

## INTEGRATED ANALYSIS FOR GENOTYPIC ADAPTATION IN RICE

S. DAS, R.C. MISRA, S.R. DAS, M.C. PATTNAIK and S.K. SINHA

Department of Plant Breeding and Genetics, College of Agriculture, Orissa University of Agriculture and  
Technology, Bhubaneswar, Orissa, India

Corresponding author: swarnalata1967@rediffmail.com

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### ABSTRACT

Development of varieties with high yield potential coupled with wide adaptability is an important plant breeding objective. The presence of genotype by environment (GxE) interaction plays a crucial role in determining the performance of genetic materials, tested at different locations and in different years. This study was undertaken to assess yield performance, stability and adaptability of thirty-six rice genotypes of three different maturity groups evaluated over 12 environments. There were highly significant ( $P < 0.05$ ) genotype-environment interaction in three different maturity groups. The AMMI analysis of variance in the maturity groups also showed significant genotype, location and G'L. Stability in yield performance was predicted using nine stability parameters ( $b$ ,  $S_d^2$ , CV, SF,  $R_1$ ,  $R_2$ , W, S1 and ASV). The rank correlation coefficient among nine parameters indicated that the stability parameters were dissimilar in for all the maturity groups. Stability index (STI) computed by integrating all the nine stability parameters indicated that genotypes Lalat and OR 2006-12 of mid-early group, genotypes OR 1912-25, OR 2310-12 and MTU 1001 of mid-late group, and genotypes OR 1898-3-16, OR 1901-14-32, OR 2109-2, OR 2001-1, Mahanadi and Jagabandhu of late group yielded higher consistently over the 3 years in the different agroclimatic zones.

*Key Words:* Adaptation, AMMI stability value, stability index

### RÉSUMÉ

Le développement de variétés à potentiel élevé de rendement couplé à une large adaptabilité est un objectif important de l'amélioration des plantes. La présence de génotype par interaction avec l'environnement (GxE) joue un rôle crucial dans la détermination des performances de matériels génétiques testés dans différentes localisations et dans des années différentes influençant le processus de sélection. L'étude était entreprise pour évaluer la performance en rendement, la stabilité et l'adaptabilité de trente six génotypes de riz de trois groupes de maturité différente évalués sur 12 environnements. L'interaction génotype-environnement était significativement élevée ( $P < 0.05$ ) dans trois groupes de maturité différente. L'analyse AMM de la variance dans les groupes de maturité avait aussi montré un effet significatif du génotype, localisation et G'L. La stabilité en performance de rendement était prédite utilisant neuf paramètres de stabilité ( $b$ ,  $S_d^2$ , CV, SF,  $R_1$ ,  $R_2$ , W, S1 and ASV). L'étude du niveau de coefficient de corrélation parmi les neuf paramètres a indiqué que les paramètres de stabilité n'étaient pas les mêmes dans leurs degré de corrélation pour tous les groupes de maturité. L'index de stabilité (STI) calculé en intégrant tous les neuf paramètres de stabilité a indiqué que les génotypes Lalat et OR 2006-12 du mi-premier groupe, les génotypes OR 1912-25, OR 2310-12 et MTU 1001 du mi-dernier groupe et les génotypes OR 1898-3-16, OR 1901-14-32, OR 2109-2, OR 2001-1, Mahanadi et Jagabandhu du dernier groupe ont produit considérablement de rendements très élevés au cours des 3 ans dans différentes zones agroclimatiques.

*Mots Cles:* Adaptation, valeur de stabilité AMMI, index de stabilité

## INTRODUCTION

Development of varieties with high yield potential coupled with wide adaptability is an important plant breeding objective. The presence of genotype by environment (GxE) interaction plays a crucial role in determining the performance of genetic materials, tested at different locations and in different years, influencing the selection process (Becker and Leon, 1988; Purchase *et al.*, 2000). Multilocation trials provide useful information on genotypic adaptation and stability (Crossa, 1990). The GxE interaction estimates help breeders to decide the breeding strategy, to breed for specific or general adaptation, which depends on stability in yield performance under a limited or wide range of environmental conditions (Romagosa and Fox, 1993).

Plant breeders generally agree on the importance of high yield stability, but disagree with the different methods used for stability analysis (Becker and Leon, 1988). Therefore, several biometrical methods including univariate and multivariate ones have been developed to assess stability (Akcura *et al.*, 2005). Among the univariate approaches, the linear regression model of Eberhart and Russell (1966) is most widely adopted by the breeders (Chowdhury *et al.*, 2002; Bose *et al.*, 2004; Francis *et al.*, 2005; Nanita Devi *et al.*, 2006; Das *et al.*, 2008) as it is mathematically simple. But this model could not determine which genotype is superior, because the genotype's response to environments is intrinsically multivariate and regression tries to transform it into a univariate problem.

The use of stability analysis other than analysis of variance (ANOVA) may also help in prediction of adaptability of genotypes. Wricke's ecovalence is an alternative method that is used by breeders to determine stability of genotypes based on GXE interaction effects (Mahapatra, 1993; Chandrasari *et al.*, 2002; Das *et al.*, 2008). It indicates the contribution of each genotype to the GXE interaction. When exposed to different environments, the responsive genotypes are not necessarily unstable, rather more desirable if there is consistency in yield

as measured by coefficient of variation (CV) (Francis and Kannenberg, 1978).

Mahapatra and Das (1998) and Chandrasari *et al.* (2002) used CV to predict adaptability in rice. Among the multivariate approaches AMMI model is widely used (Asenjo *et al.*, 2003; Mahalingam *et al.*, 2006 and Das *et al.*, 2008). In AMMI, the response patterns of the genotypes to environmental change can be extrapolated to a much wider range of environments. AMMI stability value (ASV) statistic was developed by Purchase (1997) to quantify and rank the genotypes on the basis of their yield stability. ASV is based on AMMI model's PCA 1 and PCA 2 scores for each genotype. It is in effect the distance from the co-ordinate point to the origin in a two dimensional scatter gram of PCA 1 score against PCA 2 score. Many methods are available for the analysis of GxE interaction and adaptability (Lin *et al.*, 1986; Hohls, 1995). But the prediction of adaptability of the genotypes may vary depending on the biometrical methods followed, i.e. a genotype found to be stable in one biometrical method may not be stable in other. Therefore, the integration of several biometrical approaches may give a better result than the use of a single method in predicting the adaptability and stability in yield performance. The aim of the present investigation was to analyse genotypic adaptation in rice by integrating both univariate and multivariate methods of stability analysis.

## MATERIALS AND METHODS

Thirty six rice genotypes ( Table 1) of 3 different maturity groups – 11 of mid-early (115-125), 13 mid-late (126-140) and 12 of late (145-165) group were evaluated in three multilocation trials each at 4 different agroclimatic zones of Orissa (Bhubaneswar, Chiplima, Jeypore and Ranital; Table 2), India over 3 years, during 2004-2006 in *kharij* (wet) season using a randomised block design with three replications. For all trials, nursery sowing was done during last week of June to the first week of July. Twenty-five to thirty days old seedlings were transplanted with 20 cm × 15 cm spacing and 2 seedlings per hill. In each trial, the plot size

TABLE 1. Parentage of mid-early, mid-late and late rice genotypes

Name of genotype	Parentage
<b>Mid-early (115-125 days)</b>	
1. OR 1739-47	Sankar/IR 72
2. OR 1916-19	Lalat/Ratna
3. OR 1929-4	OR 929-3-2/RP 2423-108-97
4. OR 1976-11	TRC 87-125//IR 49517/Prana
5. OR 2006-12	Sarathi/IR 36
6. OR 2168-1	IR 36/UPRI 3
7. OR 2172-7	IR 64//IR 72//Jagannath/NCJ 10
8. OR 2200-5	RP 2423-108-97/ORS 199-2
9. Konark	Lalat/OR 135-3-4
10. Lalat	Obs 677/IR 2071// Vikram/W1263
11. Bhoi	Gouri/RP 825-45-1-3
<b>Mid-late (126-140 days)</b>	
1. OR 1681-11	Bhoi/Surendra
2. OR 1912-25	Swarna/Lalat
3. OR 1914-8	Swarna/IR 36
4. OR 1964-8	RTN 14-1-1//IR 72
5. OR 1967-15	RTN 14-1-1//IR 49517/OR 1301-32
6. OR 2156-15	Swarna/IR 72
7. OR 2310-12	Swarna/Birupa
8. Pratikshya	Swarna/IR 64
9. Gouri	Rajeswari/Vikram
10. Surendra	OR 158-5/Rasi
11. Gajapati	OR 136-3/IR13429-196-1-20
12. Kharavela	Daya/IR 13240-108-2-2-3
13. MTU 1001	MTU 5249/MTU 7014
<b>Late (145-165 days)</b>	
1. OR 1885-16-34	IR 72/Kanchan
2. OR 1898-2-15	Mahalaxmi/OR 633-7
3. OR 1898-3-16	Mahalaxmi/OR 633-7
4. OR 1901-14-32	Manika/IR 72
5. OR 2001-1	RP 1125-606-32/Rambha
6. OR 2109-2	Indravati//IR 72/Salivahan
7. OR 2119-13	Manika/Manasarovar
8. Savitri	Pankaj/Jagannath
9. Salivahan	RP 5-32/Pankaj
10. Mahanadi	IR 19661/Savitri
11. Kanchan	Jajati/Mahsuri
12. Jagabandhu	Savitri/IR 4819-77-3-2//IR 27301-154-3

was 2 m × 3 m containing 10 rows of 3 m length each.

The yield data of the 12 environments (4 locations × 3 years) were subjected to stability analysis following univariate methods like regression co-efficient (b) and deviation from regression ( $S_d^2$ ) of Eberhart and Russell (1966), co-efficient of variation (CV) of Francis and Kannenberg (1978), two range parameters ( $R_1$  and  $R_2$ ) of Langer *et al.* (1979), stability factor (SF) proposed by Lewis (1954), ecovalence (W) of Wricke (1962), mean absolute rank difference (S1) of Nassar and Huhn (1987) and the multivariate method AMMI (Additive main effects and multiplicative interaction) stability value (ASV) of Purchase (1997). The models are described below.

**Linear regression model.** Adaptability and stability of performance of genotypes for grain yield were analysed, using the linear regression model of Eberhart and Russell (1966) as follows:

$$Y_{ij} = a_i + b_i I_j + d_{ij}, \quad (i=1, g; j=1, n),$$

where:

$Y_{ij}$  = mean of  $i^{\text{th}}$  genotype in  $j^{\text{th}}$  environment;

$I_j$  = environmental index of  $j^{\text{th}}$  environment, i.e.  $j^{\text{th}}$  environment mean (over all genotypes) minus the grand mean;

$a_i$  = mean of  $i^{\text{th}}$  genotype over all environments;

$b_i$  = regression coefficient which measures the response of  $i^{\text{th}}$  genotype to the varying environments;

$d_{ij}$  = deviation from regression of  $i^{\text{th}}$  genotype at  $j^{\text{th}}$  environment, i.e.,  $d_{ij} = Y_{ij} - \hat{Y}_{ij}$ .

The regression coefficient 'b' was estimated as:

$$b_i = \frac{\sum_j Y_{ij} I_j}{\sum_j I_j^2}$$

TABLE 2. Environmental variation of four experimental regions (Source: Agrometeorology, OUAT, Bhubaneswar)

Different regions	Latitude	Longitude	Average rain fall (mm)	Temperature (°C)
Bhubaneswar	18°40'-20°15'N	83°48'-87°40'N	1340.0	11.5- 39° C
Chiplima	16°15'-20°52'N	82°13'-85°15'N	1180.0	12.0- 40.0° C
Jeypore	10°20'-20°10'N	81°50'-83°20'N	1347.1	7.5- 39.1° C
Ranital	22°40'-23°48'N	86°16'-87°25'N	1488.0	24.0- 38.0° C

The stability parameter, measuring deviation from regression ( ) was estimated as follows:

$$S_{di}^2 = \frac{\sum_j d_{ij}^2}{n-2} - \frac{S_e^2}{r}$$

$$\text{where } \sum_j d_{ij}^2 = \left[ \sum_j Y_{ij}^2 - \frac{Y_{i.}^2}{n} \right] - \frac{\left( \sum_j Y_{ij} \cdot I_j \right)^2}{\sum_j I_j^2}$$

$S_e^2$  = pooled error mean square;  
 $r$  = number of replications; and  
 $n$  = number of environments.

**Coefficient of variation (CV).** Use of coefficient of variation as a stability parameter was proposed by Francis and Kannenberg (1978). The parameter was estimated as:

$$CV = \frac{SD_x}{\bar{X}} \times 100$$

where  $SD_x$  is standard deviation of the means of a genotype over environments and  $\bar{X}$  is the mean of the genotype over all environments.

**Range parameters.** Two range parameters ( $R_1$  and  $R_2$ ) were estimated as follows, after Langer *et al.* (1979).

$$R_1 = \bar{X}_H - \bar{X}_L$$

$$R_2 = \bar{X}_{HE} \text{ and } \bar{X}_{LE}$$

where  $\bar{X}_H$  and  $\bar{X}_L$  are the highest and lowest mean yields of a genotype over the range of environments and  $\bar{X}_{HE}$  and  $\bar{X}_{LE}$  are mean yields of a genotype in the highest-yielding and lowest-yielding environments.

**Stability factor.** Stability factor (SF) of a genotype as proposed by Lewis (1954) was estimated as:

$$SF = \frac{\bar{X}_{HE}}{\bar{X}_{LE}}$$

where  $\bar{X}_{HE}$  is mean of the genotype in the highest -yielding environment; and  $\bar{X}_{LE}$  is mean of the genotype in the lowest -yielding environment.

**Ecovalence (W).** According to Wricke (1962) Ecovalence ( $W_i$ ) of a genotype was estimated as:

$$W_i = \sum_j \left[ Y_{ij} - \frac{Y_{i.}}{n} - \frac{Y_{.j}}{g} + \frac{Y_{..}}{gn} \right]^2$$

where  $Y_{ij}$  = mean of  $i^{\text{th}}$  genotype in  $j^{\text{th}}$  environment;  
 $Y_{i.}$  = total of  $i^{\text{th}}$  genotype over environments;  
 $Y_{.j}$  = total of  $j^{\text{th}}$  environment over all genotypes; and  
 $Y_{..}$  = grand total.

**Mean absolute rank difference (S1).** Mean absolute rank difference' is a stability parameter proposed by Nassar and Huhn (1987). The rank of a genotype in each environment is determined first. If there are 'n' no. of environments/ locations then the possible pair-wise rank difference across the environments of the genotype would be  $n \times (n-1)/2$ . Then all the rank differences were added and the average is calculated to get mean absolute rank difference of the genotype. Mean absolute rank difference estimates are all possible pair-wise rank

differences across locations for each genotype. Genotypes with less change in rank are expected to be more stable.

**AMMI stability value (ASV).** The PCA scores of a genotype in the AMMI analysis are an indicator of the stability of a genotype over environments. The greater the IPCA (Interaction Principal Component Axis) scores, either negative or positive, indicated the specific adaptation of a genotype to certain environments. The more the IPCA scores approximate to zero, the more stable the genotype is over all the environments considered for the study. The mathematical function of the AMMI model following Zobel *et al.* (1988) is:

$$Y_{ij} = \mu + \alpha_i + \beta_j + \sum_{k=1}^n \lambda_k \gamma_{ik} \delta_{jk} + \theta_{ij}$$

where  $Y_{ij}$  = mean yield of  $i^{\text{th}}$  genotype in  $j^{\text{th}}$  environment;

$\mu$  = grand mean;

$\alpha_i$  = mean deviation/effect of  $i^{\text{th}}$  genotype;

$\beta_j$  = mean deviation/effect of  $j^{\text{th}}$  environment;

$\lambda_k$  = eigen value of  $k^{\text{th}}$  IPCA axis;

$\tilde{\alpha}_{ik}$  = genotypic score of  $i^{\text{th}}$  genotype on  $k^{\text{th}}$  IPCA;

$\delta_{jk}$  = environment score of  $j^{\text{th}}$  environment on  $k^{\text{th}}$  IPCA,

$\theta_{ij}$  = residual of G  $\times$  E interaction effect in  $Y_{ij}$ ; and

$n$  = number of IPC axes retained in the model.

A stability parameter called AMMI stability value (ASV) was estimated for each genotype using the following formula, after Purchase (1997).

$$ASV = \sqrt{(\omega\gamma_{i1})^2 + \gamma_{i2}^2}$$

where  $\omega$  = IPCA 1 SS/IPCA 2 SS (weight to IPCA 1);

$\gamma_{i1}$  = IPCA 1 score of  $i^{\text{th}}$  genotype; and

$\gamma_{i2}$  = IPCA 2 score of  $i^{\text{th}}$  genotype.

**Estimation of stability index (STI).** Stability of performance of each genotype was expressed in terms of a stability index (STI). For estimating STI, the genotypes of each maturity group were classified into stable and unstable categories on the basis of each stability parameter as discussed above and the stable genotypes were scored 1, while unstable genotypes were scored 0. Genotypes having  $b$  values of 0.8-1.2 ( $b \neq 1$ ) were considered stable and those having  $b < 0.8$  or  $> 1.2$  ( $b \neq 1$ ) were considered unstable. Non-significant  $S_d^2$  of a genotype indicated stability and significant  $S_d^2$  indicated unstable performance. Low (below average) value in case of CV, SE, R1, R2, W, S1 and ASV indicated stability and high (above average) value indicated unstable performance. Finally, the numerical scores of a genotype on all the 9 parameters were added to get stability index (STI) of the genotype. High value of this index indicated higher stability of yield performance of the genotypes.

## RESULTS

Analysis of variance (Table 3) of yield data of the three multilocation trials of mid-early, mid-late and late groups over 12 environments showed significant differences ( $P < 0.05$ ) among genotypes of each maturity group and among environments and highly significant G  $\times$  E interaction indicated differential response of the genotypes to environmental changes. Regression analysis indicated that the mean sum of squares due to environment (linear) was highly significant.

**Mid-early group.** Table 4 showed the stability parameters of Eberhart and Russell (1966). In the case of mid-early group, the regression coefficient ( $b$ ) of the genotypes OR 1916-19, OR 1976-11, OR 2006-12 and Lalat was found to be unity ( $b = 0.8 - 1.2$ ). Genotypes OR 2200-5, OR 2172-7 and Konark had ' $b$ ' values greater than unity ( $b > 1.2$ ). The remaining four genotypes had  $b$ -values less than unity ( $b < 0.8$ ).  $S_d^2$  of the genotypes Lalat, OR 2200-5, Konark, OR 1929-4, OR 1916-19 and Bhoi were not significantly different from zero. Genotypes

TABLE 3. Pooled analysis of variance for grain yield in rice

Source	df	MS	F
<b>Pooled analysis of variance for grain yield in mid-early rice genotypes</b>			
Genotypes (G)	10	24.94	3.85**
Environments (E)	11	395.70	61.16**
G x E	110	17.03	2.63**
E + G x E	121		
Environment (linear)	1	4352.71	296.65**
G x E (linear)	10	28.90	1.97*
Pooled deviation	110	14.67	2.26**
Pooled error	240	6.47	
<b>Pooled analysis of variance for grain yield in mid-late rice genotypes</b>			
Genotypes (G)	12	83.19	10.57**
Environments (E)	11	900.88	114.50**
G x E	132	24.19	3.08**
E + G x E	143		
Environment (linear)	1	9909.73	483.94**
G x E (linear)	12	44.29	2.16*
Pooled deviation	130	20.48	2.60**
Pooled error	288	7.87	
<b>Pooled analysis of variance for grain yield in late rice genotypes</b>			
Genotypes (G)	11	167.12	17.20**
Environments (E)	11	404.01	41.60**
G x E	121	39.93	4.11**
E + G x E	132		
Environment (linear)	1	4444.08	125.30**
G x E (linear)	11	52.26	1.47
Pooled deviation	120	35.47	3.65**
Pooled error	264	9.71	

\*= significant at 5%; \*\*= significant at 1% level

showing below average value for CV, SF, R1, R2, W and S1 (Table 5) ranked in the stable category, while those having above average value were classified as unstable. There were 7, 6, 5, 5, 6, and 6 genotypes showed stability on the basis of CV, SF, R1, R2 W and S1 parameters, respectively.

The AMMI analysis of variance showed that both main effect components, i.e. genotype and location and interaction component were significant (Table 6). The main effects of genotypes and locations accounted for 8.43% and 80.86%, respectively; and G x L interaction accounted for 10.71% of the total variation in

G-L data for grain yield. Table 7 indicated the AMMI 2 model IPCA 1 and IPCA 2 scores and the ASV with its ranking for the mid-early genotypes. According to ASV ranking, the most stable genotypes were OR 1976-11, Lalat, OR 1929-4, OR 2168-1, OR 2200-5 and OR 1739-47. This clearly indicated that genotype found to be stable on the basis of one method may not be stable on the basis of another method(s).

The rank correlation coefficient study among the nine stability parameters (Table 8b) revealed that b had positive significant correlation with CV, SF, R1 and R2 and negative correlation with and W. But  $S_d^2$  showed negative correlation

TABLE 4. Estimates of stability parameters (b and  $S_d^2$ ) of linear regression model for grain yield ( $t ha^{-1}$ ) of rice genotypes

Genotype	b	$S_d^2$
<b>Mid-early</b>		
1. OR 1739-47	0.78 (0)	10.21* (0)
2. OR 1916-19	0.94 (1)	6.15 (1)
3. OR 1929-4	0.76 (0)	3.09 (1)
4. OR 1976-11	0.99 (1)	19.50**(0)
5. OR 2006-12	0.92 (1)	14.46**(0)
6. OR 2168-1	0.69 (0)	24.95**(0)
7. OR 2172-7	1.23 (0)	9.28* (0)
8. OR 2200-5	1.47 (0)	0.30 (1)
9. Konark	1.35 (0)	0.34 (1)
10. Lalat	1.08 (1)	-3.95 (1)
11. Bhoi	0.79 (.0)	7.16 (1)
Average	1.00	8.20
<b>Mid-late</b>		
1. OR 1681-11	0.58(0)	16.59**(0)
2. OR 1912-25	0.83(1)	6.29 (1)
3. OR 1914-8	1.08(1)	4.26 (1)
4. OR 1964-8	1.01(1)	19.69**(0)
5. OR 1967-15	1.17(1)	7.81* (0)
6. OR 2156-15	0.59(0)	15.68**(0)
7. OR 2310-12	0.97(1)	6.00 (1)
8. Pratikshya	0.93(1)	38.26**(0)
9. Gouri	0.93(1)	12.55**(0)
10. Surendra	0.93(1)	19.01**(0)
11. Gajapati	1.49(0)	4.45 (1)
12. Kharavela	1.31(0)	15.59**(0)
13. MTU 1001	1.08(1)	-2.26 (1)
Average	1.00	12.61
<b>Late</b>		
1. OR 1885-16-34	0.71(0)	52.42**(0)
2. OR 1898-2-15	1.06(1)	11.09* (0)
3. OR 1898-3-16	1.12(1)	3.83 (1)
4. OR 1901-14-32	0.68(0)	8.11 (1)
5. OR 2001-1	0.93(1)	11.46* (0)
6. OR 2109-2	0.92(1)	22.39**(0)
7. OR 2119-13	0.39(0)	72.37**(0)
8. Savitri	1.61(0)	36.52**(0)
9. Salivahan	1.33(0)	38.50**(0)
10. Mahanadi	0.84(1)	0.46 (1)
11. Kanchan	1.64(0)	49.40**(0)
12. Jagabandhu	0.77(0)	2.47 (1)
Average	1.00	15.60

Values in brackets are the scored value, where '0' indicated unstable performance and '1' indicated stable performance. \* = significant at 5%, \*\* = significant at 1% level

with CV, SF, R1 and R2 and positive significant correlation with W. Both S1 and ASV had no significant correlation with any other stability parameters.

So to predict stability in yield performance of a genotype all the 9 stability parameters were considered together, by scoring the genotypes in a 0-1 scale for each parameter. The STI values ranged from 0 to 8 (Table 9) in mid-early group. The genotypes OR 1739-47, OR 1929-4, OR 2168-1, OR 1916-19, OR 2006-12, Lalat and Bhoi scored high STI value (> 4.63) and were considered as stable irrespective of their yield performance. In mid-early group, the genotypes Lalat, OR 2200-5, OR 2172-7, OR 2006-12, OR 1976-11 and Konark gave above average yield (Table 9) and considered as high yielder. The two high yielding genotypes, i.e., Lalat and OR 2006-12 having high STI value indicated their wider adaptability over all environments. The genotype OR 2172-7 having high yield and STI of 0 indicated that it was highly unstable.

**Mid-late group.** The regression coefficient (b-values) of the genotypes varied from 0.59 to 1.49. Nine genotypes had unity b-values. On the basis of  $S_d^2$  values (Table 4), the genotypes OR 1912-25, OR 1914-8, OR 2310-12, Gajapati and MTU 1001 were classified as stable ( $S_d^2 = 0$ ). The remaining 8 genotypes showed high deviation from regression ( $S_d^2 > 0$ ). On the basis of CV, SF,  $R_1$ ,  $R_2$ , W and S1 values 8, 6, 7, 6, 7 and 5 genotypes respectively, were found to be stable and the rest unstable. The AMMI analysis of variance showed that both main effect components, i.e., genotype and location and  $G \times E$  interaction component were significant (Table 6). Based on ASV ranking, the genotypes OR 2310-12, OR 1681-11, OR 1914-8, Gouri, MTU 1001, OR 1967-15 and Surendra were found to be stable (Table 7). The rank correlation coefficient study among the nine stability parameters (Table 8b) showed that b had positive significant correlation with CV, SF, R1 and W and negative correlation with the rest four parameters. The  $S_d^2$  showed positive significant correlation with R2 and S1. The W exhibited positive significant correlation with b, CV, SF and R1. But the multivariate statistics

TABLE 5. Estimates of stability parameters CV, SF, R1, R2, W and S1 for grain yield (t ha<sup>-1</sup>) of rice genotypes

Genotype	CV	SF	R1	R2	W	S1
<b>Mid-early</b>						
1. OR 1739-47	16.9(1)	1.41(1)	16.3(1)	12.6(1)	186.4(0)	4.02(0)
2. OR 1916-19	18.9(1)	1.97(0)	23.3(0)	23.3(0)	127.6(1)	2.77(1)
3. OR 1929-4	15.4(1)	1.39(1)	16.4(1)	11.5(1)	119.1(1)	2.94(1)
4. OR 1976-11	20.4(0)	1.90(0)	22.8(0)	22.8(0)	259.7(0)	4.21(0)
5. OR 2006-12	18.6(1)	1.43(1)	24.1(0)	13.9(1)	212.0(0)	2.92(1)
6. OR 2168-1	19.3(1)	1.28(1)	19.5(1)	9.6(1)	349.9(0)	3.68(0)
7. OR 2172-7	21.9(0)	2.61(0)	31.3(0)	31.3(0)	178.1(0)	3.54(0)
8. OR 2200-5	24.1(0)	2.18(0)	27.8(0)	27.6(0)	147.7(1)	4.30(0)
9. Konark	22.9(0)	2.24(0)	27.6(0)	25.8(0)	110.2(1)	3.23(1)
10. Lalat	17.4(1)	1.75(1)	21.1(1)	20.8(0)	28.0(1)	1.89(1)
11. Bhoi	17.1(1)	1.55(1)	19.6(1)	11.9(1)	154.5(1)	2.50(1)
Average	19.4	1.79	22.7	19.2	170.3	3.27
<b>Mid-late</b>						
1. OR 1681-11	17.9(1)	1.60(1)	24.2(1)	322.1(0)	17.6(1)	3.98(0)
2. OR 1912-25	16.4(1)	1.61(1)	25.9(1)	164.5(1)	22.2(1)	1.98(1)
3. OR 1914-8	23.5(0)	1.67(1)	32.9(0)	126.6(1)	22.5(1)	2.95(1)
4. OR 1964-8	23.0(0)	1.92(0)	25.7(1)	275.6(0)	25.7(1)	4.47(0)
5. OR 1967-15	26.1(0)	1.85(1)	32.5(0)	178.9(1)	27.2(0)	3.77(1)
6. OR 2156-15	15.7(1)	1.52(1)	23.4(1)	363.7(0)	15.0(1)	4.91(0)
7. OR 2310-12	20.6(1)	1.93(0)	27.7(1)	139.5(1)	27.7(0)	4.82(0)
8. Pratikshya	21.9(1)	2.00(0)	31.8(0)	464.9(0)	31.8(0)	4.26(0)
9. Gouri	22.4(1)	2.06(0)	29.0(1)	207.9(1)	24.9(1)	4.28(0)
10. Surendra	21.5(1)	2.17(0)	34.1(0)	272.3(0)	34.1(0)	4.08(0)
11. Gajapati	32.5(0)	2.59(0)	40.7(0)	308.4(0)	40.6(0)	3.67(1)
12. Kharavela	31.0(0)	2.17(0)	42.6(0)	308.8(0)	34.1(0)	4.07(0)
13. MTU 1001	20.9(1)	1.67(1)	29.1(1)	60.3(1)	24.0(1)	3.42(1)
Average	22.6	1.90	30.7	245.7	26.7	3.89
<b>Late</b>						
1. OR 1885-16-34	26.7(0)	1.27(1)	31.0(0)	7.7(1)	652.0(0)	3.08(1)
2. OR 1898-2-15	20.3(1)	1.56(1)	24.5(1)	15.1(1)	209.2(1)	3.46(1)
3. OR 1898-3-16	16.8(1)	1.89(0)	27.2(0)	27.2(0)	140.7(1)	3.62(1)
4. OR 1901-14-32	12.7(1)	1.37(1)	20.3(1)	12.5(1)	217.0(1)	3.47(1)
5. OR 2001-1	17.1(1)	2.01(0)	24.9(1)	24.9(0)	213.7(1)	3.10(1)
6. OR 2109-2	17.7(1)	1.59(1)	25.2(1)	20.2(0)	323.3(1)	3.18(1)
7. OR 2119-13	21.5(0)	1.30(1)	25.6(1)	8.5(1)	959.1(0)	5.06(0)
8. Savitri	29.5(0)	2.07(0)	33.2(0)	30.3(0)	600.5(0)	4.63(0)
9. Salivahan	28.4(0)	1.94(0)	28.5(0)	23.0(0)	522.8(0)	3.90(0)
10. Mahanadi	13.9(1)	1.27(1)	15.5(1)	10.2(1)	110.7(1)	3.49(1)
11. Kanchan	32.2(0)	1.83(0)	39.0(0)	27.6(0)	741.1(0)	4.17(0)
12. Jagabandhu	13.1(1)	1.25(1)	16.5(1)	9.5(1)	140.9(1)	2.74(1)
Average	20.8	1.61	26.0	18.1	402.6	3.66

Values in brackets are the scored value, where '0' indicated unstable performance and '1' indicated stable performance for each stability parameter

ASV did not show significant correlation with the univariate stability parameters.

Based on STI values (Table 9), the genotypes were identified as stable and unstable irrespective of their yield level. The genotypes

TABLE 6. AMMI ANOVA of rice genotypes for yield

Source	df	SS	(%) G-L SS	MS	F	(%) G x L interaction SS
<b>AMMI ANOVA of mid-early rice genotypes for yield</b>						
Genotype (G)	10	83.449	8.43	8.35	3.72**	
Location (L)	3	800.522	80.86	266.84	119.08**	
G x L	30	106.008	10.71	3.53	1.58*	
IPCA 1	12	65.185	6.58	5.43	2.42**	61.49
IPCA 2	10	26.503	2.68	2.65	1.18	25.00
Residual	8	14.320	1.45	1.79	0.80	13.51
Error	240	537.792		2.24		
<b>AMMI ANOVA of mid-late rice genotypes for yield</b>						
Source	df	SS	(%) G-L SS	MS	F	(%) G x L interaction SS
Genotype (G)	12	332.734	17.71	27.73	9.81**	
Location (L)	3	1286.190	68.45	428.73	151.62**	
G x L	36	260.067	13.84	7.22	2.56**	
IPCA 1	14	107.879	5.74	7.71**	2.73*	41.48
IPCA 2	12	89.167	4.75	7.43**	2.63*	34.29
Residual	10	63.069	3.36	6.30	2.24*	24.23
Error	288	814.378		2.83		
<b>AMMI ANOVA of late rice genotypes for yield</b>						
Source	df	SS	(%) G-L SS	MS	F	(%) G x L interaction SS
Genotype (G)	11	612.828	44.54	55.71	17.21**	
Location (L)	3	221.052	16.07	73.68	22.76**	
G x L	33	541.923	39.39	16.42	5.07**	
IPCA 1	13	432.662	31.45	33.28	10.28**	79.84
IPCA 2	11	96.934	7.04	8.81	2.72**	17.89
Residual	9	12.327	0.90	1.37	0.42	2.27
Error	264	854.858		3.24		

\* = significant at 5%, \*\* = significant at 1% level

OR 1912-25, OR 2310-12 and MTU 1001 with high yield and high STI value were considered as widely adapted genotypes and they were agronomically superior.

**Late group.** The regression coefficient (b-values) of the late group genotypes ranged from 0.39 to 1.64 (Table 4). Five genotypes showed unit regression ( $b = 0.8-1.2$ ). Based on  $S_d^2$  values, four genotypes were found to be stable and rest eight were unstable. There were 7, 7,

7, 6, 7 and 8 genotypes had below average values for the parameters CV, SF,  $R_1$ ,  $R_2$ , W and S1 (Table 5), respectively and were considered as stable (Table 5). The AMMI analysis of variance showed that genotype (G), location (L) and G'L interaction components were significant at 1% level. The multivariate stability statistics ASV indicated that the genotypes Mahanadi, OR 1898-3-16, Jagabandhu, OR 1898-2-15, OR 2109-2 and OR 1885-16-34 were stable. The rank and rank correlation coefficient study

TABLE 7. The IPCA1 and IPCA2 scores along with AMMI stability value (ASV) for grain yield ( $t\ ha^{-1}$ ) of rice genotypes

Genotype	IPCA Score1	IPCA Score2	ASV
<b>Mid-early</b>			
1. OR 1739-47	-0.76	-0.40	1.26(1)
2. OR 1916-19	-1.33	-0.07	2.08(0)
3. OR 1929-4	0.38	-0.12	0.61(1)
4. OR 1976-11	0.22	0.15	0.38(1)
5. OR 2006-12	1.49	-0.67	2.44(0)
6. OR 2168-1	0.59	-0.15	0.93(1)
7. OR 2172-7	-0.96	1.46	2.10(0)
8. OR 2200-5	0.64	0.72	1.23(1)
9. Konark	0.79	0.61	1.38(0)
10. Lalat	-0.06	-0.39	0.40(1)
11. Bhoi	-1.00	-1.14	1.95(0)
<b>Mid-late</b>			
1. OR 1681-11	-0.41	0.40	0.60(1)
2. OR 1912-25	1.43	0.01	1.57(0)
3. OR 1914-8	-0.51	0.33	0.65(1)
4. OR 1964-8	0.54	-1.44	1.55(0)
5. OR 1967-15	-0.49	0.77	0.94(1)
6. OR 2156-15	-0.25	1.28	1.31(0)
7. OR 2310-12	-0.05	0.56	0.56(1)
8. Pratikshya	2.34	0.47	2.61(0)
9. Gouri	-0.67	0.51	0.90(1)
10. Surendra	0.03	-1.05	1.05(1)
11. Gajapati	-0.36	-1.20	1.26(0)
12. Kharavela	-0.89	-1.14	1.50(0)
13. MTU 1001	-0.70	0.49	0.92(1)
<b>Late</b>			
1. OR 1885-16-34	-0.35	-2.21	2.33(1)
2. OR 1898-2-15	-0.38	-0.36	0.88(1)
3. OR 1898-3-16	0.33	-0.29	0.75(1)
4. OR 1901-14-32	1.15	0.08	2.43(0)
5. OR 2001-1	1.20	0.41	2.56(0)
6. OR 2109-2	0.44	0.79	1.22(1)
7. OR 2119-13	3.06	0.04	6.47(0)
8. Savitri	-1.35	0.74	2.94(0)
9. Salivahan	-1.36	1.66	3.32(0)
10. Mahanadi	-0.34	0.21	0.74(1)
11. Kanchan	-2.05	-0.64	4.37(0)
12. Jagabandhu	-0.36	-0.42	0.87(1)

Values in brackets are the scored value, where '0' indicated unstable performance and '1' indicated stable performance for the stability parameter ASV.

among the nine stability parameters (Table 8a and 8b) showed that *b* had positive significant correlation with CV, SF and R2 and limited correspondence with the rest five parameters.

The Wricke's procedure of stability statistics exhibited positive significant correlation with  $S_d^2$ , CV, and R1. The multivariate statistics ASV showed significant positive correlation with  $S_d^2$ , CV, R1 and W. But S1 did not show significant correlation with any other stability parameter.

Stability index in late group (Table 9) revealed that genotypes OR 1898-2-15, OR 1898-3-16, OR 1901-14-32, OR 2109-2, OR 2001-1, Mahanadi and Jagabandhu with above average STI value ( $>4.75$ ) had reflected consistency in their yield performance. High mean yield along with high STI value for the genotypes OR 1898-3-16, OR 1901-14-32, OR 2109-2, OR 2001-1, Mahanadi and Jagabandhu indicated their general adaptation. The high yielding genotype Mahanadi was found to be stable for each of the 9 parameters and considered as unique as compared to other high yielding genotypes.

## DISCUSSION

The present study clearly showed that genotypes of mid-early, mid-late and late group differed greatly in their yield stability for each of the univariate and multivariate stability parameters (Tables 4, 5 and 7.). According to authors knowledge integration of both the univariate and multivariate methods to assess adaptability is very scanty. Mahapatra (1993) estimated adaptability of 12 rice varieties by integrating eight univariate methods along with mean yield. In mid-early group the number of stable genotypes is highest (7) according to CV and least (4) on the basis of *b* value. In the mid-late group, the number of stable genotypes is highest (9) according to *b* value and lowest (5) on the basis of  $S_d^2$  and S1 value. In the late group, highest (8) number of stable genotypes is observed according to S1 parameter and least (4) on the basis of  $S_d^2$  value.

The rank correlation coefficient in the present investigation indicated that the stability statistics showed variation in their degree of correlation and were not the same for all the maturity groups. In the mid-early group W showed positive significant correlation with  $S_d^2$  but not with other stability statistics. However,

TABLE 8a. Ranking order of the nine stability parameters in different maturity groups of rice.

b	$S_d^2$	CV	SF	R1	R2	W	S1	ASV
<b>Mid-early</b>								
3	8	2	3	1	4	8	9	6
6	5	6	8	7	8	4	3	9
2	4	1	2	2	2	3	5	3
7	10	8	7	6	7	10	10	1
5	9	5	4	8	5	9	4	11
1	11	7	1	3	1	11	8	4
9	7	9	11	11	11	7	7	10
11	2	11	9	10	10	5	11	5
10	3	10	10	9	9	2	6	7
8	1	4	6	5	6	1	1	2
4	6	3	5	4	3	6	2	8
<b>Mid-late</b>								
1	10	3	2	2	11	2	6	2
3	5	2	3	4	4	3	1	12
10	2	10	5	10	2	4	2	3
8	12	9	7	3	8	7	11	11
11	6	11	6	9	5	8	5	6
2	9	1	1	1	12	1	13	9
7	4	4	8	5	3	9	12	1
4	13	7	9	8	13	10	9	13
5	7	8	10	6	6	6	10	4
6	11	6	11	11	7	11	8	7
13	3	13	13	12	9	13	4	8
12	8	12	12	13	10	12	7	10
9	1	5	4	7	1	5	3	5
<b>Late</b>								
3	11	9	3	10	1	10	2	6
8	5	7	6	4	6	4	5	4
9	3	4	9	8	10	2	8	2
2	4	1	5	3	5	6	6	7
7	6	5	11	5	9	5	3	8
6	7	6	7	6	7	7	4	5
1	12	8	4	7	2	12	12	12
11	8	11	12	11	12	9	11	9
10	9	10	10	9	8	8	9	10
5	1	3	2	1	4	1	7	1
12	10	12	8	12	11	11	10	11
4	2	2	1	2	3	3	1	3

b = regression coefficient,  $S_d^2$  = deviation from regression, CV = coefficient of variation, SF = stability factor, R1 = range 1, R2 = range 2, W = Wricke's ecovalence, S1 = mean absolute rank difference, ASV = AMMI stability value

S1 and ASV did not have positive significant correlation with other stability parameters.

In the mid-late group, W showed a positive significant correlation with b, CV, SF and R1;

S1 showed positive significant correlation only with  $S_d^2$  and ASV had at all no significant correlation with any other stability parameters. In late group, the highest positive significant

TABLE 8b. Rank correlation among the nine stability parameters in different maturity groups of rice

<b>Mid-early</b>									
	b	$S_d^2$	CV	SF	R1	R2	W	S1	ASV
b		-.565	.745*	.918**	.845**	.927**	-.418	.155	.100
$S_d^2$			-.063	-.418	-.245	-.382	.945**	.336	.118
CV				.727*	.818*	.745*	.081	.500	.100
SF					.863**	.963**	-.354	.100	.290
R1						.881**	-.136	.127	.454
R2							-.281	.227	.281
S1								.509	.081
ASV									-.263
<b>Mid-late</b>									
b		-.478	.862**	.577*	.769**	-.329	.643*	-.319	-.038
$S_d^2$			-.137	.087	-.242	.764**	.089	.577*	.467
CV				.709*	.775**	-.011	.687*	-.220	.082
SF					.758**	.132	.934**	.115	.143
R1						-.115	.780**	-.384	.066
R2							.137	.462	.478
S1								.071	.209
ASV									.016
<b>Late</b>									
b		.056	.566*	.741*	.552	.888**	.013	.350	.147
$S_d^2$			.811**	.252	.762**	-.007	.958**	.392	.832**
CV				.476	.874**	.378	.755**	.510	.671*
SF					.566*	.881**	.196	.398	.420
R1						.483	.727*	.482	.615*
R2							.007	.413	.216
S1								.440	.881**
ASV									.559

b = regression coefficient,  $S_d^2$  = deviation from regression, CV = coefficient of variation, SF = stability factor, R1 = range 1, R2 = range 2, W = Wricke's ecovalence, S1 = Mmean absolute rank difference, ASV = AMMI stability value

correlation was observed between W and  $S_d^2$  and ASV showed significant positive correlation with  $S_d^2$ , CV, R2 and W. Therefore, we integrate different stability parameters to predict genotypic adaptation in rice.

According to STI estimate seven genotype from each maturity group are found to be stable. The high yielding genotypes MTU 1001 of mid-late group and Mahanadi of late group are stable for each of the stability parameters and it may be supposed due to the involvement of multiple genes in controlling sensitivity to environmental

changes. The present study suggests that integration of several approaches of stability analysis is better than the use of a single approach in predicting genotypic adaptation.

## CONCLUSION

Integration of univariate and multivariate approaches in the present study indicate that the mid-early group genotypes Lalat and OR 2006-12, the mid-late group genotypes OR 1912-25, OR 2310-12 and MTU 1001 and the late group

TABLE 9. Estimates of grain yield (t ha<sup>-1</sup>) and STI value of rice genotypes

Genotype	Mean yield (t ha <sup>-1</sup> )	Yield rank	Stability index (STI)
<b>Mid-early group</b>			
1. OR 1739-47	3.604	7	5
2. OR 1916-19	3.495	10	5
3. OR 1929-4	3.524	8	8
4. OR 1976-11	3.763	5	2
5. OR 2006-12	3.772	4	5
6. OR 2168-1	3.507	9	5
7. OR 2172-7	3.782	3	0
8. OR 2200-5	3.787	2	3
9. Konark	3.687	6	3
10. Lalat	3.842	1	8
11. Bhoi	3.441	11	7
Average	3.655		4.63
<b>Mid-late group</b>			
1. OR 1681-11	4.130	8	5
2. OR 1912-25	4.745	1	8
3. OR 1914-8	4.084	9	7
4. OR 1964-8	4.241	7	3
5. OR 1967-15	4.011	10	5
6. OR 2156-15	4.305	4	4
7. OR 2310-12	4.266	6	6
8. Pratikshya	4.605	2	2
9. Gouri	3.960	12	6
10. Surendra	4.271	5	3
11. Gajapati	3.961	11	2
12. Kharavela	3.827	13	0
13. MTU 1001	4.408	3	9
Average	4.216		4.62
<b>Late group</b>			
1. OR 1885-16-34	3.215	12	4
2. OR 1898-2-15	3.702	10	8
3. OR 1898-3-16	4.394	2	6
4. OR 1901-14-32	4.445	1	7
5. OR 2001-1	4.072	7	5
6. OR 2109-2	4.299	3	7
7. OR 2119-13	4.146	6	3
8. Savitri	3.859	8	0
9. Salivahan	3.587	11	0
10. Mahanadi	4.150	5	9
11. Kanchan	3.726	9	0
12. Jagabandhu	4.265	4	8
Average	3.988		4.75

genotypes OR 1898-3-16, OR 1901-14-32, OR 2109-2, OR 2001-1, Mahanadi and Jagabandhu have wide adaptability.

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