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account for a small fraction of the total GE and could be misleading [13-15].

Additive main effects and multiplicative interaction (AMMI) has been proved to be a suitable method for depicting adaptive responses [15-17]. AMMI analysis has been reported to have significantly improved the probability of successful selection [17] and has been used to analyse G×E interaction with greater precision in many crops [13,15,18]. The model combines the conventional analysis of variance for genotype and environment main effects with principal components analysis to decompose the GEI into several Interaction Principal Component Axes (IPCA). With the biplot facility from AMMI analysis, both genotypes and environments are plotted together on the same scatter plot and inferences about their interaction can be made.

This study reports the use of AMMI model to analyse yield data of thirty genotypes of upland rice evaluate in four locations. The objectives

the smaller variance Przystalski [22] reported that, the genetic variance tends to be larger in better environments than in poorer environments.

A desirable property of the AMMI model is that, the genotypic and environmental scores can be used to construct powerful graphical representations called biplots [19] that help to interpret the GEI, the biplot showing both genotypes and environments in the same plot. The author further stated that, biplots facilitate the exploration of relationships between genotypes and/or environments. Genotypes that are more similar to each other are closer to each other in the plot than genotypes that are less similar. The same is true for environments. Genotypes/environments that are alike tend to cluster together. Result in Figure 2 indicates that, S Daga location has the highest mean yield 3692 kg/ha, while ART12-1L6P7-8-1-B-1 (2) is the genotype with the highest mean yield. The result also shows that, there is no correlation between Amakama and Yandev/ Uyo locations. The projection of ART12-1L6P7-8-1-B-1 (2) and ART16-9-3-15-3-B-1-1 (8) on to S Daga axis reflects the higher mean yield performance of the genotypes. Similarly in Amakama genotype ART3-9L9P3-1-B-2 (22) and ART2-6L6P6-1-B-1(10) performed best in the location, while genotype ART12-1L6P7-8-1-B-1 (2) and ART16-9-3-15-3-B-1-1 (8) has positive interaction with S Daga. It is also predicted that, genotype ART3-3L12P9-1-1-B (15), ART3-7L9P8-3-B-B-2(20) and ART3-6L3P9-B-B-2 (16) has negative GEI values in S Daga because their projection were towards the negative direction of S Daga arrow. Also genotype FARO55 (23), ART16-22-1-1-2-B-1-1 (7) and WAB706-27-K5-KB-2 (28) have negative interaction with Amakama location. Generally, there was a poor yield performance in Yandev and Uyo locations as shown in Figure 2.

#### AMMI 2 biplot display

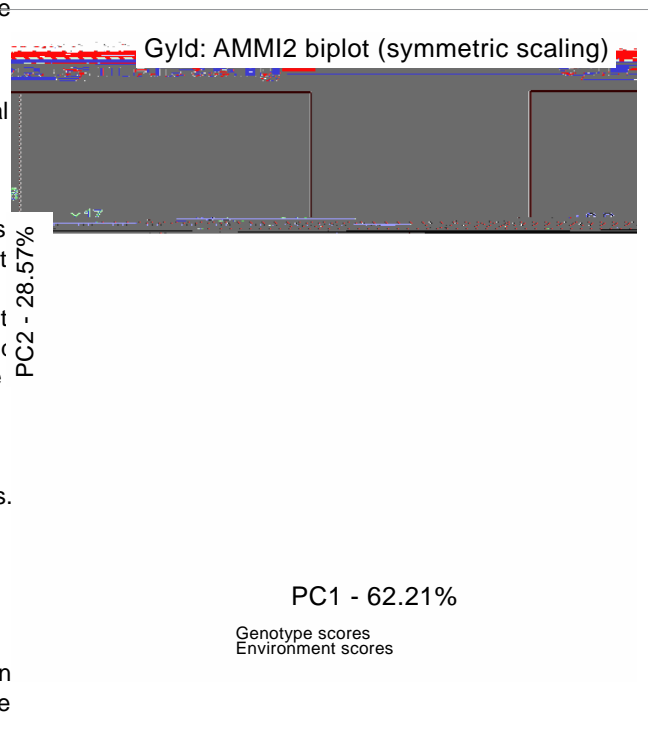
In the AMMI 2 biplot, (Figure 2) the environmental scores (locations) are joined to the origin by side lines. Sites with short vectors do not exert strong interactive forces (Uyo and Yandev). While those that long vectors exert strong interaction (S.Daga and Amakama). Weikai Yan reported that, a short vector indicates a location in which there is a small range of genotype performance.

The vertical Y axis is showing the best one dimension measure of the GE effect for each genotype. Thus, genotypes close to the X axis have a small GE effect, while those far away the X axis in either the positive or negative directions has a large GE effect. Figure 2 shows that, genotype ART10-1L12P2-1-B-1(1) and ART16-16-5-23-1-B-1-1 (6) has a small GE effect, which is considered stable and less influenced by the environments.

Weikai Yan reported that, If the angle between two genotype vectors is less than 90 degrees, then the genotypes are positively correlated, tending to do well, or badly, in the same environment. But if the angle between the vectors of two genotypes is greater than 90 degrees, then they tend to perform differently over the trial environments. If the angle between two genotype vectors is 90 degrees, their performance is independent, of each other. Figure 2 shows that, ART16-9-3-15-3-B-1-1 (8), ART3-9L9P3-1-B-2 (22) and ART3-6L3P9-B-B-3 (17) are

positively correlated. However, there is negative correlation between ART16-9-3-15-3-B-1-1 (8), ART10-1L12P2-1-B-1 (1) and ART16-16-5-23-1-B-1-1(6). Also, there is no correlation between ART16-9-3-15-3-B-1-1 (8) and ART3-12L11P2-B-B-1 (11) ART16-12-22-4-1-B-1-1 (5), ART3-8L6P6-5-B-2(21) and FARO58 (24). The ideal genotype is the genotype with high performance combined with good stability.

GGE biplot also allows the partitioning of environment into



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