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G × E Interaction of Mid-Late Rice Genotypes in LR and AMMI Model and Evaluation of Adaptability and Yield Stability

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Abstract

Multilocation yield trials of 13 mid-late (125—140 days) rice genotypes were conducted at Bhubaneswar, Chiplima, Jeypore and Ranital over 3 years 2003–2005, during *kharif* of season. G × E interaction analysis of yield data revealed highly significant differences among genotypes and environments and significant G × E interaction indicated differential performance of genotypes over environments. Considering mean and LR parameters b and S^2d jointly, 3 of the 7 higher yielding genotypes viz. OR 1912-25, MTU 1001 and OR 2310-12 showed stability of performance and all these genotypes exhibited wide adaptability over all environments. Stability assessment on the basis of parameters like CV, SF, R_1, R_2, W and ASV revealed that OR 1681-11, OR 1912-25, Gouri and MTU 1001 showed stability of performance according to 5 of the 6 parameters and OR 2156-15 and OR 2310-12 showed stability in 4 parameters. AMMI (additive main and multiplicative interaction) analysis showed differential performance of genotypes in the 4 locations. OR 1912-25 and Pratikshya, the two genotypes showing highest average yield, showed high G × L interaction-positive interaction at Chiplima and negative interaction at Jeypore. MTU 1001and OR 2156-15, which were the third and fourth highest yielder, showed negative interaction at Chiplima. AMMI-II predicted yield showed that OR 1912-25 and Pratikshya were high yielder and possessed broad adaptation to all locations and MTU 1001 would be more suitable for Jeypore and Ranital. The genotypes showing good adaptation to specific locations were OR 2156-15 for Bhubaneswar, OR 1964-8 for Chiplima and Surendra for Jeypore.

Key words : Rice, G × E interaction, LR model, AMMI model, Adaptability and stability.

Stability of yield performance of varieties is the most important prerequisite for improvement in crop production.Though more than 1000 rice (*Oryza sativa* L.) varieties have been released in India many of them have been out of cultivation within 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. Evaluation of interaction of genotypes with locations and other agro-ecological conditions would help in getting information on adaptability and stability of performance of genotypes. The Linear Regression model (1) is the most frequently used for analysis of genotype × environment interaction, adaptability and stability of performance of genotypes. Other workers have suggested use of parameters like coefficient of variation, stability factor, R_1 and R_2, Wricke's ecovalence and AMMI stability value as measures of stability. The AMMI (additive main and multiplicative interaction) model is considered to be a better model for analysis of G × E interaction in yield data of multilocation varietal trials (2). It not only gives estimate of total G × E interaction effect of each genotype but further partitions it into interaction effects due to individual environments. The present multilocation trial of 13 mid-late duration rice genotypes was conducted to analyze G × E interaction and evaluate the adaptability and stability of yield performance of the genotypes.

Methods

Multilocation yield trials of thirteen mid-late (125–140 days) rice genotypes were conducted at four different locations–Bhubaneswar, Chiplima, Jeypore and Ranital over 3 years during *kharif* of 2003–2005. The genotypes included seven pre-release varieties and six released varieties (Pratikshya, Gouri, Surendra, Gajapati, Kharavela and MTU 1001). Nursery sowing was done during last week of June to first week of July. All trials were laid out in randomized block design with three replications. In each trial, the plot size

Table 1. Pooled analysis of variance for grain yield of mid-late rice genotypes.

Source	df	MS	*F*
Genotypes (G)	12	83.19	10.57**
Environments (E)	11	900.88	114.50**
G × E	132	24.19	3.08**
E + G × E	143		
Environment (linear)	1	9909.73	483.94**
G × E (linear)	12	44.29	2.16*
Pooled deviation	130	20.48	2.60**
Pooled error	288	7.87	

was 2 m × 3 m and 25–30 days old seedlings were transplanted with 20 cm × 15 cm spacing. Fertilizers were applied at 80 kg N, 40 kg P_2O_5 and 40 kg K_2O per hectare. Normal cultural practices and plant protection measures were followed in each trial and data on net plot grain yield was recorded.

Grain yield data of the 12 environments were taken for G × E interaction analysis using the Linear Regression model (1) and adaptability and stability parameters of genotypes were estimated. Stability of yield performance of genotypes was also estimated using other like coefficient of variation CV (3), stability factor SF (4), R_1 and R_2 (5), Wricke's ecovalence W (6) and AMMI stability value ASV (7). The year component of the environment variables was eliminated by averaging over years and genotype × location interaction was analyzed by AMMI model (2) and the genotypes best adapted to each location were identified.

Results and Discussion

The genotypes showed significant differences in grain yield in all four locations during the 3 years. Average trial yield during 2003, 2004 and 2005 were 36.51, 30.25 and 35.29 q/ha at Bhubaneswar, 32.72, 39.50 and 56.96 q/ha at Chiplima, 51.36, 38.22 and 43.26 q/ha at Jeypore and 52.33, 43.18 and 46.49 q/ha at Ranital, respectively. Thus the 12 environments showed wide variation in yield ranging from 30.25 to 56.96 q/ha. Ranking of the genotypes on the basis of grain yield in different environments showed interaction of genotypes with environmental conditions. Analysis of variance for G × E interaction in LR model of Eberhart and Russell revealed significant differences among genotypes and environments (Table 1) and highly significant G × E interaction indicated differential response of the genotypes to environmental changes. Partitioning of E + G × E effects revealed that E (linear) component was highly significant and accounted for a major part of the total variation. Both G × E (linear) and pooled deviation components were significant, indicating that some genotypes had predictable linear response to environments, while others showed large deviation from linear response. There are many reports (8—12), to cite a few, on G × E interaction analysis of multilocation yield data in rice, using Eberhart and Russell's LR model. In all these studies, G × E interaction was significant indicating differential response of genotypes to changes in environment and some genotypes showed stable per-

Table 2. Stability parameters of mid-late rice genotypes for grain yield (q/ha) on linear regression model. LYE : Lowest yielding environment, HYE : Highest yielding environment.

	Genotype	Mean	a	b	SE (b)	r^3	DMS	S^2d	Predicted yield LYE	Predicted yield HYE
1.	OR 1681-11	41.30	12.59	0.58	0.18	59.11	24.46	16.59**	33.19	51.37
2.	OR 1912-25	47.45	12.61	0.83	0.14	78.62	14.16	6.29	37.59	59.66
3.	OR 1914-8	40.84	-4.86	1.08	0.13	88.07	12.13	4.26	27.93	56.88
4.	OR 1964-8	42.41	-0.10	1.01	0.19	73.77	27.56	19.69**	30.39	57.31
5.	OR 1967-15	40.11	-9.24	1.17	0.14	86.94	15.68	7.81*	26.16	57.41
6.	OR 2156-15	43.05	18.18	0.59	0.18	52.97	23.55	15.68**	36.02	51.78
7.	OR 2310-12	42.66	1.87	0.97	0.14	83.73	13.87	6.00	31.12	56.95
8.	Pratikshya	46.05	6.79	0.93	0.25	58.90	46.13	38.26**	34.95	59.82
9.	Gouri	39.60	0.37	0.93	0.16	76.37	20.42	12.55**	28.50	53.34
10.	Surendra	42.71	3.42	0.93	0.19	71.12	26.88	19.01**	31.61	56.50
11.	Gajapati	39.61	-23.34	1.49	0.13	93.24	12.32	4.45	21.83	61.71
12.	Kharavela	38.27	17.05	1.31	0.18	84.83	23.46	15.59**	22.64	57.68
13.	MTU 1001	44.08	-1.22	1.08	0.09	94.01	5.61	-2.26	31.30	60.01
	Average	42.16	-	1.00	-	-	20.48	12.61	-	-

Table 3. Estimates of different stability parameters (CV, SF, R_1, R_2, W and ASV) for grain yield (q/ha) of mid-late rice genotypes.

Genotype	Mean	CV	SF	R_1	R_2	W	ASV
1. OR 1681-11	41.30	17.9	1.60	24.2	322.1	17.6	0.60
2. OR 1912-25	47.45	16.4	1.61	25.9	164.5	22.2	1.57
3. OR 1914-8	40.84	23.5	1.67	32.9	126.6	22.5	0.65
4. OR 1964-8	42.41	23.0	1.92	25.7	275.6	25.7	1.55
5. OR 1967-15	40.11	26.1	1.85	32.5	178.9	27.2	0.94
6. OR 2156-15	43.05	15.7	1.52	23.4	363.7	15.0	1.31
7. OR 2310-12	42.66	20.6	1.93	27.7	139.5	27.7	0.56
8. Pratikshya	46.05	21.9	2.00	31.8	464.9	31.8	2.61
9. Gouri	39.60	22.4	2.06	29.0	207.9	24.9	0.90
10. Surendra	42.71	21.5	2.17	34.1	272.3	34.1	1.05
11. Gajapati	39.61	32.5	2.59	40.7	308.4	40.6	1.26
12. Kharavela	38.27	31.0	2.17	42.6	308.8	34.1	1.50
13. MTU 1001	44.08	20.9	1.67	29.1	60.3	24.0	0.92
Average	42.16	22.6	1.90	30.7	245.7	26.7	1.19

formance over the range of environments, while many showed unstable performance due to high G × E interaction.

Stability Parameters of Genotypes on Linear Regression Model

Stability parameters like regression coefficient (b), deviation from regression (S^2d) and coefficient of determination (r^2) of genotypes were estimated following Eberhart and Russell's LR model (Table 2).In this model, genotypes giving b-value close to unity are considered to be adapted to all environments, while those showing b-value greater than or less than unity would show specific adaptation to rich or poor environment, respectively. The genotypes showing low and non-significant S^2d and high r^2 values are considered to possess stability of performance over the range of environmental conditions.

Average yield of the 13 genotypes ranged from 38.27 to 47.45 q/ha with grand mean of 42.16 q/ha. The genotypes OR 1912-25, Pratikshya, MTU 1001, OR 2156-15, Surendra, OR 2310-12 and OR 1964-8 gave above average yield. The intercept (a) values ranged from –23.34 to 18.18. The genotypes OR 2156-15, OR 1681-11 and OR 1912-25 giving high positive 'a'-values would be better adapted to poorer environments, while Gajapati and Kharavela giving high negative 'a'-values would be poorly adapted to low yielding environments. Regression coefficients (b-values) of the genotypes varied from 0.59 to 1.49. The coefficient of determination (r^2) of regression was more than 70% for 10 of the 13 genotypes, indicating good fit of the response of these genotypes to linear regression model. The genotypes Gajapati and Kharavela had b-values greater than unity (> 1.2), indicating their specific adaptation to better environments and OR 1681-11 and OR 2156-15 had b-values less than unity (< 0.8) indicating their specific adaptation to poorer environments. The remaining nine genotypes showed

Table 4. AMMI ANOVA of mid-late rice genotypes for yield (q/ha).

Source	df	SS	% of G-L SS	MS	*F*	% of G × L interaction
Genotype (G)	12	332.73	17.71	27.73	9.81**	
Location (L)	3	1286.19	68.45	428.73	151.62**	
G × L	36	260.07	13.84	7.22	2.56**	
IPCA 1	14	107.88	5.74	7.71**	2.73*	41.48
IPCA 2	12	89.17	4.75	7.43**	2.63*	34.29
Residual	10	63.07	3.36	6.30	2.24*	24.23
Error	288	814.38		2.83		

Table 5. Interaction effects of mid-late rice genotypes for yield (q/ha) in different locations.

Genotype	Location Bhubaneswar	Chiplima	Jeypore	Ranital
1. OR 1681-11	1.89	-0.65	0.93	-2.17
2. OR 1912-25	-0.06	2.87	-3.55	0.74
3. OR 1914-8	0.42	-1.84	0.68	0.74
4. OR 1964-8	-4.09	2.69	0.14	1.26
5. OR 1967-15	1.05	-2.81	-0.09	1.86
6. OR 2156-15	2.54	-2.85	-1.18	1.49
7. OR 2310-12	2.62	0.16	0.03	-2.81
8. Pratikshya	1.10	4.13	-6.28	1.05
9. Gouri	1.14	-2.23	0.99	0.10
10. Surendra	-0.81	3.04	1.98	-4.21
11. Gajapati	-4.21	-0.11	1.70	2.62
12. Kharavela	-2.55	-0.03	3.63	-1.04
13. MTU 1001	0.96	-2.36	1.02	0.38

Table 6. Predicted yield (q/ha) of mid-late rice genotypes in different locations in AMMI II model.

Genotype	Location Bhubaneswar	Chiplima	Jeypore	Ranital
1. OR 1681-11	33.92	40.85	43.99	46.44
2. OR 1912-25	39.36	51.33	46.08	53.04
3. OR 1914-8	33.43	40.18	43.79	45.95
4. OR 1964-8	30.79	46.55	44.96	47.35
5. OR 1967-15	33.75	38.84	42.50	45.34
6. OR 2156-15	37.94	41.53	44.23	48.49
7. OR 2310-12	35.81	42.65	44.22	47.97
8. Pratikshya	39.09	51.15	41.93	52.03
9. Gouri	32.62	38.33	42.74	44.71
10. Surendra	32.01	45.22	46.01	47.60
11. Gajapati	28.55	41.52	44.03	44.35
12. Kharavela	27.32	38.97	43.91	42.87
13. MTU 1001	37.05	42.79	47.32	49.18

unity regression (b = 0.8—1.2) indicating their adaptation to all environments.

The deviation from regression (S^2d) of the genotypes ranged from –2.26 to 38.26. S^2d values of genotypes OR 1912-25, OR 1914-8, OR 2310-12, Gajapati and MTU 1001 were not significantly greater than zero, indicating stability of performance of these genotypes over environments. S^2d of the remaining eight genotypes were significantly greater than zero, indicating lack of stability in performance. Considering mean, b and S^2d values of the genotypes jointly, three of the seven genotypes i.e., OR 1912-25, OR 2310-12 and MTU 1001 giving above average yield showed stability of performance and all the three genotypes exhibited wide adaptability over all environments. Predicted yield of the genotypes on LR model in the lowest- and highest- yielding environment (LYE and HYE) showed that OR 1912-25, OR 2156-5 and Pratikshya would show better performance in poorer environments, while Gajapati, MTU 1001 and OR 1912-25 would perform better in rich environments.

Stability Parameters of Genotypes on Other Models

Stability of performance of genotypes was also assessed by six other parameters, i.e. CV, SF, R_1, R_2, W and ASV. Genotypes showing lower values for these parameters are considered to possess stability of performance. The 13 genotypes showed wide variation in estimates of these stability parameters (Table 3). A genotype showing below-average value for a parameter was classified as stable genotype. On this basis, the genotypes OR 1681-11, OR 1912-25, Gouri and MTU 1001 showed stability of performance according to five of the six parameters and OR 2156-15 (6) and OR 2310-12 showed stability in four parameters. The remaining seven genotypes showed poor stability of performance according to most of these parameters. OR 1912-25, MTU 1001 and OR 2310-12 were also found to be stable on the basis of S^2d of LR model. So, estimating the parameters like CV, SF, R_1, R_2, W and ASV would be a useful supplement to assessing stability by LR model.

Genotype-Location Interaction on AMMI Model

In the LR model of Eberhart and Russell, a stable genotype should have low deviation from regression (S^2d). So many genotypes having high yield potential often get rejected due to unstable performance over the range of environments. A genotype showing high positive interaction at certain environments and negative interaction at some other environments is likely to show high S^2d and would be considered as unstable. The LR model does not provide for critical analysis of interaction of genotypes in specific environments and does not help in identifying promising genotypes to take advantage of their high positive interaction with specific locations or specific agro-ecological or agro-management conditions.

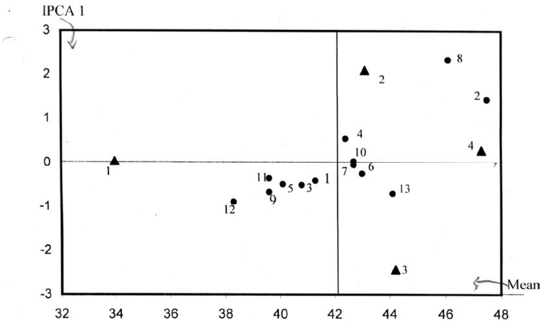

Figure 1. AMMI 1 biplot of main effects and G × L interaction of mid-late rice genotypes. Location (solid triangle) : 1. Bhubaneswar, 2. Chiplima, 3. Jeypore. 4. Ranital. Genotype (solid circle) : 1. OR 1681-11, 2. OR 1912-25, 3. OR 1914-8, 4. OR 1964-8, 5. OR 1967-15, 6. OR 2156-15, 7. OR 2310-12, 8. Pratikshya, 9. Gouri, 10. Surendra, 11. Gajapati, 12. Kharavela, 13. MTU 1001.

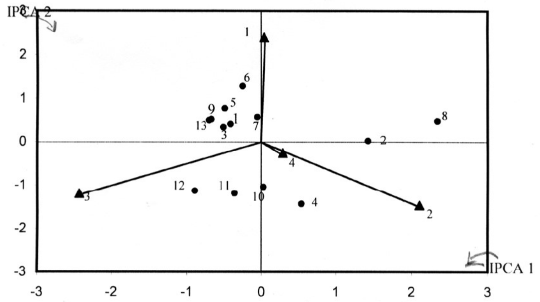

Figure 2. AMMI II biplot of G × L interaction of mid-late rice genotypes.

AMMI analysis gives estimate of total G × E interaction effect of each genotype and also partitions it into effects due to individual environments. Low G × E interaction of a genotype indicates stability of the genotype over the range of environments. A genotype showing high positive interaction in an environment obviously has the ability to exploit the agro-ecological or agro-management conditions of specific environment and is therefore best suited for that environment. AMMI analysis permits estimation of interaction effect of a genotype in each location and it helps to identify genotypes best suited for specific locations.

The AMMI analysis of variance of G-L data on yield showed that all three components–genotype (G) and location (L) and G × L interaction, were significant (Table 4). The main effects of the genotypes and locations accounted for 17.71 and 68.45%, respectively and G × L interaction accounted for 13.84% of the total variation in G-L data. The G × L interaction of the genotypes in different locations (Table 5) showed that the genotypes OR 2156-15 and OR 2310-12 had high positive interaction and Gajapati, OR 1964-8 and Kharavela had high negative interaction with environmental conditions of Bhubaneswar, while the remaining eight genotypes had low to moderate interaction. At Chiplima, the genotypes Pratikshya, Surendra, OR 1912-25 and OR 1964-8 showed high positive and OR 1967-15, OR 2156-15, MTU 1001and Gouri had high negative interaction. The interactions of most genotypes at Jeypore were small. However, Kharavela showed high positive and Pratikshya and OR 1912-25 had high negative interaction at Jeypore. At Ranital location, Gajapati had positive interaction while Surendra, OR 2310-12 and OR 1681-11 had negative interactions.

Using AMMI analysis, the G × L interaction for grain yield was further partitioned into IPCA 1, IPCA 2 and residual effects and both the IPCA components were significant IPCA 1and IPCA 2 accounted for 41.48 and 34.29% respectively, of the G × L interaction sum of squares (Table 4). The most powerful interpretive tool in analysis of G × L interaction by AMMI model is biplot analyses. It permits easy visulization of difference in interaction effects. In AMMI I biplot, the IPCA I scores of genotypes and locations are plotted against their respective means and in AMMI II biplot, the IPCA 1 and IPCA 2 scores of genotype and location are plotted against each other AMMI I biplot for grain yield of the 13 genotypes at four locations is presented in Figure 1. The main effects (genotypes and locations) accounted for 86.16% and IPCAI accounted for 5.74% of total variation in G × L data and so the AMMI I biplot gave a model fit of 91.90%.

The scatter of genotypes points in AMMI I biplot (Fig. 1) showed that OR 1964-8, Surendra, OR 2310-12 and OR 2156-15 formed one adaptive group. Similarly, Gajapati, Gouri and OR 1967-15 ; OR 1914-8 and OR 1681-11 formed two other adaptive groups. The genotypes within a group do not differ in main effects and interactions, but the three groups differ from each other both in main effect and/or interaction. The remaining four genotypes exhibited wide variation among them in main effects and in interactions and formed three adaptive groups. The genotypes OR 1912-25 and Pratikshya had quite high main effects and also positive interaction. Among the locations, Bhubaneswar had the lowest main effect, while Ranital had the highest main effect and both the locations showed negligible interaction. Chiplima had moderate main effect and large positive interaction, while Jeypore had moderate main effect and large negative interaction.

Figure 2 gives the AMMI-II biplot for yield. The IPCA 1 and IPCA 2 accounted for 41.48 and 34.29% of the G × L interaction and thus the biplot gave a model fit of 75.77%. Scatter of genotypes in the biplot indicated that genotypes OR 1681-11, OR 1914-8, OR 2310-12, MTU 1001, Gouri, OR 1967-15 and OR 2156-15 grouped together and these genotypes had small interaction effects. The genotypes Kharavela, Gajapati, Surendra and OR 1964-8 had similar negative IPCA 2 effects but differed much in the IPCA 1 effects. The genotypes OR 1912-25 and Pratikshya showed high positive IPCA 1effects and small IPCA 2 effects. On the basis of length of spokes of locations, it was observed that interactive forces at Chiplima and Jeypore locations were strong, while it was moderate at Bhubaneswar and lowest at Ranital.

Interaction of geotypes with specific locations was judged by the projection (perpendicular) of genotype points onto location lines (Fig.2). On this basis, the genotypes Kharavela, Gajapati, Surendra and OR 1964-8 showed high positive interaction at Chiplima and Ranital and high negative interaction at Jeypore. The remaining ten genotypes showed low to moderate positive interactions at these three locations. Reports on AMMI analysis of multilocation grain yield data in rice (12—15) showed G × E interaction and the reports stressed the usefulness of AMMI analysis for selection of genotypes for specific locations/environments.

AMMI-Predicted Performance and Adaptation of Genotypes

To identify better genotypes for specific locations, predicted yield of the genotypes in different locations were estimated using. AMMI II model taking into taking into account the main effects of genotypes and locations and interaction effect of IPCA 1 and IPCA 2. AMMI II gave model fit of 96.65% for grain yield (Table 6). The range of variation of AMMI-predicted yield of the genotypes at Bhubaneswar, Chiplima, Jeypore and Ranital locations were 27.32 to 39.36, 38.33 to 51.33, 41.93 to 47.32 and 42.87 to 53.04 q/ha, respectively. Three top ranking genotypes in each location were : Bhubaneswar : OR 1912-25, Pratikshya and OR 2156-15 ; Chiplima : OR 1912-25, Pratikshya and OR 1964-8 ; Jeypore : MTU 1001, OR 1912-25 and Surendra ; Ranital : OR 1912-25, Pratikshya and MTU 1001.

The genotype OR 1912-25 ranked among the top three in all four locations–first at Bhubaneswar, Chiplima and Ranital and second at Jeypore. Pratikshya ranked second on 3 locations and MTU 1001 ranked among top three in two locations. OR 2156-15, OR 1964-8 and Surendra ranked among the top three in one location each. Thus, OR 1912-25 and Pratikshya had high yield and possessed broad adaptation to most locations. Genotypes showing good adaptation to specific locations were MTU 1001 for Jeypore and Ranital, OR 2156-15 for Bhubaneswar, OR 1964-8 for Chiplima and Surendra for Jeypore.

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