

Yield Stability and Genotype by Environment Interaction of Fifteen Rice (*Oryza Sativa* L) Genotypes Evaluated under Rainfed and Irrigated Conditions in Northern Ghana

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Abstract

In order to determine stable rice genotypes (*Oryza Sativa* L.) with high grain yield through a single parameter, field experiment was conducted using fifteen rice genotypes in two different conditions (irrigated and rainfed) in a complete randomized block design with three replications across four locations within two rice producing hubs in Northern Ghana; the Savelugu hub in the Northern Region and the Navrongo hub in the Upper East Region. Combined analysis of variance showed significant differences for the interaction between the genotypes and the environments, indicating the possibility of selecting stable genotypes. The results of the additive main effects and multiplicative interaction analysis revealed that 12.31% of variability was justified by the interaction between the genotype and the environment. The scores of the principal interaction components showed high variability for the environments relative to the variety effects. The study identified genotypes *Perfume (short)*, *Basmati 370-1*, genotypes *GH1837*, *Good and new (JP)* and genotype *Perfume (short)* as stable entries. The genotypes *Perfume (short)*, *GH1837*, *Basmati 370-1*, and *Good and new (JP)* were observed to be stable with high grain yield across both rainfed and irrigated conditions.

Keywords

Genotype, Rank Sum, Rice (*Oryza sativa* L.), Yield Stability Index

INTRODUCTION

Rice is one of the main sources of food in the world, and its increased demand is expected to enhance production in many parts of Asia, Africa and Latin America [20]. It is the main food for more than 2.5 billion people of the world, and it covers 9 percent of the earth's arable land. It supplies 21 percent of global human per capita energy and 15 percent of per capital protein. Asian countries contribute over 90 percent of the world's production of rice [13, 14]. Food security programs depends on high yielding varieties which are obtained by increasing yield potential and yield stability [17]. The yield stability performance is one of the most desirable properties for a genotype to be released as a variety for cultivation. Stability is a complex product of genetic yield potential to stress conditions. References [1] and [2], defines yield stability of a cultivar as a similarity (consistency) degree of its yield response function across environments to mean of all studied cultivar yield response function.

A genotype may be considered stable if its environmental variance is small, if its response to environment is parallel to the mean response of all genotypes in the trial, or if the residual mean square from a regression model on the environmental index is small. References [15] and [16] reported that Stability should however not be the only selection parameter because the most stable genotypes would not necessarily give the best yield performance hence, there is a need for approaches that incorporate both mean yield and stability in a single index.

According to [19] there are a number of statistical methods for consideration of genotype by environment interaction and its relationship with stability. From all of these methods, regression of mean of each genotype on environmental index is one of the most applicable methods [21]. This method has been suggested by [9], and modified by [5].

This study sought to determine stable rice genotypes (*Oryza Sativa* L.) with high grain yield through a single parameter using Analysis of Variance (ANOVA) and Additive Main effects and Multiplicative Interaction analysis (AMMI).

MATERIALS AND METHODS

The experiment was conducted in 2013 within two rice producing hubs in Northern Ghana; the Savelugu hub, situated at latitude 9°37'North and longitude 0°50'West and the Navrongo hub, situated at 11°10'North and longitude 10°1' West. Fifteen rice genotypes were evaluated for yield under multi-locational trials at four locations across the two hubs. The experiment was laid out in a Randomized Complete Block Design (RCBD), where blocks consisted of rainfed and irrigated fields located in Boggu and Libga respectively for the Savelugu hub, and Kologo and Gongnia respectively for the Navrongo hub. Three (3) replications of the rice genotypes were used in all locations, with the plots laid 5m by 3m giving a total block size of 15m². The rainfed fields were direct seeded at stake in population density of 20cm x 20cm, with three seeds per stand. Seeds were placed in dibbled holes of approximately 3 to 5 cm depth. Seeds for the irrigated fields were transplanted from nurseries (3 weeks old), onto a well bundled plot of size 15m². The plant Population density was maintained as that of the rainfed fields. Fertilizer was applied at a recommended rate of 60-60-30 NPK kg/ha, with the Nitrogen (N) component applied as a split dose. The names and source of planting materials are indicated in Table 1. All good agronomic practices were undertaken to raise a healthy crop. At harvest, grain yield were adjusted for 14% moisture level and converted to yield/ha.

Table 1: Names and sources of germplasm materials used for the experiment

Genotype	Source
<i>Basmati 370-1</i>	IRRI, Philippines
<i>GH1837</i>	CSIR-PGRI, Ghana
<i>Good and new (JP)</i>	Japan
<i>GR 18 RED</i>	CSIR-PGRI, Ghana
<i>IR 72 (Ph)</i>	IRRI, Philippines
<i>Kawawa red</i>	CSIR-PGRI, Ghana
<i>Koshihikari</i>	Japan
<i>Local Basmati – 2</i>	IRRI, Philippines
<i>Local red</i>	Farmer collection
<i>Matigey</i>	CSIR-PGRI, Ghana
<i>Perfume (short)</i>	Thailand
<i>Sebota1</i>	Cameroun
<i>Sebota33</i>	Cameroun
<i>Sebota41</i>	Cameroun
<i>Sebota69</i>	Cameroun

Statistical Analysis

Data on grain yield were subjected to a combination of analysis of variance (ANOVA) and AMMI analysis. The genotypes deviations from the grand mean yield, environment deviation and the interaction between the genotype and the environment (GxE) were partitioned using ANOVA. The multiplicative effects analysis was subsequently used to partition the GxE deviations into two interactive principal component (IPCA1 and IPCA2) axes.

Additive Main effects and Multiplicative Interaction Analysis

AMMI analysis was used to adjust the main or additive genotype and environmental effects, in addition to the adjustment of the multiplicative effects for the GxE interaction by principal component analysis. The AMMI model is as follows:

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

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 axes k

α_{ik} and γ_{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 , that is environment

PCA score = $\lambda_k^{0.5} \gamma_{jk}$; genotype PCA score = $\lambda_k^{0.5} \alpha_{ik}$ [22].

The sum of squares of the interaction (G×E) was divided into an n singular axis or Interaction Principal Component Axis (IPCA), which reflects the standard portion in which each axis corresponded to a particular AMMI model. The selection of a model that best describes the G×E interaction was based on the F-Test (F_R) test as proposed by [3].

Various yield-stability statistics were also calculated in addition to the above stability parameters as follows:

AMMI stability Value (ASV)

The AMMI stability value (ASV) measure of yield stability, which is the distance from the coordinate point to the origin in a two dimensional IPCA1 score against IPCA2 scores in the AMMI model described [18] is calculated as follows:

$$ASV = \sqrt{\left[\frac{SS_{IPCA1}}{SS_{IPCA2}} (IPCA1score) \right]^2 + (IPCA2score)^2} \quad (2)$$

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 higher the IPCA score, either negative or positive, the more specifically adopted a genotype is to certain environments. Lower ASV score indicate a more stable genotype across environments.

Yield Stability Index and Rank Sum

These two measures of yield stability are calculated as follows:

$$\text{Yield Stability Index, YSI} = \text{RASV} + \text{RY} \quad (3)$$

Where RASV is the rank of the AMMI stability value and RY is the rank of the mean grain yield of genotypes (RY) across environment.

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 parameters show desirable genotypes with high mean yield and stability.

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

$$S_i^2 = \frac{\sum_{j=1}^m (R_{ij} - \bar{R}_i)^2}{l-1} \quad (4)$$

Where R_{ij} is the rank of X_{ij} in 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 adaption across environments

The joint Analysis of Variance (ANOVA) for the fifteen rice genotypes grown under rainfed and irrigated conditions showed differences ($P < 0.01$) for environments (E), genotypes (G) and the interaction between the environments and genotypes (GxE) ($P < 0.05$) as seen in Table 2, thereby corroborating the findings of [6], [8], [7]. The experimental coefficient of variation for the joint analysis was low (16.9%), indicating good experimental precision. A significant effect of the genotype by environment (GxE) interaction demonstrates the differential performance of genotypes in different environments.

Table 2: ANOVA for grain yield under rainfed and irrigated conditions

Source of variation	Df	F-values
Environment (E)	3	64.84**
Genotype (G)	14	10.13**
Genotype*Environment(GxE)	42	1.53*
Error	120	
Total	179	
CV %		16.9

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

The significant genotype by environment interaction also suggested that the grain yield of genotypes varied across irrigated and rainfed conditions. The significant differences for the components of the environment (E), genotype (G) and Interaction (GxE) indicated the effects of environments in the GxE, genetic variability among entries and the possibility of selecting high yielding genotypes. Since the interaction between the environment and genotype is significant, we proceed to find phenotypic stability [7]. The mean grain yield of genotypes ranged from 3.77t/ha for genotype *GH1837* to 2.45t/ha for genotypes *Sebota41* and *Sebota69*.

AMMI analysis of Genotype by Environment Interaction

This method of AMMI analysis is widely used in stability and adaptability analyses because it provides an initial diagnosis of the model and is well-suited for data analysis with many environmental influences; it also allows greater unfolding of the GxE interaction and summarizes the patterns and relationships between genotypes and environments; Accuracy of trait estimates is also improved [10, 22, 4].

The results of the AMMI analysis (Table 3) indicated that about 12% of the total variation was accounted for by the interaction between the genotype and environment, 37% by the environment and 27% by the genotypes. The large contribution of environment indicates that the environments were diverse, with large differences among environment means causing most of the variation in the grain yield.

Table 3: AMMI analysis of grain yield in 15 rice genotypes under rainfed and irrigated conditions

Source	Df	SS	MS	% of total SS	% of GxE
Genotypes (G)	14	34.37	2.46**	27.25	
Environments (E)	3	47.14	15.71**	37.38	
GxE	42	15.53	0.37**	12.31	
IPCA 1	16	7.94	0.49**		51.13
IPCA 2	14	5.76	0.41		37.09
Residuals	12	1.84	0.153		
Error	112	27.70	0.25		
Total	179	126.11	0.71		

** = Significant ($P < 0.05$)

The significant genotype by environment interaction showed that there was a considerable difference in the genotypic response across environments.

The results of AMMI analysis also showed that the first interaction principal component axis (IPCA1) explained for 51.13% of the interaction Sum of squares, whilst IPCA2 explained 37.09% of GxE interaction sum of squares.

AMMI stability value

A quantitative stability measure is essential to quantify and rank genotypes in terms of yield stability but this is not provided by the AMMI model [11, 12]. The AMMI stability value (ASV), proposed by [18] to quantify and rank genotypes according to their yield stability was therefore used. The ASV is the distance from zero in a two-dimensional scattergram of IPCA1 (interaction principal component analysis axis 1) scores against IPCA2 scores. Since the IPCA1 score contributes more to GE sum of squares (Table 3), it has to be weighted by the proportional difference between IPCA1 and IPCA2 scores to compensate for the relative contribution of IPCA1 and IPCA2 to the total GE sum of squares. The distance from zero is then determined using the Pythagorean Theorem [18].

In the ASV method, a genotype with the lowest ASV score is the most stable; accordingly (Table 4), genotype *Perfume (short)* was more stable, followed by genotype *Basmati 370-1*. The genotype *Matigey* was however observed to be less stable in terms of yield performance across both rainfed and irrigated conditions.

Table 4: First and second IPCA, mean yield, and various yield-stability statistics under rainfed and irrigated conditions

Genotype	IPCA1	IPCA2	Grain Yield (t/ha)	ASV	YSI	RS
<i>Basmati 370-1</i>	0.01	-0.30	2.71	0.10	11	9.10
<i>GH1837</i>	-0.20	0.18	3.77	0.30	7	1.30
<i>Good and new (JP)</i>	-0.26	0.01	3.63	0.36	9	2.36
<i>GR 18 RED</i>	-0.14	-0.21	3.44	0.24	9	4.24
<i>IR 72 (Ph)</i>	-0.03	0.34	2.95	0.16	8	5.16
<i>Kawawa red</i>	0.29	0.12	2.48	0.41	22	13.41
<i>Koshihikari</i>	0.63	0.31	2.63	0.96	25	11.96
<i>Local Basmati – 2</i>	-0.23	-0.74	2.84	0.87	19	6.87
<i>Local red</i>	0.08	-0.27	2.71	0.18	12	8.18
<i>Matigey</i>	-0.74	0.36	2.79	1.15	22	8.15
<i>Perfume (short)</i>	-0.03	-0.08	3.53	0.05	4	3.05
<i>Sebota1</i>	-0.32	0.33	2.66	0.55	21	10.55
<i>Sebota33</i>	0.26	-0.30	2.61	0.45	22	12.45
<i>Sebota41</i>	0.41	0.18	2.45	0.59	26	14.59
<i>Sebota69</i>	0.28	0.06	2.45	0.39	23	15.39

IPCA1 = Interactive Principal Component Analysis 1, IPCA2 = Interactive Principal Component Analysis 2

ASV = AMMI Stability Value, YSI = Yield Stability Index, RS = Rank Sum

Yield Stability Index and Rank Sum

This approach of estimating yield stability is done by ranking the mean grain yield of genotypes (RY) across environments and the rank of AMMI stability value (RASV). This approach incorporates both mean yield and stability in a single index. Low value of the YSI shows stable genotypes with a high mean yield. By using these measures, suitable rice varieties can be identified for varying existing environmental conditions.

Since the ASV takes into account both IPCA1 and IPCA2, a greater proportion of the variation in the interaction between the genotype and the environment (GxE) is justified, therefore the rank of ASV and yield mean is such that the lowest ASV is rank one, while the highest yield mean is rank one, and ranks are then summed in a single simultaneous selection index of yield stability called the yield stability index (YSI). The genotype with the lowest YSI is considered the most stable genotype. The most stable genotype with high grain yield based on the YSI (Table 4) is the genotype *Perfume (short)*. The genotypes *Sebota41* and *Sebota69* had high YSI values for grain yield, and hence assumed less stable in terms of yield performance across rainfed and irrigated conditions.

The Rank Sum measure of yield stability (Table 4) showed genotypes *GH1837*, *Good and new (JP)* and *Perfume (short)* as the most stable genotypes with high grain yield.

CONCLUSION

The study provided an evaluation of genotypic and environmental performance of fifteen rice genotypes over a range of environments across the two hubs. The significant differences exhibited among the genotypes and environments for yield suggests a wide variability between the genotypes and the environments. Based on the stability parameters, the genotypes

Perfume (short), *GH1837*, and *Good and new (JP)* were stable with high grain yield making them suitable for environments across the two hubs.

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