Genotype x Environment Interaction and Grain Yield Stability Analysis of Rice (*Oryza sativa* L.)

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Abstract

Background: Upland rice has been introduced in to Ethiopia recently and widely produced in different parts of the country particularly after it was adopted as the "millennium crop" in 2000. However, limited availability of improved varieties hampers production of the crop.

Objective: To determine the nature and magnitude of genotype x environment interaction and to identify stable high yielding, blast, and brown spot diseases tolerant varieties for upland rice-growing environments.

Materials and Methods: The experiment was conducted at Gutin and Bako (2010–2011) and Boneya and Chewaka districts in the 2011 main cropping seasons. Eleven rice genotypes [WAB272-B-B-8-H1, YIN LU20, IRGA370-38-1-1-F-B1-1, CNAX3031-15-2-1-1, WAB502-8-5-1, WABC165(IAC165), WAB450-11-11P31-HB, WAB376-B-10-H3 and WAB368-B-1-H2-HB] including standard checks (IRAT 355 and SUPERICA 1) were laid out in a randomized complete block design with three replications. Grain yield data were collected and analyzed.

Results: The results showed significant variations among the genotypes in grain yield. The mean grain yield obtained over four environments ranged from 2.36 tons ha⁻¹ (IRAT 355) to 4.23 tons ha⁻¹ for Chewaka variety (YIN LU20) and SUPERICA-1 produced 2.54 tons ha⁻¹. Regression analysis based on Eberhart and Russell Model showed that Chewaka variety and WABC165 (IAC165) had mean grain yield that were higher than the average for all genotypes. Regression coefficient (b_i) did not differ significantly from unity and the squared deviations (s²di) approached zero. On the other hand, IRGA370-38-1-1-F-B1-1, WAB450-11-11P31-HB and WAB376-B-10-H3 had regression coefficient (b_i) differ significantly from unity showing that these genotypes are sensitive to different environmental conditions and tend to give higher yield at favorable environments.

Conclusion: Among the tested genotypes, YIN LU20 and CNAX3031-15-2-1-1 were stable and high yielding and proposed as candidate varieties. In addition, genotype YIN LU20 was preferred by farmers for its stability, high seed yield and resistance to rice blast and brown spot diseases and released for cultivation in western Ethiopia and other areas in the country with similar agro-ecology, named as Chewaka variety.

Keywords: AMMI; Genotype; Grain yield; Regression Coefficient; Stability; Upland rice

1. Introduction

Rice (*Oryza sativa* L.) is an important cereal crop grown for its diverse uses in Asia, Africa, and Australia (Dogara and Jumare, 2014). The crop ranked third most important cereal crop in the world next to maize (*Zea mays* L.) and wheat (*Triticum aestivum* L.) based on the total grain

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production (FAO, 2017). It is staple food for more than half of the world's population (Muthayya *et al.*, 2014). The rapid increase of the world population also dictates to produce greater quantities of cereal crops such as rice, wheat and maize (Kang and Priyadarshan, 2007). Rice is recently (in 1970s) introduced crop to Ethiopia and now

*Corresponding author: germame2004@gmail.com ©Haramaya University, 2022 ISSN 1993-8195 (Online), ISSN 1992-0407(Print) it has been grown in different parts of the country (Tariku *et al.*, 2013, MoARD, 2010). It ranks second after maize in terms of productivity among other cereal crops, which play a significant role for food security in Ethiopia. The national average productivity of rice 2.8 tons ha⁻¹ and it is very low as compared to global mean productivity of 4.4 tons ha⁻¹ (Dessie *et al.*, 2018). Rice production and productivity is affected by various factors such as lack of improved varieties, diseases, pre and postharvest machineries (MoARD, 2010).

Nowadays, the crop has received attention from farmers and investors due to its suitability to make into pancake Ethiopian bread locally called 'Injera'. Among suitable areas to grow upland rice, Western part of Oromia, which has suitable climatic and soil conditions. Breeders evaluate different genotypes in order to identify high yielding, widely adaptable and stable over the testing environments. Genotypes exhibiting fluctuating yield when grown in different environments or agro-climatic zones complicate demonstrating the superiority of a particular variety. Multi-environment yield trials are crucial to identify adaptable high yielding cultivars and discover sites that best represent the target environment. The performance of a genotype is dependent on the genetic capacity of the variety, the environment where the variety is grown, and the interaction between the genotype and the environment (Yan, 2001; Yan and Hunt, 2001).

Genotypes x environment interactions occur when the responses of two genotypes to different levels of environmental factors fail to be parallel (Allard and Bradshaw, 1964). The regression model proposed by Eberhart and Russell (1966) allows for the computation of a complete analysis of variance with individual stability estimates and departure from linearity of a regression line. The model considers a stable variety as the one with a high mean yield, $b_i=1$ and $s^2d_i = 0$. Similarly, genotypes with a high s²d_i deviate significantly from linearity and have a less predictable response for the given environments (Eberhart and Russell, 1966). Additive Main effects and Multiplication Interaction (AMMI) model, involves correlation or regression analysis that also relates the genotypic and environmental score derived from a principal component analysis of the genotype x environment interaction matrix to genotypic and environmental covariates (Zobel et al., 1988).

Upland rice has been introduced recently to Ethiopia, now it is widely produced in different parts of the country including Western Oromia. However, limited availability of improved varieties hampers production of the crop. Rice genotypes were evaluated and developed in the northern parts of the country (Lakew *et al.*, 2017; Lakew *et al.*, 2014; Tariku *et al.*, 2013; Zewdu *et al.*, 2020). However, no study was conducted on stability of rice genotypes in western Oromia. Therefore, this study was done to determine the nature and magnitude of genotype x environment interaction and identify superior and stable upland rice genotypes for the test environments and similar agro-ecologies.

2. Materials and Methods

2.1. Description of the Study Areas

The study was conducted at Gutin [1200–1799 meter above sea level (m.a.s.l.)] and Bako (1650 m.a.s.l) during the 2010 and 2011 cropping seasons, and Boyena (1300 m.a.s.l) and Chewaka (900 to 1400 m.a.s.l) in the 2011 main cropping season. The study was executed under rainfed upland conditions.

2.2. Experimental Materials, Design and Procedures

Eleven rice genotypes including standard checks (IRAT 355 and SUPERICA 1) were used in the study (Table 1). At all locations, the experiment was laid out as a randomized complete block design with three replications. Seeds of each genotype were sown in six rows of 5 m long with 0.2 m spacing between rows and 1 m between blocks. A seed rate of 80 kg ha⁻¹ was used. Fertilizer rate of 100 kg DAP ha-1 (46 kg P2O5 ha-1) and 50 kg Urea ha⁻¹ (23 kg N ha⁻¹) were used. All rate of the DAP fertilizer was applied at planting; however, Urea was applied in split twice, i.e., $\frac{1}{2}$ at planting and the other $\frac{1}{2}$ at knee height (panicle initiation) growth stage of the crop. Management practices were done according to recommendations. Plants in the four middle rows were harvested and grain yield was adjusted at 12% seed moisture content before weighing and data processing for analysis.

S/N	Genotype name	Origin
1	WAB272-B-B-8-H1	AfricaRice
2	YIN LU20	IRRI
3	IRGA370-38-1-1-F-B1-1	IRRI
4	CNAX3031-15-2-1-1	Unknown
5	WAB502-8-5-1	AfricaRice
6	WABC165(IAC165)	AfricaRice
7	WAB450-11-11P31-HB	AfricaRice
8	WAB376-B-10-H3	AfricaRice
9	WAB368-B-1-H2-HB	AfricaRice
10	IRAT-335	Standard check
11	SUPERICA-1	Standard check

Table 1. Rice genotypes used in the study.

2.3. Data Analysis

The combined data across locations and years were used to compute analysis of variance (ANOVA) using R (2016) statistical software. The responses of the genotypes were evaluated based regression coefficients (Eberhart and Russel, 1966) and Additive Main-effect and Multiplicative Interaction (AMMI) models in Agrobase software (Agrobase, 2000). A linear model proposed by Eberhart and Russell (1966) is:

 $Y_{ij} = \mu_{i} + b_i I_j + S^2 d_{ij}$

Where, Y_{ij} is the mean performance of ith variety (I = 1, 2, ..., n) environment; μ_i is the mean of ith variety over all the environments; b_i is the regression coefficient which measures the response of ith variety to varying environments; S^2d_{ij} is the deviation from regression of ith variety in the jth environment; and I_j is the environmental index of jth environment.

AMMI model (Gauch and Zobel, 1996):

$$Y_{ger} = \mu + \alpha_g + \beta_e + \sum n \, \lambda_n \gamma_{gn} \delta_{en} + \rho_{ge} + \varepsilon_{ger}$$

Where, Y_{ger} is the observed yield of genotype g in environment e for replication r; Additive parameters: μ the grand mean; α_g the deviation of genotype g from the grand mean; and β_e the deviation of environment e; the multiplicative parameters: λ_n the singular value for interaction principal component axis (IPCA) n, γ_{gn} the genotype eigenvector for axis n, and δ_{en} the environment eigenvector; ρ_{ge} PCA residuals (noise portion) and

 \mathcal{E}_{ger} error term.

3. Results and Discussion

3.1. Analysis of Variance

The combined analysis of variance for the two seasons and four locations was performed following Shapiro-Wilk normality test. The analysis of variance revealed that the main effects, genotype (G), location (L), and year (Y) showed significant (P ≤ 0.001) differences for grain yield (Table 2). The G x L and G x Y also showed highly significant ($P \le 0.01$) differences, whereas G x L x Y and L x Y showed significant and non-significant differences, respectively. Highly significant mean squares due to G x L interaction revealed that the genotypes interacted considerably with environmental conditions. Similar trends were reported in previous studies by Tariku et al. (2013), Waghmode and Mehta (2011), Akter et al. (2015), Oladosu et al. (2017), Zewdu et al. (2020) for rice. Significant differences were observed for grain yield among the test genotypes across the six environments. This suggests the presence of genetic variability among the genotypes in the tested locations. The mean grain yield over six environments ranged from 2.36 tons ha-1 (IRAT 355) to 4.23 tons ha-1 (YIN LU20) with a grand mean of 2.28 tons ha-1 and the standard check (SUPERICA-1) gave 2.54 tons ha⁻¹ (Table 3).

Source of variations	Degrees of freedom	Mean squares	
Replication	2	5.08***	
Genotype(G)	10	4.90***	
Location(L)	3	37.00***	
Year(Y)	1	13.78***	
GxL	30	1.19**	
GxY	10	1.71**	
LxY	1	0.35	
GxLxY	10	1.54*	
Residuals	120	0.63	

Table 2. Combined analysis of variance for eleven upland rice varieties evaluated in western Ethiopia.

Note: ***, ** and * refer to statistical significance at P < 0.0001, P < 0.001 and P < 0.05 probability level, respectively.

Table 3. Mean seed yield (ton ha-1) of rice genotypes across six environments.

S/N	Genotype	Mean seed yield in tons ha ⁻¹					Mean	
		2010		2011			_	
		Gutin	Bako	Boneya	Bako	Gutin	Chewaka	
1	WAB272-B-B-8-H1	2.85	1.72	3.70	3.72	2.70	2.84	2.92
2	YIN LU20	2.67	2.18	4.56	5.89	4.88	5.17	4.23
3	IRGA370-38-1-1-F-B1-1	3.66	1.78	4.50	1.82	5.71	3.53	3.50
4	CNAX3031-15-2-1-1	3.30	1.74	4.18	3.40	4.61	3.76	3.50
5	WAB502-8-5-1	3.42	2.41	3.25	2.82	5.17	2.99	3.34
6	WABC165(IAC165)	3.23	1.94	4.47	2.27	4.26	3.26	3.24
7	WAB450-11-11P31-HB	2.96	1.94	4.21	2.20	5.40	2.88	3.27
8	WAB376-B-10-H3	2.93	2.10	4.80	2.76	5.02	3.56	3.53
9	WAB368-B-1-H2-HB	2.43	1.55	3.81	3.10	3.39	2.69	2.83
10	IRAT-335	1.73	1.29	3.75	2.44	2.79	2.16	2.36
11	SUPERICA-1	2.50	1.74	3.72	2.46	2.50	2.29	2.54
	MEAN	2.88	1.85	4.09	2.99	4.22	3.19	3.20
	LSD	0.902	0.2383	0.5478	0.7016	0.7968	0.4866	0.6890

Note: *LSD* = *least significant difference*.

3.2. Regression Analysis3.2.1. Eberhart and Russell model

Mean square due to genotypes was found to be significant (P < 0.01) (Table 4). Non-significance of genotypes x environments (linear) showed that there were no differences in yield performance among the genotypes under the different environments. The mean performance, regression coefficient (b_i) and squared deviations (s²d_i) from regression values are presented in Table 5. Genotypes YIN LU20 and WABC165(IAC165) showed mean yield higher than average, regression coefficient (b_i) did not differ significantly from unity and deviation from regression (s²d_i) approaching to zero. This

suggests these genotypes are stable and widely adaptable to the six environments. Genotypes, IRGA370-38-1-1-F-B1-1, WAB450-11-11P31-HB and WAB376-B-10-H3, had b_i value significantly different from unity showing that these genotypes are sensitive to change in environment and tend to give high yield at favorable environment. The results consistent with the earlier reports on rice (Panwar *et al.*, 2008; Kumar *et al.*, 2010; Bose *et al.*, 2012; Patel *et al.*, 2015; Satoto *et al.*, 2016; Shrestha *et al.*, 2020a; Shrestha *et al.*, 2020b)

Source of variation	DF	Mean squares	
Total	43		
Genotype	10	1.22**	
Environment + Genotype x Environment	33	0.74	
Environment in linear	1	16.13	
Genotype x Environment (linear)	10	0.33	
Pooled deviation	22	0.21	
Residual	88	0.61	

Table 4. Analysis of variance for grain yield using Eberhart-Russel Regression model.

Note: ** = Significant level at P < 0.001 probability level.

Table 5. Stability analysis for grain yield of rice genotypes grown across six environments in Western Oromia.

Genotypes	Regression slope	Deviation from linearity	Mean grain
	bi	(S^2d_i)	yield (tons ha ⁻¹)
WAB 272-B-B-8-H1	0.5113	0.1741	2.92
YIN LU20	1.0190	1.4531	4.23
IRGA370-38-1-1-F-B1-1	1.5212	0.4665	3.50
CNAX3031-15-2-1-1	1.1060	-0.1963	3.50
WAB502-8-5-1	0.8256	0.2445	3.34
WABC165(IAC165)	1.0798	-0.0731	3.24
WAB450-11-11P31-HB	1.3534	0.1459	3.27
WAB376-B-10-H3	1.3007	-0.1594	3.53
WAB368-B-1-H2-HB	0.8543	-0.1652	2.83
IRAT335	0.8707	-0.0569	2.36
SUPERICA-1	0.5580	-0.0341	2.54
Mean			3.20

Note: *Standard error of beta* = 0.3365.

3.2.2. Additive main effects and multiplicative interaction (AMMI) model

Analysis of variance revealed significant (P<0.01) differences among environments, genotypes, and genotype x environment. These results are in agreement with the findings of Nassir and Ariyo (2011), Tariku *et al.* (2013), Islam *et al.* (2020), Zewdu *et al.* (2020) for rice at different locations. Interaction principal component analysis (IPCA) 1 and (IPCA) 2 showed significant (P < 0.01) differences, whereas the remaining IPCAs were not significant (Table 6). The percentage of G x E interaction explained by IPCA 1 was 64.55% of the G x E interaction sum of squares. Since IPCA 1 (at P \leq 0.01) axis was significant and AMMI analysis was performed to identify stable genotypes. The AMMI analysis result revealed that

CNAX3031-15-2-1-1 was the most stable genotype having IPCA score closer to zero (Table 7 and Figure 1). However, YIN LU20, IRGA370-38-1-1-F-B1-1 and WAB450-11-11P31-HB with IPCA score deviate from zero are suitable for specific adaptation. In agreement with the current finding Yan *et al.* (2007), Dewi *et al.* (2014), and Sharifi *et al.* (2017) explained the importance of AMMI and Biplots in identification of stable varieties. Environments such as Gutin, Boneya and Chewaka, produced higher environmental mean yield than the others. This indicates that the varieties performed well in those environments due to proper agronomic practices and favorable environmental condition.

Source of variation	DF	Mean squares	% G x E interaction explained
Total	197	·	
Environments	5	24.997**	
Reps within Env.	12	2.422	
Genotype	10	4.908**	
Genotype x Env.	50	1.361**	
IPCA 1	14	3.138**	64.55
IPCA2	12	1.263**	22.26
Residual	120	0.634	

Table 6. Analysis of variance for Additive Main effects and Multiple Interaction (AMMI).

Note: Grand mean = 3.204; $R^2 = 0.7810$; CV (%) = 24.84; Reps = Replications; and Env. = Environment. ** = Significant level at P < 0.01 probability level.

Table 7. IPCA1 Scores of genotypes and environments.

Designation of genotypes	Genotype	IPCA 1 score	Mean grain yield (tons ha ⁻¹)
A	WAB 272-B-B-8-H1	0.7227	2.92
В	YIN LU20	1.0929	4.23
С	IRGA370-38-1-1-F-B1-1	-0.9768	3.50
D	CNAX3031-15-2-1-1	0.0345	3.50
E	WAB502-8-5-1	-0.4173	3.34
F	WABC165(IAC165)	-0.3407	3.24
G	WAB450-11-11P31-HB	-0.6955	3.27
Н	WAB376-B-10-H3	-0.3265	3.53
Ι	WAB368-B-1-H2-HB	0.3187	2.83
J	IRAT335	0.2937	2.36
K	SUPERICA-1	0.2944	2.54
Environments			
А	Gutin2010	-0.4856	2.88
В	Boneya2011	-0.1066	4.09
С	Bako2010	-0.0575	1.85
D	Bako2011	1.4795	2.99
E	Gutin2011	-1.1372	4.22
F	Chewaka2011	0.3073	3.19

Note: *IPCA* = *Interaction principal component analysis*.

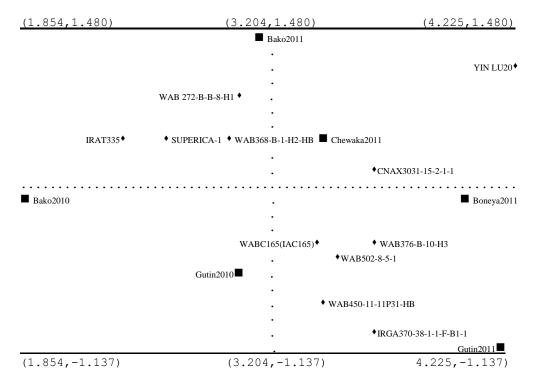


Figure 1. Biplot with abscissa (X-axis) plotting means from 1.854 to 4.225 and with ordinate (Y-axis) plotting IPCA1 from -1.137 to 1.480.

4. Conclusions

The results of this study have demonstrated that, according to Eberhart and Russell Model (regression analysis), genotypes YIN LU20 and WABC165 (IAC165) were found to be stable and widely adaptable. In addition, genotype YIN LU20 was found to be a high yielder in most locations. The regression analysis and AMMI models revealed that CNAX3031-15-2-1-1 was the most stable genotype. However, genotypes IRGA370-38-1-1-F-B1-1 and WAB450-11-11P31-HB with IPCA scores deviating from zero are suitable for adaptation to specific locations and sensitive to change of environmental conditions. However, genotypes YIN LU20 and CNAX3031-15-2-1-1 were found to be stable and high yielding and proposed as candidate varieties. Accordingly, YIN LU20, which was finally named as Chewaka variety was selected by farmers for its high seed yield, stability, and resistance to blast and brown spot diseases and therefore, officially released for production in the test environment and areas in the country with similar agroecology.

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