The Journal of Animal & Plant Sciences, 24(6): 2014, Page: 1885-1897
ISSN: 1018-7081

ADDITIVE MAIN EFFECTS AND MULTIPLICATIVE INTERACTION (AMMI) ANALYSIS OF GRAIN YIELD STABILITY IN EARLY DURATION RICE

L. K. Bose[1], N. N. Jambhulkar[2] and O. N. Singh[3]

Central Rice Research Institute, Cuttack - 753006, India
[*1] Corresponding author - Senior Scientist, Crop Improvement Division, Central Rice Research Institute, Cuttack – 753006, India. [2]- Scientist, Division of Social Sciences, Central Rice Research Institute, Cuttack – 753006, India
[3]- Head, Crop Improvement Division, Central Rice Research Institute, Cuttack – 753006, India
Corresponding Author Email: lotanrice@gmail.com

ABSTRACT

Genotype × Environment interaction of 17 early duration rice genotypes tested over four seasons was analyzed to identify stable high yielding genotypes. Genotypes were grown in a randomized complete block design with three replications. Genotype × environment interaction (GEI) was analyzed following Additive Main effects and Multiplicative Interaction (AMMI) as well as regression models. AMMI analysis of variance showed highly significant genotype and environment mean squares. First two interaction principal component axes (IPCA) cumulatively explained 93.76% of total interaction effects. Integrating biplot display and genotypic stability statistics enabled four groupings of genotypes based on similarities in their performance across environments. The biplot generated using genotypes and environmental scores for first two IPCAs revealed positioning of the four genotype groups (GG) into three sectors of the biplot. Among them, three genotype in GG-3 (G-6, G-13 and G-15) exhibited high yields across environments, low IPCA-1 scores, low stability index (D_i) values, unit regression coefficient and minimum deviation from regression. Hence these genotypes were recognized as possessing stable high yielding attributes. Although, both AMMI model and regression models were equally potential in partitioning GEI, AMMI analysis and biplot display was more informative in differentiating the genotype response over environments and recognizing the most discriminating environments.

Key words: Early rice, AMMI model, regression model, G×E interaction, stability parameters.

INTRODUCTION

Rice is the staple food for a large proportion of the world's population (Zhang, 2007). Asia is considered as rice bowl of the world, where nearly 90 % of world's rice is produced (Hossain and Narciso, 2004). India is the largest rice growing country in the world; however, its productivity per unit area is low. In India, rice is cultivated on 43.77 million hectares with a production of 96.43 million tons and productivity of 2.20 t/ha, (Economic Survey, 2007).Though more than 900 rice varieties have been released in India, many of them have been out of cultivation within a few years due to inconsistent performance in diverse environments and only few varieties with stable performance continue to be under cultivation even after 15 - 20 years of release. Among the rice production areas in the country, it is the most diverse in hydrology and other soil and climatic factors that combine to make a difference in rice yield (Singh *et al*., 1997). In Wet season, rice is grown with supplemental irrigation from which assured production and productivity is obtained. Due to natural calamities when crop is not assured in wet season, dry season irrigated rice provides food security and income generation. Analysis of interaction of genotypes with locations and other agro-ecological conditions would help in getting information on adaptability and stability performance of genotypes. The method commonly used for analysis of G×E interaction is the Linear Regression model of Eberhart and Russell (1966) in which the b-values give information about adaptability and S^2_{di} and R^2 are used as measures of stability of performance. Other workers have suggested use of AMMI stability value (ASV) as measure of stability. The Additive Main and Multiplicative Interaction (AMMI) is a better model for analysis of G×E interaction in multilocation varietal trials (Zobel *et al*., 1988). It not only gives estimate of total G×E interaction effect of each genotype but also partitions it into interaction effects due to individual environments. Adaptation and yield stability studies help in identifying varieties that have either specific or general adaptation which can be exploited for varietal recommendation. The present study was undertaken to analyze G×E interaction and evaluate the adaptability and stability of yield performance of seventeen early rice genotypes. Genotype by environment interaction has been studied by various researchers (Singh *et al*., 1987; Jain and Pandya, 1988; Zubair and Ghafoor, 2001). Specific- adapted cultivars may raise crop yields by exploiting G×E (location) interaction effects (Annicchiarico, 2002) and site specific cultivar recommendation can be defined if the best yielding material differs depending on site. Therefore,

recommending more than one cultivar per region or a sub-region will be preferred so as to limit the risk of disasters arising from unforeseen biotic or abiotic stress of one cultivar recommended for a wide range of environments (Annicchiarico, 2002). Rather than just the observed data, modeling of the data by various techniques has been used for cultivar recommendation. The adaptability of a variety over a diverse environment is usually tested by the degree of its interaction with different environments under which it is planted (Ashraf *et al*., 2001). Eberhart and Russel (1966) developed a model to test the stability of varieties under various environments and defined a stable variety as having unit regression over the environments (b = 1.00) and with minimum deviation from the regression (S^2_{di} = 0). Also the joint linear regression method (Finlay and Wilkinson, 1963) has been used. Other new models now being used include AMMI (Gauch, 1992) and Factorial Regression (Hardwick and Wood, 1972). This article exploits combined advantages of some of these models to evaluate the suitability of early and mid early varieties for small and marginal farmers of Odisha state.

MATERIALS AND METHODS

The present experiment was conducted to determine the yield stability of 17 popular early duration (60 to 115 days) rice genotypes specially released for rain fed to irrigated ecosystems. Some of the genotypes are of long slender to short bold grain types, possess drought tolerance and cold tolerance, resistance to different diseases like Blast, Brown spot, Sheath blight, Bacterial blight, Rice tungro disease and insect pests like Stem borer and Green leaf hopper. Seeds of these rice genotypes were sown in wet seed beds. Twenty one day-old healthy seedlings were transplanted in well puddle plots of 3m × 4m size. The plant density was maintained at 33 plants m^2 with spacing of 20 × 15 cm line to plant basis. Fertilizer was applied @ 90:60:60 of N: P: K ha^{-1}. The entire dose of P and K along with 30kg of N was applied as basal dose, while the rest of the 60kg of N was applied in two split doses, one 21 days after transplanting and the other at flowering stage. Appropriate cultural practices like weeding, intermittent irrigation and need based plant protection measures were undertaken in order to raise a healthy crop. The experiment was conducted in a completely randomised block design with three replications. The experiment was repeated in four consecutive wet seasons from 2008 to 2011 at Central Rice Research Institute, Cuttack, India with diverse environmental conditions. At harvest, grain yields were recorded on a plot basis and then converted to yield $hectare^{-1}$.

Analysis of variance was computed for individual environment to test the homogeneity, then a combined analysis of variance was performed, considering both environments and genotypes as fixed by using IRRISTAT package (IRRISTAT, 2007), so that significance of all effects were tested against mean square of error. The stable performance of 17 rice genotype tested over four environments was assessed following the regression models of Eberhart and Russell (1966), Perkins and Jinks (1968) and Freeman and Perkins (1971). The stability analysis was carried out with the help of the statistical package IRRISTAT (2007). The association among different stability parameters was determined following Pearson's correlation coefficients (Pearson, 1920).

The AMMI model was applied, with additive effects for the 17 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

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

where, Y_{ij} is the yield of the i^{th} genotype in the j^{th} environment,

g_i is the mean of the i^{th} genotype minus the grand mean,

λ_k is the square root of the eigen value of the PCA axis k

γ_{ik} and δ_{jk} are the principal component scores for PCA axis k of the i^{th} genotype and the j^{th} environment, respectively and

e_{ij} is the residual.

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

The AMMI stability index 'D_i', which is the distance of interaction principal component (IPC) point with origin in space, was estimated according to the formula suggested by Zhang *et al* (1998) as:

$$D_i = \sqrt{\sum_{s=1}^{c} Y_{is}^2}$$

where, c is the number of significant IPCs,

Y_{is}^2 is the scores/yield of the rice genotype i in IPCs.

The AMMI analysis was conducted using the computer software IRRISTAT for windows, version 5. In addition to the above stability parameters, various yield-stability statistics were also calculated as follows:

AMMI stability value (ASV): The AMMI stability value (ASV) as described by Purchase *et al*. (2000) was calculated as follows:

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

Where $\frac{SS_{IPCA1}}{SS_{IPCA2}}$ is the weight given to the IPCA1-value by dividing the IPCA1 sum of squares by the IPCA2 sum of squares. The larger the IPCA score, either negative or positive, the more specifically adapted a genotype is to certain environments. Smaller ASV scores indicate a more stable genotype across environments.

Sustainability index (SI): The sustainability index was calculated by the following formula as suggested by Babarmanzoor *et al*. (2009):

$$S.I. = [(Y - \pm n)/YM] \times 100$$

Where, Y = Average performance of a genotype,

$\pm n$ = Standard deviation and

YM = Best performance of a genotype in any year.

The values of SI were classified arbitrarily into five groups *viz.* very low (up to 20%), low (21-40%), moderate (41-60%), high (61-80%) and very high (above 80%).

Stability index (I): The stability index (*I*) was computed by the nonparametric stability analysis (Bajpai and Prabhakaran, 2000) to identify stable and high-yielding genotypes as follows:

$$I = \left(\frac{\bar{y}_i}{\bar{y}_{..}} + \frac{1}{\pm_i^2}\right) / \left[\frac{1}{n}\sum_i \left(\frac{1}{\pm_i^2}\right)\right]$$ Rao *et al* (2004)

Where, Y_i = average performance of the *i*th genotype,

Y = overall mean,

$\pm_i^2$ = Shukla's (1972) stability variance of the *i*th genotype and

n = number of environments.

Yield stability index (YSI) and Rank-Sum (RS): The YSI and RS were calculated as:

YSI = RASV+RY

where, RASV is the rank of AMMI stability value and RY is the rank of mean grain yield of genotypes (RY) across environments.

RS = Rank mean (R) + Standard deviation of rank (SDR)

The RS incorporates both yield and yield stability in a single non parametric index, while YSI incorporates both mean yield and stability in a single criterion. Low values of both the parameters show desirable genotypes with high mean yield and stability.

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*th environment, $\bar{R}_{i.}$ is the mean rank across all environments for the *i*th genotype and

$$SDR = (S_i^2)^{0.5}$$

RESULTS AND DISCUSSION

Yield response of rice genotypes: The 17 cultivars included in the present investigation were dwarf to semi-dwarf, high yielding and early duration cultivars specially bred for direct seeding / transplanting under rain fed upland / favorable shallow land ecologies with yield attributes of 2.0 to 5.0 t/ha. The highest mean yield of 5.292 t/ha was obtained for G-15, followed by 5.042 t/ha for G-2 (Table 2). The lowest mean yield of 2.658 t/ha was obtained for G-8, followed by 3.308 t/ha for G-4 and the grand mean yield was 4.207 t/ha.

AMMI analysis of variance: The AMMI analysis of variance of 17 rice genotypes tested over four environments revealed that 74.67% of the total sum of squares (SS) was attributable to the genotypes (G), 13.60% to the environments (E) and 11.73% to GE interaction effects (Table 1). A large SS due to G indicated that the genotypes were diverse with large differences among the mean yields. The small proportion of SS due to E indicated that the differences among the environmental means (seasonal fluctuations) were not very high. The magnitude of GE SS was 6.38 times smaller than that for the SS due to G, thus, indicating that the differences in the response of the genotypes across environments were not that substantial and the genotypes need multi-locational testing. However, the AMMI-1 and AMMI-2 biplots and a few other nonparametric stability parameters provided good information leading to recognition of stable rice genotypes.

The first interaction principal component axis (IPCA-1) accounted for 62.59% of the interaction SS in 37.50% of the interaction degrees of freedom. Similarly, IPCA-2 explained further 31.15% of the interaction SS. The MS for both IPCA-1 and IPCA-2 were significant at P = 0.01 level and cumulatively contributed to 93.74% of the total interaction. Therefore, the post-dictive evaluation using F-test at P = 0.01 suggested that these two IPCAs of the interaction were significant for the model with 34 degrees of freedom. IPCA-3 captured noise, since the MS was not significant and explained

only 6.26% of the total SS and, therefore, did not help in prediction of validation observations. Thus, the interaction of the 17 rice genotypes across four environments was best predictable by the first two principal components of genotypes and environments.

Previous reports reveal that the most accurate model for AMMI can be predicted by using the first two IPCAs (Gauch and Zobel, 1996; Yan *et al*., 2000; Yan and Rajcan, 2002; Nayak *et al*., 2008). Conversely, Sivapalan *et al* (2000) recommended a predictive AMMI model with first four IPCAs. These results indicate that the number of the terms to be included in an AMMI model can not be specified a priori without first trying AMMI predictive assessment. The factors like the type of the crop, the diversity in the germplasm and the range of environmental conditions will affect the degree of complexity of the best predictive model (Crossa *et al*., 1990).

AMMI-1 biplot display: The graphical representation (Figure 1) of AMMI analysis reveals the main effect means on the abscissa and IPCA-1 scores of both genotypes as well as environments, simultaneously on the ordinate. The interaction is described in terms of differential sensitivities of the genotypes to the most discriminating environmental variable that can be constructed. Displacement along the abscissa reflects differences in main effects, whereas displacement along the ordinate illustrates differences in interaction effects. Genotypes or environments appearing almost on a perpendicular line have similar means and those falling almost on a horizontal line have similar interaction patterns. Genotypes with IPCA-1 scores close to zero have small interactions and hence show wider adaptation to the tested environments (Carbonell *et al*., 2004). A large genotypic IPCA-1 score (either positive or negative) have high interaction and reflects more specific adaptation to the environments with IPCA-1 values of the same sign.

The environments showed variability in both main effects and interactions (Figure 1). The high potential environment E-3 can be seen in quadrant-II, with minimum interaction effects, high negative IPCA-1 as well as IPCA-2 scores. The low potential environments E-1 and E-4 were distributed in quadrant-IV, with negative environmental index, high positive IPCA-1 score to low negative IPCA-2 scores. The E-2 showed the second highest yield potentiality, had a negative environmental index, negative IPCA-1 and high positive IPCA-2 scores. Thus, the biplot indicated E-3 as the highest yielding environment and E-4 as the lowest yielding environment. The rice genotypes also showed wide variability in yield.

The scores and main effects can be read from the graph and used to predict the expected level of yield for any G-E combination. For any G-E combination in the AMMI biplot (Figure 1), the additive part (main effects) of the AMMI model equals the G mean plus E mean minus the grand mean. The multiplicative part (interaction effects) is the product of G and E IPCA-1 scores (Zobel *et al*., 1988). For example, the genotype-2 with environment-3 had a main effect of 5.042+4.671-4.207=5.506 (Table 1). The interaction effects would be the products of the respective IPCA-1 scores i.e. 0.731 x -0.767= -0.561. The AMMI model estimated the yield of genotype-2 in environment-3 as 5.506 - 0.561=4.945 t/ha., which fits the observed yield level of 5.067 t/ha (Table 2). Genotypes and environments with IPCA-1 scores of the same sign produce positive interactions effects, while the combinations of IPCA-1 scores of opposite signs have negative specific interactions.

Four genotype groups (GG) are evident from the biplot generated from the present study (Figure 1):

GG-1 includes five genotypes viz. 5, 9, 10, 12 and 16 with mean yield of 4.368 t/ha, which is higher than the grand mean (4.207 t/ha). This group of genotypes has small positive to negative IPCA-1 scores ranging from -0.435 to +0.266 and small D_i values. They are well adapted to E-2 and E-3; have high interactions and possess relatively stable yields.

GG-2 consists of six genotypes viz. 1, 4, 7, 11, 14 and 17 with a mean yield of 3.676 t/ha, which is less than the grand mean. They have small positive and negative IPCA-1 scores ranging from -0.581 to +0.422, smaller IPCA-2 scores ranging from -0.342 to +0.615, small D_i values and are well adapted to the environments E-2, 3 and 4. These genotypes have small interactions and hence possess relatively stable low yielding attributes.

GG-3 includes five genotypes *viz.* 2, 3, 6, 13 and 15 with a mean yield response of 4.992 t/ha, which is much above the grand mean. This group of genotypes have small negative to high positive IPCA-1 scores ranging from -0.118 to 0.731 and small negative IPCA-2 scores ranging from -0.025 to -0.312. They show small D_i values. This group of genotypes is well adapted to the environments E-1, 3 and 4. They have high interactions and hence are highly stable across the environments.

***GG*-4** consists of the single genotype G-8 with lowest mean yield level of 2.658 t/ha, which is much lower than the grand mean. This group has smallest negative IPCA-1 score of -0.006 and positive IPCA-2 score of +0.254, small D_i value, and is well adapted to the environment E-2. This genotype group has high interactions and hence is highly stable across tested environments, but for low yields.

The environments show variability in both main effects and interactions. Two environments, E-1 and E-4 show positive IPCA-1 scores, while E-2 and E-3 show negative IPCA-1 scores (Table 3 and Figure 1), while E-1, E-3 and E-4 show small negative IPCA-2 score and E-2 show high positive IPCA-2 scores. The highest mean yield response (4.671 t/ha) was shown in E-3 which was higher than grand mean yields, while E-1, E-2 and E-4 show yield response smaller than the grand mean yield.

The direction and magnitude of differences among genotypes along the abscissa and ordinate (IPCA-1 scores) can be read from the graph. The most stable genotypes should show high yield levels and should be stable across the tested environments. Any genotype showing higher absolute IPCA-1 score would produce a higher absolute G×E interaction effect than that with lower absolute IPCA-1 score and is less variable in yield response (i.e. more stable) across the environments. The genotype stability ranking based on higher absolute IPCA-1 scores was GG-3 (-0.118 to +0.731), GG-2 (-0.581 to 0.422), GG-1 (0.435 to +0.266) and GG-4(-0.006).The groups of genotypes are depicted on the horizontal axis in AMMI-1 biplot display (Fig. 1). GG-3 exhibit highest mean yield levels of 4.992 t/ha, much above the grand mean yield, small negative to high positive IPCA-1 scores and hence was recognized as possessing stable yield attributes. GG-1 exhibit second highest mean yield level of 4.368 t/ha and small negative to positive IPCA-1 scores. GG-2 exhibit mean yield level of 3.676 t/ha and small negative to moderate positive IPCA-1 scores, while GG-4 exhibit lowest yield level of 2.658 t/ha, much below the grand mean and the smallest negative IPCA-1 score and hence possessed stable yield attribute of lowest magnitude.

The four environments show variability in the main effects and interactions, the IPCA-1 scores showing clear higher negative or positive interactions (Figure 1) due to the 2 groups of environments (EG). EG-1 constituting of E-1 and E-4 showed highest main effects and large positive IPCA-1 scores, while EG-2 consisting of E-2, and E-3 showed high response to the genotypes with high negative interaction IPCA-1 scores.

The estimates of yield response, environmental index and first two IPCA scores in respect of four environments presented in (Table 3) revealed highest yield response of E-3 (4.671 t/ha), followed by E-2(4.176 t/ha), E-1 (4.104 t/ha) and E-4 (3.876 t/ha). High positive environmental index was evidenced for E-3, while it was negative for rest of the three environments. The IPCA-1 scores were high and positive for E-1 and E-4, while it was negative for E-2 and E-3. The IPCA-2 scores were high and positive for E-2, while it was negative for E-1, E-3 and E-4.

Response of four genotype groups to environments: Yields of four genotype groups averaged over four environments ranged from 2.658t/ha for GG-4 to 4.992t/ha for GG-3 (Table 4). The ranking of the GGs in descending order of their average yield levels was GG-3>GG-1>GG-2>GG4. The genotypes in GG-3 exhibited highest mean yield levels of 4.992 t/ha across four environments. GG-1 and GG-2 exhibited varied degrees of yield response ranging from 2.667 t/ha to 5.500 t/ha. The only genotype in GG-4 exhibited consistently low yield response across all the four environments.

AMMI-2 biplot display: The AMMI is an explorative technique by which the G×E relationship can be expressed in terms of interaction patterns derived in biplot. A biplot is generated by using genotypic and environmental scores of the first two AMMI components in which both genotypes and environments are displayed simultaneously (Vargas and Crossa, 2000). In the plotting of AMMI-2 biplot, Purchase (1997) pointed out that the closer the genotypes scores to the center of the biplot, the more stable they are. The interaction is described in terms of differential sensitivities of the genotypes to the most discriminating environmental variables (AMMI-axes) that can be constructed. These environmental variables and the genotype sensitivities are estimated from the table itself (Schneider and Van den Boogert, 1999). For simple interpretation of the biplot, the genotypes with vector end points far from the origin contribute relatively more to the interaction than those with vector end points close to the origin. In the present experiment, the genotypes 14 in GG-2 and 16 in GG-1 have relatively greater contribution to the interaction than the others (Figure 2). Genotypes with vector end points far apart, show considerable interactions like those of 2 in GG-3, 4 and 7 in GG-2 and 10 in GG-1 with rest of the genotypes. Genotypes, for which the directions of the vectors almost coincide, have similar pattern of interactions like those of G-2 in GG-3, G-4 and G-7 in GG-2 and G-10 in GG-1. On the other hand, when the directions are opposite, the interaction patterns of the corresponding genotypes show negative correlation like those within GG-1, GG-2 and GG-3. Thus, the genotypes and environments showing considerable interactions could be easily identified from the biplot.

AMMI analysis extracted values of the scores for IPCA-1 to IPCA-2 in respect of 17 genotypes (Table 2) as well as 4 environments (Table 3). A biplot is generated using the IPCA-1 and IPCA-2 scores for the 17 rice genotypes and 4 environments with the first principal component axis on the abscissa and the second on the ordinate (Figure 2). The biplot displayed both the genotypes and environments simultaneously in four sectors of a single scattered plot depending upon the positive or negative signs of the scores on the first two principal components. Sector-1 represents host genotypes or environments with positive IPCA-1 as well as IPCA-2 scores, while sector-2 represent positive IPCA-1 and negative IPCA-2 scores. Sector-3 represents negative IPCA-1 as well as IPCA-2 scores and sector-4 represents negative IPCA-1 and positive IPCA-2 scores. In the present study, the environments were distributed into three sectors in the following manner: E-1 and E-4 in sector-2; E-3 in sector-3; and E-2 in sector-4 (Figure 2). The ranking of the environments in order of their level of response to yields was E-3>E-2>E-1>E-4. Among the genotypes, G-12, 16 and 17 fell into sector-1, G-2, 3, 6, 14 and 15 fell into sector-2; G-4, 9, 10, 11 and 13 into sector-3 and G-1, 5, 7 and 8 into sector-4. The ranking of

genotypes according to their yield levels was G-15>2>6>3>13>12>5>16>10>9>14>7>11>1>17>4>8 and the ranking of the genotype groups according to their mean yield levels was GG-3>GG-1>GG-2>GG-4. Thus, the biplot not only displayed the GEI but also facilitated in visual description of 'which win where' pattern described by Li *et al.* (2006).

A polygon drawn in the biplot (Figure 2) by joining the genotypes located farthest from the biplot origin, encompassing all other genotypes, facilitates identification of the genotypes that are high yielders in specific environments (Yan *et al*., 2000). The vertex genotype in a sector is highest or lowest yielders in the environment falling in that sector. In the present study, the vertex genotypes 2, 4, 7 and 10 exhibit such attributes in all the environments. The five genotypes in GG-3 exhibited highly stable yield response in all the four environments. However, the only genotypes G-8 in GG-4 showed stable low yielding response in all the four environments.

There was a significant correlation between the mean yields and the IPCA-1 scores ($r = 0.491^{*}$). Hence, the 'G' main effects can be represented by the IPCA-1 scores for the genotypes. The genotypes with lower IPCA-1 scores would produce a lower absolute G×E interaction effect than those with higher absolute IPCA-1 scores and have less variable degree of yields (more stable) across genotypes. The stability ranking of the genotypes in ascending order of absolute IPCA-1 scores was GG-4> GG-3> GG-1> GG-2. Thus, the genotypes in GG-4 and GG-3 possessed high stability across the tested environments. Among them, the genotype G-8 in GG-4 exhibited least mean yields and hence possessed stable yields of lower magnitude. The five genotypes in GG-3 exhibited highest mean yield levels for which these were considered as stable high yielders.

The discriminating ability of the environments can be judged by calculating the distance of each environment from the biplot origin. In this regard, the environments E-1, E-2 and E-3 are most discriminating as indicated by long distance from the biplot origin. Genotypes with IPCA-1 scores >0 responded positively (adaptable) to the environments that had IPCA-1 scores > 0 (i.e. their interaction is positive), but responded negatively to the environments that had IPCA-1 scores <0. The reverse applies for the genotypes that had IPCA-1 scores < 0 (Samonte *et al*., 2005). The biplot revealed that the genotypes G-2, 3, 6, 12, 14, 15, 16 and 17 with IPCA-1 scores >0 responded positively to the environments E-1 and E-4 and hence their interaction is high, positive and these genotypes are adaptable to the corresponding environments. On the other hand, the rest of the genotypes, G-1, 4, 5, 7, 8, 9, 10, 11 and 13, with IPCA-1 scores <0 are adapted to the environments E-2 and E-3.

AMMI stability index 'D_i': The distance of interaction principal component point with the origin in space is the AMMI stability coefficient 'D_i'. The estimate of the stability index 'D_i' incorporates the IPCA scores of the significant IPCs depending upon their contributions towards the interaction SS (Zhang *et al*., 1998). The stability index is useful in evaluation and identification of genotypes possessing stable yields. The lower D_i values indicate high stability across the tested environments and *vice versa*. The ranking of genotype groups in ascending order of 'D_i' values was those in GG-4 (0.254) < GG-3 (0.126 to 0.753) < GG-1 (0.273 to 0.544) < GG-2 (0.106 to 0.630). The single genotype G-8 in GG-4 exhibited low D_i values with lowest mean yield level of 2.658 t/ha and smallest negative IPCA-1 score (-0.006). Hence this genotype was recognized as possessing stable yield of lowest magnitude. The top yielding five genotypes in GG-3 possessed highest level of mean yields (4.992 t/ha), second lowest level of stability index across the environments, low negative to high positive IPCA-1 scores but low negative IPCA-2 scores and hence were identified as possessing high yield stability. The five genotypes in GG-1 showed second highest yield (4.368 t/ha) with low stability index ranging from 0.273 to 0.544 and hence possessed average stability for yield. The six genotypes in GG-2 showed third highest mean yields of 3.676 t/ha with stability index ranging from 0.106 to 0.630 and negative to positive IPCA-1 as well as IPCA-2 scores and hence were recognized as possessing average stability for yield.

Interaction pattern from response plot: Response plots indicated the nature of GEI with the main effects of genotypes and environments removed. The values plotted for each genotype group by environments are the deviations from additive main effects predictions of each variable. The larger the deviation, the greater is the interaction of the GG with the environment. The response may be positive or negative depending upon whether or not the GG resulted in more or less effects than the main effects expectation. In the present study, 5 genotypes in GG-1 showed positive interactions with E-1, E-2, E-3 and negative interactions with E-4 (Figure 3); second highest mean yields (Table 4); located near the centre of the biplot (Figure 2) with low negative to positive IPCA-1 as well as IPCA-2 scores and hence were recognized as possessing stable yields. The six genotypes in GG-2 showed negative interactions with E-1, E-2, E-3 and positive interactions with E-4 located near the centre of the biplot (Figure 2) with low negative to positive IPCA-1 as well as IPCA-2 scores; and hence were considered as possessing stable yields. The five genotypes in GG-3 showed high to low positive interactions with E-1, E-2, E-3 and high negative interactions with E-4, highest mean yields with high to low positive and negative IPCA-1 scores and low negative IPCA-2 scores; located nearer to away from the centre of biplot even at the apex

of the polygon and mean yields (4.992 t/ha) much above the grand mean (4.207 t/ha). Hence this group of genotypes was considered to be possessing high stable yields. The single genotype (G-8) in GG-4 showed negative interactions with E-1, E-2, E-3 and high positive interactions with E-4, low negative IPCA-1 and low positive IPCA-2 scores; located away from the centre of the biplot, showed lowest mean yields and hence was recognized as highly stable low yielding genotype.

Stability analysis by regression models: Comparison among the three regression models (E and R, P and J, F and J) based on GEI from ANOVA tables and genotype rankings based on the regression coefficient (B_i) and deviation from regression (S^2_{di}) revealed similar trends. Hence, the ANOVA and GEI for E and R model only are presented here (Table 5). The highly significant G and E mean squares revealed that the yield responses for 17 genotypes are significantly different from each other and the environments also represented an array of diverse conditions for disease development. The pooled ANOVA showed that the GEI was a linear function of the additive environmental component. Further partitioning of GEI into linear and nonlinear components revealed highly significant mean squares (MS) for these components indicating the presence of both predictable and unpredictable components of GEI. Highly significant G × E (linear) interaction indicated the presence of genetic differences among the genotypes for their regression on the environmental index. Significantly larger pooled deviation over pooled error indicated the existence of a significant departure from linearity and, therefore, some of the GEI cannot be predicted from the linear regressions.

The mean grain yield of 17 rice genotypes ranged from 2.658 t/ha for G-8 to 5.292 t/ha for G-15 (Table 2). Eberhart and Russell (1966) emphasized that both linear (B_i) and nonlinear (S^2_{di}) components of GEI are necessary for judging the stability of a genotype. A regression coefficient B_i approximating 1.0 coupled with an S^2d_i of zero, indicates average stability. Regression values above 1.0 describe genotypes with higher sensitivity to environmental changes (below average stability) and greater specificity of adaptability to high yielding environments. A regression coefficient below 1.0 provides a greater resistance to environmental changes (above average stability) and, thus, increases the specificity of adaptability to low yielding environments. Linear regression for average grain yield of a single genotype on the average yield of all genotypes in each environment resulted in B_i values ranging from 0.144 to 2.101 for grain yield. This large variation in regression coefficients indicated the differential responses of genotypes to environmental changes (Table 2 and Figure 4). jhjhjhj

The results of stability analysis based on Eberhart and Russell (1966) revealed that the regression coefficients of nine genotypes *viz.*1, 3, 5, 6, 7, 8, 13, 15 and 17 were close to 1.0 *i.e.* within the confidence limits for regression. Among them, the genotypes 3, 5, 6, 13 and 15 were high yielders (above the grand mean yield) and their deviation from regression were also minimum (S^2_{di} = 0). Hence, these genotypes were best adaptable to all environments. The G-8 was also adaptable to all environments but possessed lowest yielding ability and, thus, was recognized as stable low yielding genotype.

The genotypes 2, 12 and 16 although were high yielders (> than grand mean yields), their B_i values were significantly lower than unit (B_i <1.0) and the deviation from regression for G-2 was highest while that for 12 and 16 was low negative. Hence these three genotypes were recognized as possessing above average yield stability. The genotype 14 showed regression coefficient significantly less than unit (B_i <1.0), low grain yields and was insensitive to environmental changes and have adapted to poor environments. Rest of the genotypes viz. 4, 9, 10 and 11 exhibited mean yield levels less than the grand mean, regression coefficients significantly greater than unit and minimum deviation from regression, less adaptable to environmental changes and hence possessed below average stability.

Comparison between AMMI and regression models: Association among different stability parameters estimated following E and R model, P and J model, F and P models and AMMI model was verified by calculating Pearson's correlations (Table 6). There was a highly significant correlation among the stability parameters, except the stability index D_i which was not correlated with any of the other regression parameters. The strong relationship among the parameters indicated that all the regression parameters as well as the AMMI parameter IPCA-1 are equally efficient in identification of genotypes possessing stable high yielding potentials. A critical comparison of 17 rice genotypes for their stability across four environments revealed perfect agreement between the regression and AMMI models in expression of stable high yield attributes of G-2 in GG-3, G-5 in GG-1 and G-3, 13 and 15 in GG-3 with B_i =1.0, S^2_{di} = 0 and high yields. The only genotype G-8 in GG-4 possessed stable low yielding attributes in both regression as well as AMMI models. Rest of the genotypes *viz.* G-1, 7, 8 and 17 in GG-2, although showed stable attributes of B_i =1.0, S^2_{di} = 0, were low yielders (below the grand mean yield) and hence were recognized as stable low yielders.

Out of the five genotypes in GG-3 those exhibited stable high yielding attributes and high stability, with low negative to high positive IPCA-1 scores and low D_i values in AMMI model, the genotype G-2, although showed high yielding potential, was not stable since its IPCA-1 score was high positive, D_i value was also high in AMMI model and also the regression coefficient was significantly lower than unit indicating above average stability. Rest of the four genotypes G-3,

6, 13 and 15 exhibited low negative IPCA-1 scores, low D_i values in AMMI model and B_i values well within the confidence limits as well as S^2_{di} values equals to zero in regression model. Hence this group of genotypes was recognized as possessing stable high yielding attributes. The genotypes G-8 in GG-4, G-1, 7 and 17 in GG-2; although exhibited stable attributes of unit regression coefficients and minimum S^2_{di} values in regression models and low IPCA-1 scores in AMMI model; were low yielders (below the average yields) and hence were recognized as stable low yielding genotypes.

Stability of genotypes by different yield stability statistics: Among the 17 rice genotypes G-2, G-3, G-6, G-13 and G-15 were the best five in order of their mean yields (Table 3). The AMMI model recognized these genotypes are stable high yielders (Table 4). Regression analysis recognized G-3, G-5, G-6, G-13 and G-15 as stable high yielders (Figure 4). These genotypes were among the top ranking 10 genotypes according to the stability parameters $B_{i\ ER}$, IPCA1, ASV, I, YSI, SI and RS. On the contrary, SI and I were not consider as suitable stability indices for discriminating stable genotypes with high grain yield (Farshadfar *et al*., 2011). In the present study, IPCA-1, ASV, SI, I, YSI and RS were recognized as most desirable indices for discriminating most stable genotypes with high grain yields. Based on above suitable stability indices the genotypes G-2, G-3, G-6, G-13 and G-15 were recognized as the most stable high yielding genotypes. The ranking of genotypes based on all stability statistics recognized G-13 (Tara) and G-15 (Annada) as highly stable high yielders across four environments. Annada is well known for its stable high yield performance since its release in 1987 and very popular among the farmers of eastern India.

Table 1. AMMI analysis of variance for grain yields of 17 rice genotypes tested across four environments

Sources of variation	d.f.	SS	MS	% variance explained
Trials	67	41.96	0.63***	
Genotypes (G)	16	31.33	1.96***	74.67
Environments(E)	3	5.71	1.90***	13.60
G x E interaction	48	4.92	0.10	11.73
AMMI IPCA-1	18	3.08	0.17***	62.59
AMMI IPCA-2	16	1.53	0.10**	31.15
AMMI IPCA-3	14	0.31	0.02	6.26
Pooled residual	14	0.31	0.02	

** and *** Significant at P < 0.01 and 0.001 levels, respectively.

Table 2. Mean yield response (t/ha) of 17 rice genotypes across four environments, estimates of IPCA scores, AMMI stability index and stability parameters in three regression models.

Variety	Mean	IPCA-1	IPCA-2	D_i	$B_{i\ ER}$	S^2d_i	$B_{i\ PJ}$	S^2d_i	B_{iFP}	S^2d_i
1 Vanaprava	3.667	-0.201	0.305	0.365	1.041	0.049	0.041	0.049	1.038	-0.118
2 Kalyani-II	5.042	0.731	-0.179	0.753	-0.144**	0.228	-1.144	0.228	-0.543	0.100
3 Kalinga-II	4.875	0.123	-0.025	0.126	1.136	0.081	0.136	0.081	0.898	-0.029
4 Vandana	3.308	-0.581	-0.064	0.585	2.101**	0.053	1.101	0.053	1.487	-0.116
5 Daya	4.533	-0.217	0.243	0.326	1.214	0.032	0.214	0.032	0.870	0.029
6 Pathara	4.942	0.204	-0.312	0.373	0.916	0.054	-0.084	0.054	0.633	0.160
7 Ghantes	3.842	-0.136	0.615	0.630	0.586	0.180	-0.414	0.180	0.285	-0.053
8 Heera	2.658	-0.006	0.254	0.254	0.654	-0.012	-0.346	-0.012	0.839	0.000
9 Neela	4.083	-0.435	-0.129	0.454	1.836**	0.018	0.836	0.018	1.445	-0.087
10 Anjali	4.200	-0.263	-0.476	0.544	1.894**	0.024	0.894	0.024	1.346	-0.005
11Dhalaheera	3.767	-0.299	-0.342	0.454	1.833**	-0.009	0.833	-0.009	1.727	-0.118
12 Parijat	4.550	0.266	0.062	0.273	0.487**	-0.023	-0.513	-0.023	0.366	-0.118
13 Tara	4.808	-0.118	-0.199	0.231	1.368	-0.029	0.368	-0.029	1.009	-0.118
14 Sankar	3.867	0.422	-0.004	0.422	0.190**	0.009	-0.810	0.009	-0.147	0.128
15 Annada	5.292	0.240	-0.126	0.271	0.752	0.009	-0.248	0.009	0.587	-0.099
16 Kalinga-I	4.475	0 225	0.282	0.361	0.338**	-0.023	-0.662	-0.023	0.172	-0.126
17 Kalinga-III	3.608	0.042	0.097	0.106	0.797	-0.042	-0.203	-0.042	0.688	-0.130

** B_i is significantly different from 1.00

Table 3. Mean yield response (t/ha), environmental index and estimates of first two IPCA scores in respect of four environments.

Environments	Mean yield	Environmental index	IPCA-1 scores	IPCA-2 scores
1	4.104	-0.103	0.803	-0.090
2	4.176	-0.030	-0.529	0.849
3	4.671	0.464	-0.767	-0.712
4	3.876	-0.330	0.493	-0.048

Table 4. Mean response of four genotype groups (GG) to four environments (E), range of IPCA-1 and IPCA-2 scores.

GG	Genotypes*	Mean(t/ha)	D_i range	IPCA-1 range	IPCA-2 range
GG-1	5,9,10,12,16	4.368	0.273 to 0.544	-0.435 to +0.266	-0.476 to +0.282
GG-2	1,4,7,11,14,17	3.676	0.106 to 0.630	-0.581 to +0.422	-0.342 to +0.615
GG-3	2,3,6,13,15	4.992	0.126 to 0.753	-0.118 to +0.731	-0.312 to -0.025
GG-4	8	2.658	0.254	-0.006	+0.254

*The numerals for genotypes are provided in Table-2

Table- 5. ANOVA for stability E and R model

Source of variations	Df	Sum of squares	Mean squares	F Ratio	Probability
Rep within Env.	8	0.566	0.071	0.897	0.530
Genotypes (G)	16	31.326	1.958	24.833	0.000***
E+ (GxE)	51	10.628	0.208	2.643	0.002**
Environment (E)	3	5.707	1.902	24.130	0.000***
G×E	48	4.921	0.103	1.300	0.212
E (Lin.)	1	5.707	5.707	72.389	0.000***
GxE (Lin.)	16	2.240	0.140	1.776	0.078
Pooled Deviation	34	2.681	0.079	1.884	0.006**
Pooled Error	128	5.356	0.042		
Total	67	41.955	0.626		

Table 6. Correlation among the stability parameters for 17 rice genotypes tested across four environments

	D_i	B_i ER	B_i PJ	B_i FP
IPCA-1	-0.033	-0.894**	-0.894**	-0.892**
Di		0.014	0.014	-0.164
Bi ER			1.000**	0.953**
Bi PJ				0.953**

** Significant at P < 0.01 level

Table 7. The mean yields, first and second IPCAs and various yield-stability statistics for 17 early rice genotypes.

Variety	IPCA-1	IPCA-2	Mean	ASV	YSI	SI (%)	I	RS	D_i
Vanaprava	-0.20	0.31	3.67	0.51	21	79.646	0.225	14.729	0.365
Kalyani-II	0.73	-0.18	5.04	1.48	19	83.884	0.053	6.523	0.753
Kalinga-II	0.12	-0.03	4.88	0.25	6	82.978	0.166	5.225	0.126
Vandana	-0.58	-0.06	3.31	1.17	32	60.031	0.072	16.000	0.585
Daya	-0.22	0.24	4.53	0.50	13	81.381	0.254	8.737	0.326
Pathara	0.20	-0.31	4.94	0.52	11	83.107	0.216	5.225	0.373
Ghantes	-0.14	0.62	3.84	0.67	23	77.465	0.086	14.121	0.630
Heera	-0.01	0.25	2.66	0.25	20	81.659	0.426	17.000	0.254
Neela	-0.44	-0.13	4.08	0.89	25	69.195	0.119	11.225	0.454
Anjali	-0.26	-0.48	4.20	0.71	22	67.917	0.106	11.836	0.544
Dhalaheera	-0.30	-0.34	3.77	0.69	25	66.698	0.138	14.389	0.454
Parijat	0.27	0.06	4.55	0.54	16	91.239	0.335	8.535	0.273

Tara	-0.12	-0.20	4.81	0.31	9	92.995	0.638	5.414	0.231
Sankar	0.42	0.00	3.87	0.85	25	90.955	0.129	14.000	0.422
Annada	0.24	-0.13	5.29	0.50	6	87.856	0.352	2.000	0.271
Kalinga-I	0 23	0.28	4.48	0.53	17	94.448	0.226	9.679	0.361
Kalinga-III	0.04	0.10	3.61	0.13	16	84.196	0.688	15.049	0.106

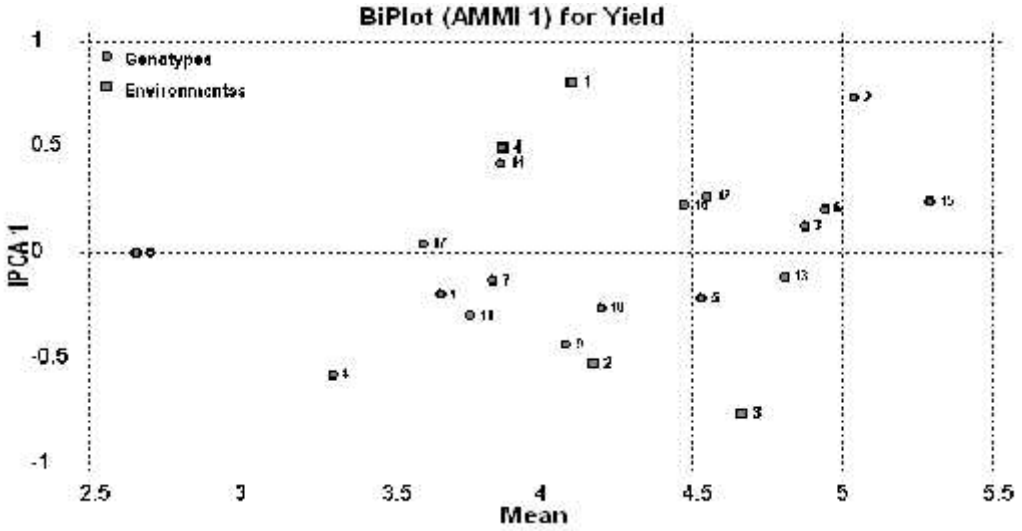

Figure 1. AMMI-1 biplot display of mean yields and IPCA-1 scores of 17 rice genotypes (◦) across four environments (□). The numerals for rice genotypes and environments are provided in Table-2 and Table-3, respectively.

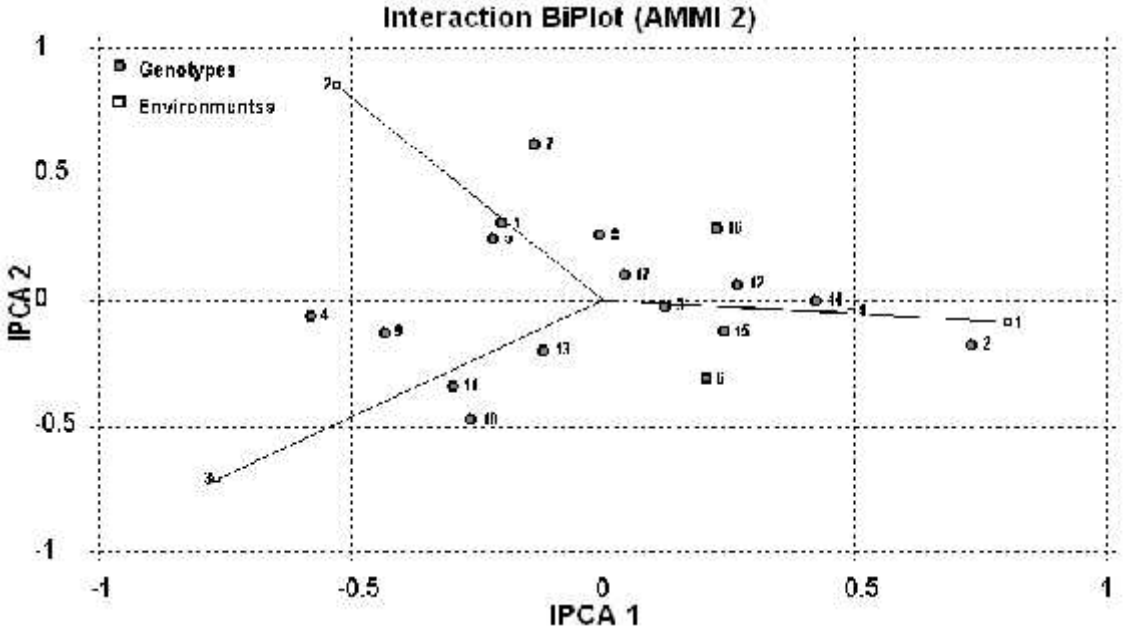

Figure 2. AMMI-2 biplot display of 17 rice genotypes and four environments for their yield response. Environment points are at the end of the spike. The numerals for genotypes and environments are provided in Table-2 and Table-3, respectively.

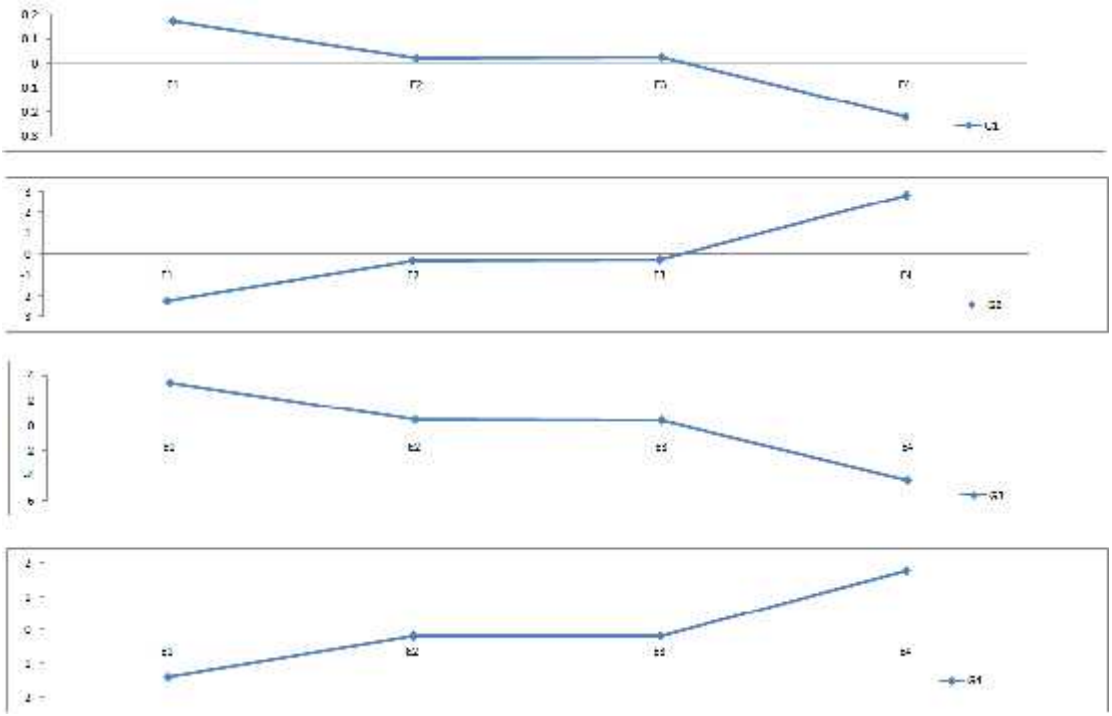

Figure 3. Response plot for the four genotype groups and four environments

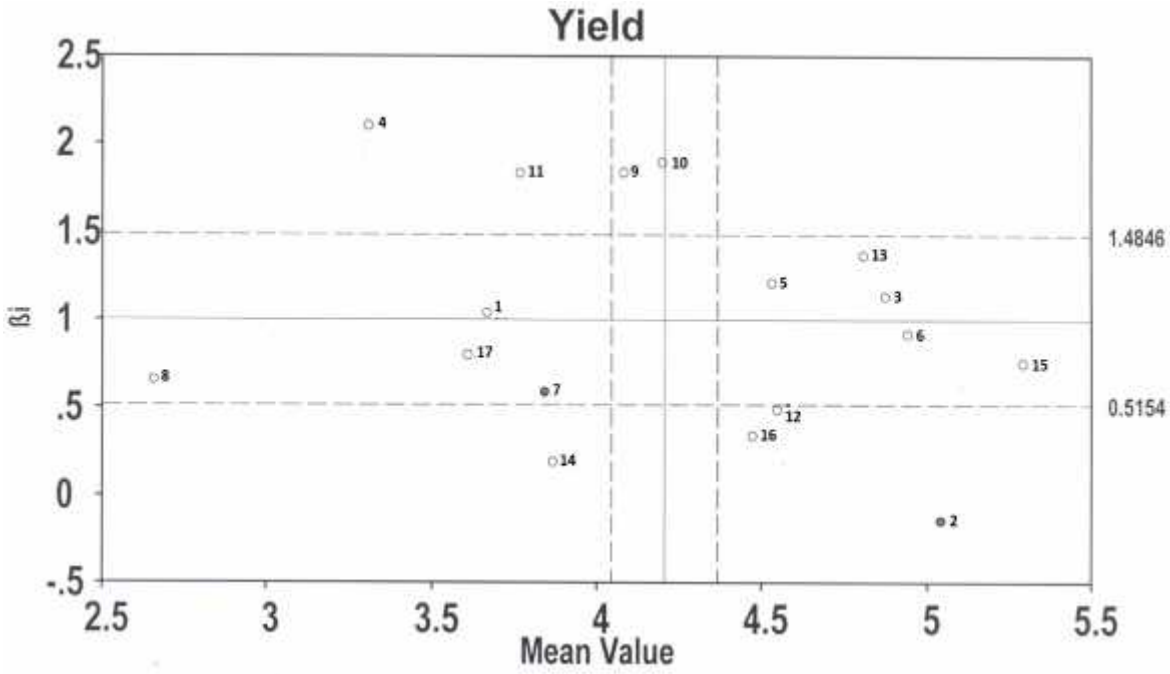

Figure 4. Relation of yield and stability of 17 rice genotypes.

Conclusion: The AMMI analysis provided (i) a better understanding of the GEI through analysis of variance, (ii) facilitated identification of genotypes possessing stable yields as well as discriminating environments through the biplot display and (iii) specificity in adaptability of the genotypes to specific environments in a 'which won where' pattern. The genotypes Kalyani-II, Kalinga-II, Pathara, Tara and Annada were identified as most stable across four environments. The scientific information obtained, could be of considerable importance in developing location specific breeding

strategies and selecting stable genotypes in breeding programme.

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