NIGERIAN STATISTICAL ASSOCIATION

2009

CONFERENCE PROCEEDINGS

THEME:

STATISTICS AND IMPLEMENTATION OF THE SEVEN POINT
AGENDA OF THE FEDERAL GOVERNMENT

VENUE:

CITY KING HOTEL AND TOWERS, GUSAU, ZAMFARA STATE

DATE:

12TH - 14TH AUGUST, 2009

ADDITIVE MAIN EFFECTS AND MULTIPLICATIVE INTERACTIONS ANALYSIS OF PADDY YIELD PERFORMANCE OF RICE CULTIVARS ACROSS LOCATIONS UNDER THE INFLUENCE OF *RICE YELLOW MOTTLE SOBEMOVIRUS*

[1]Rasheed A. Adeyemi*, [1]Muhammadu T. Salaudeen, [2]Basheer Bature

[1]Department of Crop Production, Federal University of Technology, P.M.B. 65, Minna, Nigeria
[2]Department of Maths & Statistics, Nuhu Bamalli Polytechnic, P.M.B.1061, Zaria, Nigeria

* Correspondence Author:
Mobile: +234 08035861447
Email: adeyemira@yahoo.ca

Abstract: This study was carried out under the paddy yield performance of 14 rice cultivars resistance to *Rice yellow mottle* sobemovirus (RYMV) across two locations in northern Nigeria in 2005/2006 planting season. The experimental layout was randomized complete block design with three replications. Additive main effects and multiplicative interactions (AMMI) analysis indicated that the paddy yield of the cultivars (genotypes) was under major location (environmental) influence and cultivar x environmental interactions. The first principal component (PCA I) was significant ($P< 0.05$) while second principal component (PCA 2) was not significant ($P> 0.05$) and it had a cumulative contribution of 80 % to the total variance in paddy yield performance by environmental interactions. Genotype and environmental interaction was also significant ($P<0.05$). A biplot using cultivar means and environment scores of the first 2 AMMI components showed that cultivars with larger PCA 1 and lower PCA 2 score gave higher yield value (stable cultivar). FARO 37 (G9) was found to be most stable cultivar and cultivar with lower PCA 1 and larger PCA 2 scores had low paddy yield (unstable cultivar, that is G6) with respect to the locations.

Key Words: *Principal Component Analysis, AMMI, Rice yellow mottle sobemovirus, paddy yield,*

INTRODUCTION   In northern Nigeria, upland rice ((*Oryza Sativa* L.) is an annual crops that is typically cultivated on dry land. Rice in Nigeria is the sixth major crop in area cultivated after sorghum, millet, cowpea, cassava and yam (FAO, 1994). It is grown in four major rice growing environment: upland, rainfed lowland, irrigated lowland and deep water ,(Singh et.al., 1997). Rice is a staple crop in Nigeria (Adagba et.al. 2005). It is not only consumed by human and fed to livestock, but it is also a major raw material to agro-allied industries as it can be processed into acetic acid, glucose and starch while its husks can serve as a fuel and ash use as fertilizers (Schalbroceck, 2001).   In spite of the continually increase in the land area that is cultivated with rice, Nigeria still imports rice annually and is now rated the world's second largest importer spending over $300 million annually on rice imports alone (Anonymous, 2003b).Grain yield of rice is usually limited by individual or combined influence of diseases(Singh et.al.1997), drought, wind, soil nutrient status, salinity, variety sowing date and rate (Lingle and Michael, 2000; Fischer et.al., 2001 Slaton et.al.,2003) and attack by parasitic weeds (Adagba et.al., 2005). Schalbroceck, (2001) reported that rice yellow mottle (*Rice yellow mottle virus*) is a major disease of rice after the rice blast (*Pyricularia oryzae*).

Analysis of variance (ANOVA) was Invented by Fisher (1918). For a two-way factorial design, ANOVA partitions the variation into the row main effects, column main effects, and row x column interaction effects. For yield trials, the most common outcome is that the environment main effects are largest, followed by the interaction effects and then the genotype main effects. In this work, AMMI was employed as a multivariate statistical technique to estimate the cultivar stability in paddy yield performance of rice cultivars in the two locations. However, a combined analysis of variance can quantify the interactions and describe the main effects. ANOVA may not be informative enough to explain the genotypes and environment interactions (GEI) (Yuksel Kaya *et al.*,2002).

AMMI model is effective statistical tool that incorporates both the additive and multiplicative components of the two-way data structure. AMMI biplot analysis considered is used to diagnose GEI pattern graphically. Then, the principal component analysis (PCA), which is incorporated in AMMI, takes care of the interaction effect from the additive ANOVA model. The biplot display of PCA scores plotted against genotype means provides a visual display for inspection and easy interpretation of the GEI components.

The biplot displayed and genotypic stability estimate enable genotypes to be grouped based on similarity of performance across the environments as suggested by Thillainathan and Fernandiz (2001). This idea was employed in this work to study rice cultivars paddy yield performance in response to locations.

There are past documents on the use of AMMI in multi-environmental traits, which partition the GEI matrix into individual genotypic and environmental scores. An example was provided by Yan *et al.* (2001), who applied AMMI on yield data of Ontario winter wheat performance traits, and suggested two winter wheat mega-

environments in Ontario. Another example was provided by Yan and Rajian (2002), who applied the method, to genotype by trait biplot analysis soybean multiple traits and MET data found that selection for seed yield alone was not only the simplest, but also the most effective strategy in the early stages of soybean breeding.

The objectives of this study were to (i) interpret cultivars and location interaction (ii) obtain by AMMI analysis paddy yield performance of 14 rice cultivars across two locations/ environments (iii) virtually assess how to vary these two parameters observed based on the biplot and (iii) determine cultivars with high stability with respect to paddy yield in response to environments.

METHODOLOGY

Additive Main Effect and Multiplicative Interaction (AMMI) models

There are multivariate methods for study of genotypic stability including AMMI as discussed by Crossa (1990), Gauch Junior (1985), Gauch Junior and Zobel (1988), Zobel *et al.* (1988). Many studies have applied both multivariate and univariate techniques and these methods have been useful for identifying stable and adapted genotypes (Dias & Krzanowski, 2003; Flores *et al.*, 1998; Vargas *et al.*,1999).

The AMMI model was developed by Gabriel (1971) and Gollob (1968) and has been applied by many other authors. This model is defined by:,

$$ = \quad - \quad - \quad - \quad \sum \quad \quad + \quad + \quad $$

The interaction effect is $\quad = \quad \sum \quad = \quad$

Where

$\quad$ = observed paddy yield for the ith cultivar type and jth environment.

$\quad$ = grand mean

$\quad$ = deviation of cultivar type (i) mean from grand mean

$\quad$ = deviation of environment (j) from grand mean

$\quad$ = singular value for interaction kth principal component axis (IPCA)

$\quad$ = cultivar type (i) eigenvector value for kth PCA axis

$\quad$ = environment (j) eigenvector value for kth PCA axis, $\quad$ = residual effect and

$\quad$ = error-term; (Gauch and Zobel, 1996)

Cultivars (genotypes) were used as nominal variable to produce a cultivar type-environment biplot. On the biplots, location with similar cultivar performance lies close to each other (Ter Brak and Prentice, 1988). Sites located in the sector of the biplot were associated with species located in that sector, cultivar located far away from the origin are the most important in the analysis compared to those near the centre of the biplot (Ter Brack, 1996).

Let be the matrix of GE interactions parametric effects defined by

$$ X = \begin{bmatrix} ge_{11} & \cdots & ge_{1p} \\ \vdots & \ddots & \vdots \\ ge_{n1} & \cdots & ge_{np} \end{bmatrix} $$

The X matrix (n x p) with rank $\quad = \quad - \quad - \quad - \quad$ is submitted to the singular value decomposition in the following way: $\quad = \quad$ where R (n x r) and S (p x r), R and S are column orthonomal,

$\quad = \quad$ and $\quad = \quad$, $\quad = \quad$ is the $\quad$ non null eigenvalue of $\quad$ or $\quad$, R and S are matrix of eigenvector of the related $\quad$. Let $\quad$ non – null eigenvalues retained, these variables will explain most of the total variation given by

$$ \quad = \quad = \quad \quad = \frac{\quad}{\quad} $$

If the proportion of explanation is large for small $\quad$, the technique is considered efficient. There, the interaction effects can be predicted by:
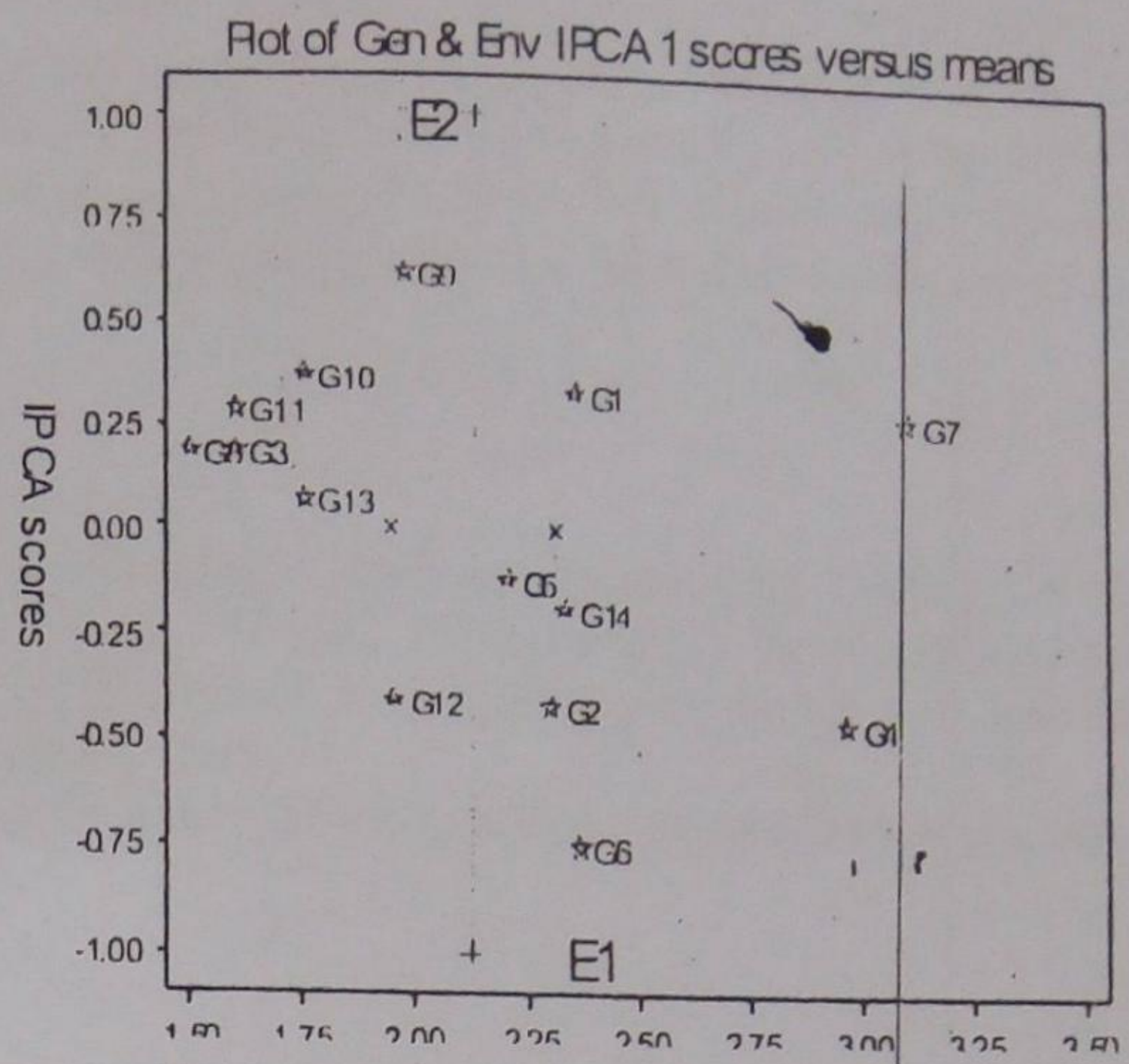
For a formal evaluation to lack of fit for the AMMI model, an analysis of variance can be accomplished as predicted for retained principal components.

RESULTS AND DICUSSION

Table 1: Environment means and variances

Location	No. of observation	Mean	Variance
1	42	2.307	0.800
2	42	1.940	0.4864
Combine	84	2.124	0.6695

Table 2: The ANOVA table for AMMI model

Source	df	SS	MS	F	F_prob
Treatments	27	33.61	1.2447	3.45	0.00006
Genotypes	13	18.76	1.4430	4.01	0.00016
Environ.	1	2.82	2.8233	3.49	0.0672
Block	4	3.23	0.8080	2.24	0.0770
Interactions	13	12.02	0.9249	2.57	0.00812
IPCA 1	13	12.02	0.9249	2.57	0.00812
IPCA 2	11	0.00	0.0000	0.00	1.00000
Error	52	18.73	0.3603		
Total	83	55.57	0.6695		

Plot of Gen & Env IPCA 1 scores versus means

Fig. 1: Plot of Gen & Env IPCA 1 scores versus mean yield for the 14 cultivars

A biplot using cultivar means and environment scores of the first 2 AMMI components showed that cultivars with larger PCA1 and lower PCA 2 score gave higher yield value (stable cultivar). FARO 37 (G9) and G12 are found to be most stable cultivars, that is cultivars close PCA1 axis. An undesirable genotype has low stability as well low mean yield had low paddy yield and far away from the origin (unstable cultivar, that is G7 and G4) with respect to the locations.

CONCLUSION The use of appropriate statistical tools is necessary for identifying the most adapted, responsive and stable variety in the final phases of the plant breeding program, where the high costs and the time spent in assays are powerful justifications to search for improved methods.