose of P, K and  $ZnSO_4$  along with 50kg of N was applied as basal dose, while the rest of the 50kg of N was applied in two split doses, one 21 days after transplanting and the other at flowering stage of the crop. Appropriate cultural practices like weeding, intermittent irrigation and need based plant protection measures were undertaken in order to raise a healthy crop. At harvest, grain yields were recorded on a plot basis and then converted to yield tons  $ha^{-1}$ .

### 2.1 Statistical analysis

The grain yield data were subjected to both combined analysis of variance and AMMI analysis. Analysis of variance was used to partition into genotype deviations from the grand mean, environment deviations from the grand mean, and GE deviations from the grand mean. Subsequently, multiplication effect analysis (AMMI) was used to partition GE deviations into different interaction principal component axes (IPCA). The SAS 9.2 software was used for combined analysis of variance and AMMI analysis.

#### 2.1.1 AMMI analysis

The AMMI model was applied, with additive effects for the nine rice genotypes (G) and four seasons of testing (Environments=E), and multiplicative term for G×E interactions. The AMMI analysis first fits additive effects for host genotypes and environments by the usual additive analysis of variance procedure and then fits multiplicative effects for G×E by principal component analysis (PCA). The AMMI model is

$$Y_{ij} = \mu + g_i + e_j + \sum_{k=1}^n \lambda_k \alpha_{ik} \gamma_{jk} + \varepsilon_{ij}$$

where  $Y_{ij}$  is the yield of the  $i^{\text{th}}$  genotype in the  $j^{\text{th}}$  environment,  $g_i$  is the  $i^{\text{th}}$  genotype mean deviation,  $e_j$  is the  $j^{\text{th}}$  environment mean deviation,  $\lambda_k$  is the square root of the eigen value of the PCA axis k,  $\alpha_{ik}$  and  $\gamma_{jk}$  are the principal component scores for PCA axis k of the  $i^{\text{th}}$  genotype and the  $j^{\text{th}}$  environment, respectively and  $\varepsilon_{ij}$  is the residual.

The environment and genotypic PCA scores are expressed as unit vector times the square root of  $\lambda_k$  i.e. environment PCA score =  $\lambda_k^{0.5} \gamma_{jk}$ ; genotype PCA score =  $\lambda_k^{0.5} \alpha_{ik}$  (ZOBEL *et al.*, 1988).

#### 2.1.2 AMMI stability value (ASV)

The AMMI stability value (ASV) was used following the formula of PURCHASE *et al.* (2000)

$$ASV = \sqrt{\left[ \frac{IPCA1_{sumofsquare}}{IPCA2_{sumofsquare}} (IPCA1_{score}) \right]^2 + (IPCA2_{score})^2}$$

Where  $\frac{SS_{IPCA1}}{SS_{IPCA2}}$  is the weight given to the IPCA1-value by dividing the IPCA1 sum of square by the IPCA2 sum of square.

#### 2.1.3 Yield stability index (YSI)

Yield stability index (YSI) was calculated using formula  $YSI = RASV + RY$  proposed by FARSHADFAR (2011). For calculation of YSI, ranks of the genotypes based on mean yields over environments added to ranks of the genotypes based on ASV. The genotypes with low YSI was taken as high yielding and stable genotypes.

#### 2.1.4 Rank-Sum (RS)

Rank-sum was calculated using following formula (FARSHADFAR and ELYASI, 2012):

$$RS = \text{Rank mean (R)} + \text{Standard deviation of rank (SDR)}$$

The standard deviation of rank (SDR) was measured as:

$$S_i^2 = \frac{\sum_{j=1}^m (R_{ij} - \bar{R}_{i.})^2}{l-1}$$

Where,  $R_{ij}$  is the rank of  $X_{ij}$  within the  $j^{\text{th}}$  environment,  
 $\bar{R}_{i.}$  is the mean rank across all environments for the  $i^{\text{th}}$  genotype and  
 $SDR = (S_i^2)^{0.5}$

Low value of RS was taken as most stable genotypes with high yield.

## RESULTS

The combined analysis of variance of Genotype (G), Environment (E) and Genotype × Environment (G×E) Interaction were significant ( $P \leq 0.01$ ) for grain yield (Table 1). The significant genotype × environment interaction effect showed that the genotypes responded differently to the variation in environmental conditions. The factors explained (%) show that rice grain yield was affected by genotype (76.28%), environment (4.67%) and their interaction (8.12%). The G×E interaction effect was twice as that of environmental effect, while genotype effect was found to be nine times that of G×E interaction effect.

Table 1. ANOVA of grain yield for 9 rice genotypes

Source	df	SS	MS	Explained SS
Rep (R)	2	0.201	0.100	0.160
Env (E)	3	5.867	1.956 *	4.668
Gen (G)	8	95.881	11.985 *	76.285
Gen×Env	24	10.206	0.425 *	8.120
Error	70	13.533	0.193	10.767
Total	107	125.687		
CV		8.665		

\* Significant at 1% probability level

The AMMI analysis of variance for grain yield ( $\text{t ha}^{-1}$ ) of nine rice genotypes was tested in four environments. The AMMI result shows that 85.64% of the total sum of squares was attributed to genotypic effects, 9.12% due to genotype × environment (GE) interaction effects and 5.24% due to environmental effects. The IPCA1 and IPCA2 explained 53.34% and 38.32% of the G×E interaction sum of squares respectively (Table 2). Hence, they cumulatively captured 92% of the total G×E interaction using 18 degrees of freedom. The biplot of IPCA1 against IPCA2 was given in Figure 1.

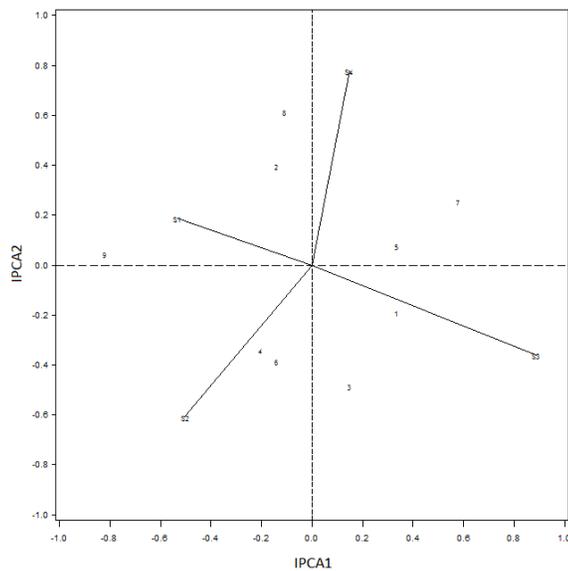


Figure 1. Biplot of nine genotypes and four environments for grain yield using genotype and environmental scores.

Table 2. AMMI analysis of grain yield for 9 rice genotypes

Source	df	SS	MS	SS explained (%)
GEN	8	31.960	3.995*	85.643
ENV	3	1.956	0.652*	5.241
G*E	24	3.402	0.142*	9.116
IPCA1	10	1.814	0.181 *	53.336
IPCA2	8	1.304	0.163 **	38.324
IPCA3	6	0.284	0.047 ns	8.341
Total	35	37.318		

\* Significant at 1% probability level \*\* Significant at 5% probability level ns Non-Significant

The values of yield and different stability parameters viz. IPCA1, IPCA2, ASV, YSI and RS for the nine genotypes were given in Table 3. To find out the relationship among different parameters, rank correlation was performed. GY is positively and significantly correlated with YSI and RS ( $P < 0.05$ ) but not with ASV. The correlation (Table 4) of YSI with all parameters is significant ( $P < 0.05$ ).

Table 3. Yield, first and second IPCA, ASV, YSI and RS of 9 rice genotypes

No.	Name	GY	IPCA1	IPCA2	ASV	YSI	RS
1	Annada	4.942	0.337	-0.189	0.506	11	6.25
2	Satabdi	4.225	-0.140	0.397	0.442	11	8.25
3	Naveen	5.667	0.152	-0.482	0.527	10	5.01
4	WITA12	5.958	-0.204	-0.337	0.441	4	3.50
5	Lalat	4.458	0.338	0.078	0.477	11	7.75
6	MTU1010	6.050	-0.137	-0.385	0.429	2	3.75
7	IR64	5.433	0.579	0.256	0.846	13	5.41
8	Vandana	3.067	-0.108	0.617	0.635	16	9.00
9	Ratna	5.867	-0.818	0.046	1.139	12	4.97

GY- Grain yield, IPCA- Interaction principal component axis, ASV- AMMI stability value, YSI- Yield stability index, RS- Rank sum

Table 4: Correlation matrix of four stability measures

Variables	GY	ASV	YSI	RS
GY		0.267	0.667 **	0.983 *
ASV			0.783 **	0.250
YSI				0.650 **
RS				

\* Significant at 1% probability level \*\* Significant at 5% probability level

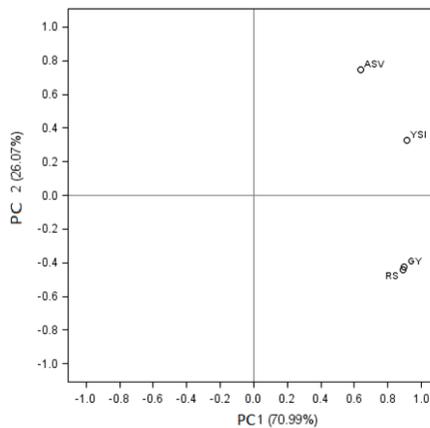


Figure 2. Biplot of yield – stability statistics models of nine rice genotypes

The relationship among different stability parameters with grain yield can be visualized graphically with the help of principal component analysis. PC1 explained 71% while PC2 explains 26% of the total variation (Figure 2).

#### DISCUSSION AND CONCLUSION

The genotype  $\times$  environment interaction effect using combined analysis of variance for nine genotypes in four environments is significant. This showed that genotypes responded differently across the environment with variation in environmental conditions. The G $\times$ E interaction effect was twice as that of environmental effect, while genotype effect was nine times greater than that of G $\times$ E interaction effect. The significant G $\times$ E interaction effect was partitioned into principal component axis following AMMI analysis. The first two principal components i.e. IPCA1 and IPCA2 were significant and sufficient to explain the G $\times$ E interaction. This is in accordance with GAUCH and ZOBEL (1996) which recommended that first two IPCAs are sufficient to predict the most accurate AMMI model. The genotype GEN6 is high yielder and ranks first based on ASV, YSI and RS with values 0.429, 2 and 3.75 respectively followed by GEN4 with values 0.441, 4 and 3.50 respectively (Table 3). Hence, GEN6 is stable genotype followed by GEN4. The genotype will be stable across all environments with its score near to zero in the interaction of IPCA1 versus IPCA2 (SANNI *et al.*, 2009). The biplot of the first two IPCA does not show the best adapted genotype and/or genotypes to most environments. The genotypes suitable of for ENV1 were GEN2, GEN8 and GEN9; whereas GEN4 and GEN6 were best for ENV2. The best genotypes with respect to ENV3 were GEN1 and GEN3; on the other hand GEN5 and GEN7 were best for ENV4. Considering the environments tested in this study, no single environment had both IPCA 1 and IPCA2 scores close to zero line. This indicates that all the environments had potential for large G $\times$ E interaction. The significant correlation of GY with RS ( $P < 0.01$ ) and YSI ( $P < 0.05$ ) indicates the good potential of these statistics for selecting the most stable high yielding genotypes. The principal component according to the rank correlation matrix showed that 97% of the total variance was explained by the first two PCs. The two parameters GY and RS were found to be very close indicates that they were highly correlated. Hence, in the experiment conducted on nine genotypes in four environments GEN6 was found to be stable using all the stability measures followed by GEN4. GY was correlated significantly with RS ( $P < 0.01$ ) and YSI ( $P < 0.05$ ).

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## ANALIZA INTERAKCIJE GENOTIPA I SPOLJNE SREDINE I STABILNOSTI GENOTIPOVA BORO PIRINČA

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### I z v o d

Vršena je analiza interakcije 9 genotipova pirinča (G) tolerantnih na hladne uslove u četiri različite spoljne sredine (E) u cilju definisanja stabilnih visokoprinosnih genotipova.

Ispitivanja su vršena u slučajnom blok sistemu u tri ponavljanja. Interakcija je analizirana kombinacijom različitih statističkih metoda (AMMI, ASV, RS i YSI). Kombinovanim analizama utvrđena je visoka značajnosti genotipa (G), spoljne sredine (E) i njihove interakcije (G×E). Istraživanja su pokazala da su GEN6 i GEN4 stabilni. Ovaj zaključak je dobijen primeom svih statističkih analiza. Statistika stabilnosti može da bude korisna u identifikaciji stabilnih visokoprinosnih genotipova i da olakša vizuelno poređenje visokoprinosnih genotipova u većem broju uslova sredine.

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