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ADAPTABILITY AND PHENOTYPIC STABILITY OF UPLAND RICE GENOTYPES IN MOZAMBIQUE

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Abstract: The alternative adopted in rice (*Oryza sativa* L.) breeding programs to decrease the effect of genotype x environment to reduce the effect of the interaction of genotype x environment (G x E), consists in the evaluation of genotypes in different environments and years, for an accurate recommendation of the most stable and adapted genotypes. Therefore, the objective of this work was to evaluate the phenotypic adaptability and stability of the productive upland rice genotypes in Mozambique, using the graphical tool for data analysis, the GGE biplot. We used data on grain yield, derived from the evaluation of five upland rice genotypes from the Rice Genetic Improvement Program of the Institute of Agrarian Research from Mozambique - Northeastern, Zonal Center (IIAM-CZnd). The trials were conducted in the complete block design with four repetitions in the agricultural years 2019/2020, 2020/2021, and 2021/2022. The trials were conducted in a total of five environments divided into three agricultural years, located in northern Mozambique. It was concluded from this work that genotypes G4 and G2 were superior to the overall average for productivity and genotype G3 showed high stability. The genotype G4 can be recommended for all mega-environments, for presenting good adaptability and phenotypic stability.

Keywords: *Oryza sativa*; Grain yield; GGE Biplot.

Introduction

The environments where upland rice is cultivated are the most varied possible, due to different soil types, climates, and irregular rainfall distribution, which often causes partial or total crop losses. Thus, upland rice breeding programs seek to identify and select lines with characteristics related to stability and adaptability (Soares et al., 2010). Adaptability and stability studies have highlighted the great importance and difficulties of dealing with the interaction genotypes by environments (G x A), that is, when genotypes do

not maintain the same relative performance in the different environments in which they are grown (Neto et al., 2013).

The interaction between genotype and environment is one of the subjects that has most aroused the attention of breeders and biometricians, with special attention to tropical conditions, since in these regions there is a greater environment heterogeneity which results in greater chances of interaction occurring (Ramalho et al., 2012), as is the case of Mozambique. The differentiated response of genotypes in various environments is a natural phenomenon resulting from the interaction of genotypes with environments (Eberhart and Russel, 1966), and its effects allow the identification of genotypes suitable for a specific environment, or of general behavior, suitable for various environments (Bueno et al., 2012), the interaction represents a problem, requiring efficiency in the analysis and use of appropriate methodologies (Neto et al., 2013).

Adaptability and stability analysis methodologies are intended for the evaluation of a group of genotypes, tested in a series of environments, and should be employed when significant genotype x environment interactions occur. Currently, there are a large number of methodologies to estimate the adaptability and stability of cultivars tested in a series of environments (Cargnin et al., 2008). The use of biplots to quantify the environment, genotype, and interaction is widespread, as interaction effects can be visualized in a single graph, which facilitates the comparison of genotypes and their interaction with the environment (Gauch and Zobel, 1996). The GGE biplot methodology is indeed the most effective, most powerful, and presents an elegant way to visualize data from multi-environment trials and genotype-by-environment interactions, and to address issues that breeders, geneticists, and agronomists have to deal with (Yan et al., 2000; Yan and Kang, 2002; Yan and Tinker, 2006).

Therefore, this work aimed to evaluate the adaptability and productive stability of upland rice genotypes from the Rice Genetic Improvement Program of the Institute of Agrarian Research from Mozambique - Northeastern Zonal Center (IIAM-CZnd), using the graphical tool the GGE biplot, resulting in the selection of stable and high yielding genotypes in various environments.

Material and Methods

Grain yield data from the evaluation of upland rice genotypes from the rice genetic improvement program of the Institute of Agrarian Research from Mozambique - Northeastern Zonal Center (IIAM-CZnd) were used (Table 1). The trials were conducted in a complete block design with four repetitions in the agricultural years 2019/2020, 2020/2021, and 2021/2022, being in Nampula and 2020/2021, 2021/2022 in Namapa respectively. The experiments were conducted in a total of five environments divided within the three agricultural years in the districts of Nampula (15° 7' S 39° 15' W) and Namapa (13º56'17'' S and 39º56'36'' E), all located in northern Mozambique (in agro-ecological region R7 Nampula:-15.147796,39.309723 and Namapa:-13.725419,39.772064). The plots consisted of five rows of four meters, spaced 0.2 x 0.2 meters between rows and between plants, with the three central rows considered useful. The cultural treatments were performed according to the recommendations of the culture in the region.

Table 1. Genotypes (G) used in experiments in the five agricultural seasons.

Identification	Genotypes	Source	Cycle	Aroma
G1	Boro Kupata	Mozambique	Precoce	Absent
G2	Montanha Aromática	Brazil	Precoce	Presence
G3	Pepita	Brazil	Precoce	Presence
G4	Sertaneja	Brazil	Precoce	Presence
G5	Serra Dourada	Brazil	Precoce	Presence

Source: Authors.

Individual analysis of variance was performed for each environment and joint analysis for all environments using the software GENES (Cruz, 2016). Once the interaction genotype x environment was verified, we proceeded to the analysis of adaptability and stability considering the productivity character. The evaluation was done using the GGE-Biplot method (Genotype and Genotype-Environment Interaction) by the model (YAN et al., 2000), according to the following statistical model:

$$Y_{ijk} = m + G_i + B/A_{jk} + A_j + GA_{ij} + E_{ijk}$$

Effects: G fixed and A random.

Where:

Y_{ijk} = production of the i-th plot in the k-the block and the j-the environment

m = general average

G_i = fixed effect of the i-the genotype (i = 1, 2,..., 5)

B/A_{jk} = effect of the k-the block in the j-the environment (k=1, 2...,4)

A_j = random effect of the j-the environment (j=1, 2...5)

GA_{ij} = effect of the interaction of the i the genotype with the j the environment

E_{ijk} = random error

The plots were obtained from the scores to improve the understanding of the interrelationship between genotypes and environments, according to Yan and Tinker (2006), constructed from the decomposition of the means, showing which genotype has the best performance. The biplots were constructed from the first two principal components of the effect of genotypes plus the interaction (G x E) (PCA1 and PCA2).

Results and discussion

The results of the simple analysis of variance showed the existence of statistical differences among the means of the genotypes at the 1% probability level. The ratio between the largest and smallest mean square of the residual was less than seven, indicating homogeneity of variances (Table 2), which allowed the joint analysis of the data. The effect of environment and G x E interaction was significant at 1 and 5% probability levels by F Test, showing the existence of variations and differentiated performance of genotypes compared to the observed variations (Table 3). Similar results were found by (Silva et al., 2019; Nuvunga et al., 2021), who observed significance between environments and the interaction genotypes and environments.

Table 3. Joint analysis of variance of the yield of five upland rice genotypes in five environments.

[1]FV	[2]GL	[3]SQ	[4]QM
BLOCKS/ENVIRONMENT	15	31.10	207.15
GENOTYPES	4	27.15	6.78 ns
ENVIRONMENTS	4	54.33	13.58**
GxE	16	56.57	3.53**
RESIDUE	60	49.83	0.83
TOTAL	99	218.94	
AVERAGE		4.20	
[5]CV(%)		21.69	

**Significance at 1% probability, by F test. 1FV = Source of Variation, 2GL = Degree of Freedom, 3SQ = Sum of Squares, 4QM = Mean Squares, 5CV = Coefficient of Variation.

Table 4 shows the distribution of cultivars based on the productivity averages of each in the five environments considered in the study. We can observe that there was a change in the ranking of the genotypes as the environment changes. This G x E interaction, therefore, consists of the complex type.

Table 2. Results of the individual yield analyses of five upland rice genotypes in five environments.

ENVIRONMENT	QMB	QMG	QMR	F	P	F+	P+
Nampula 19/2021	1.97	2.93	0.38	7.60	0.002	3.53	0.01
Nampula 20/2021	3.44	1.03	0.99	1.04	0.42	1.25	0.29
Nampula 21/2022	2.95	12.86	0.39	3.27	0.0	15.49	0.0
Namapa 20/2021	1.67	0.10	1.57	0.06	1.0	0.13	1.0
Namapa 21/2222	0.29	3.98	0.81	4.91	.014	4.8	.002

Ratio higher (QMR)/lower(QMR) = 4.07424;   (+) Note: test done considering the QMR of the joint analysis.

Table 4. Yield averages of five genotypes (G) in five environments (E).

| ID	Genotypes	E1	E2	E3	E4	E5	Averages
1	Boro Kupata	48008a	49847a	27875 a	51.175	21450 b	39671 bc
2	Montanha Aromática	38177b	49807a	42972 a	50.625	45650 a	454462 ab
3	Pepita	33910b	39981a	26082 a	50.500	22050 b	345047 c
4	Sertaneja	50337a	53491a	70855 a	48.250	25975 b	497817 a
5	Serra Dourada	30926a	46303a	41603 a	52.750	31825 b	406813 bc

Averages followed by the same lower case letters vertically constitute a statistically homogeneous group. E1- district of Nampula harvest 2019/2022; E2- district of Nampula harvest 2020/2021; E3-district of Nampula harvest; district of Namapa harvest 2020/2021; district of Namapa harvest 2021/2022.

The "which-won't-where" GGE biplot visualization

The GGE biplot analysis, in which PC1 and PC2 together, constitute a GGE biplot, explained from 22.27% to 68.97% of the total 91.24% (Figure 1), showing good efficiency.

Mega-environments are defined as a group of sub-regions that consistently share a single genotype or a group of similar genotypes specifically adapted and the best in performance (Gauch and Zobel, 1996; Yan and Rajcan, 2003). Environments that are contained within the same mega-environment are considered similar with respect to the response of genotypes (Alves et al., 2020). The

polygonal view of a GGE biplot not only shows the best cultivar for each test environment but also divides the test environments into groups (Yan and Kang, 2002). In Figure 1 it is possible to visualize the clustering of the environments based on the best genotypes forming the mega-environments. The environments were divided into two groups according to the red lines that came out from the origin of the biplot, thus forming two mega-environments. The winning genotypes for the sectors are the genotypes of the vertices at the intersection of the two sides of the polygon whose perpendicular lines form the boundary of that sector (Yan et al., 2007) and are classified as the most reactive to the en-
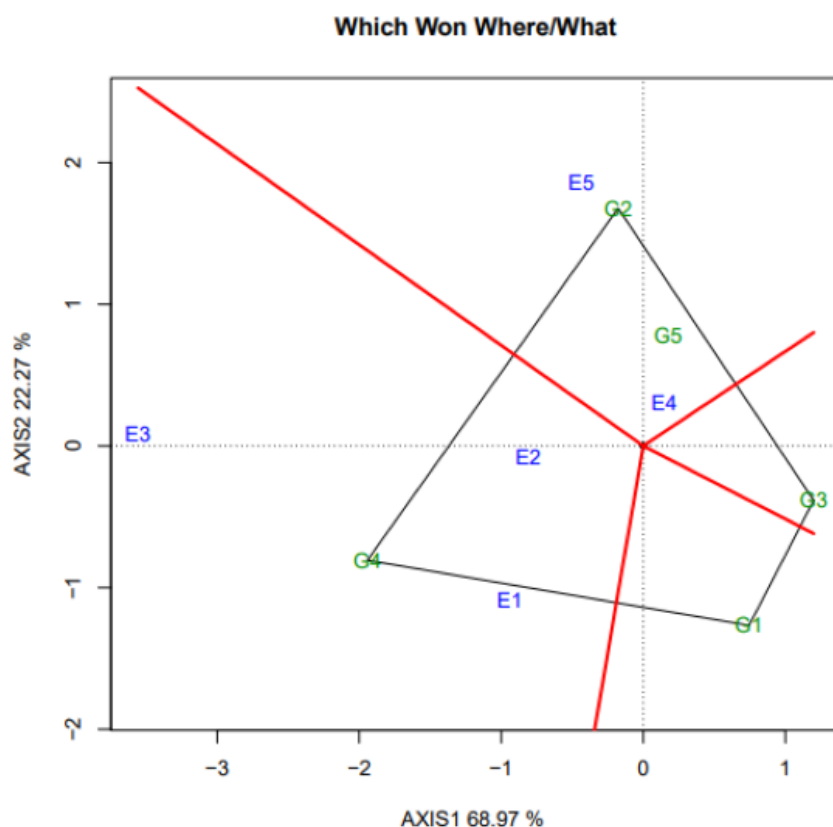
Figure 1. GGE biplot "Which-won-where" for the productivity of five upland rice genotypes in five different environments.

vironmental stimulus, however, those within the polygon are less reactive (Yamamoto et al., 2021).

Therefore, the vertices of the polygon are formed by the genotypes G1, G2, G3, and G4 being the most reactive to the environmental stimulus. When genotypes are in the vertices where it is not possible to define which sector they belong to or have no related environments these genotypes were not sensitive to any of the grouped environments (Yamamoto et al., 2021). Genotype G4 is the vertex of the sector that encompasses the mega-environment1 composed of environments E1, E2, and E3. This evidences that genotype G4 performed well in this mega-environment. In the mega-environment composed of environments E4 and E5, genotype G2 presented the best performance, with 4.5 t/ha. In this case, genotype G2 had the highest yield in the mega-environment followed by G5 with 4.05 t/ha. In some sectors none of the environments were found, revealing that these genotypes are considered unfavorable and of low productivity (G1 and G3).

The mean vsstability visualization

The GGE biplot visualization "Mean vs Stability" (Figure 2) is an effective tool for evaluating genotypes considering both the productivity and stability of the genotypes in the environments under study. In this graph it is possible to identify the genotypes that have a high mean associated with high stability, an association much desired by breeders (Yan and Kang, 2002; Yan and Tynker, 2006; Yan, 2007), where stable genotypes interact less with environments (Eberhart and Russell, 1966).

The line passing through the origin of the graph is the average environment axis (AEA). The arrow indicates the direction of higher yields. The line perpendicular to the axis of the average environment is related to the stability of the genotype, so the longer the length of the dashed green line is, the more unstable the genotype is (Yan and Tinker, 2006; Alves et al., 2020).

Therefore genotypes G4 and G2 are located above average, i.e., with higher average productive performance among the respective
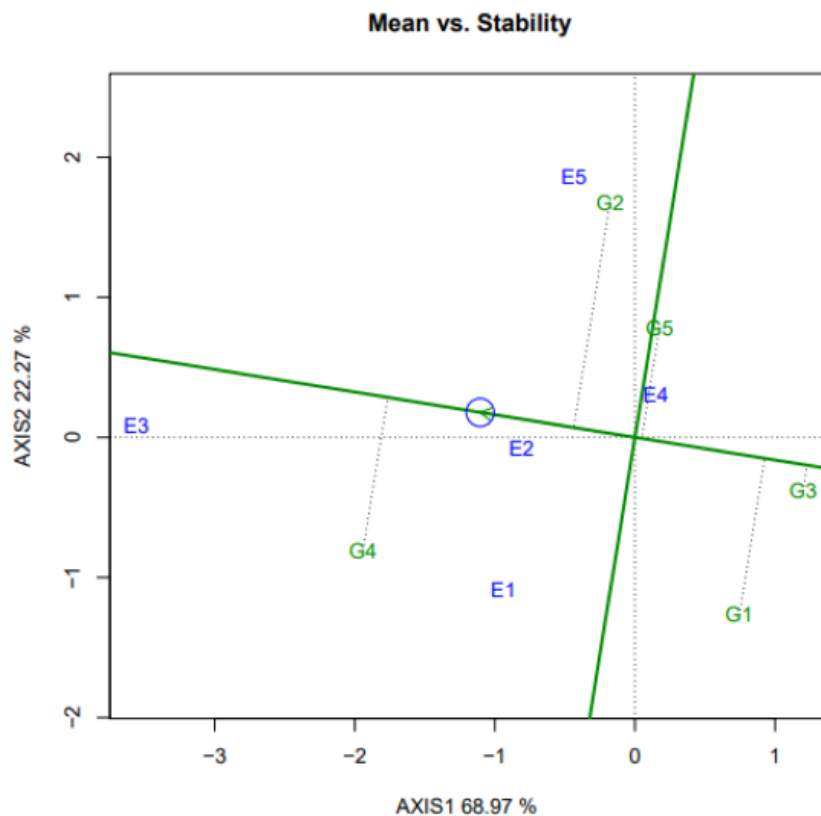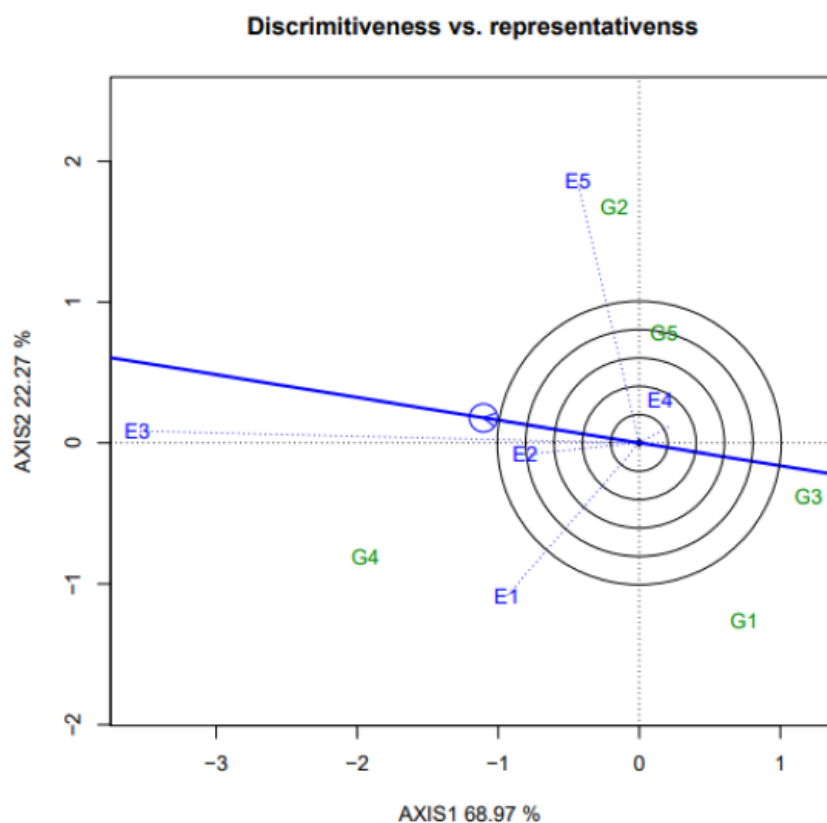

Figure 2. Visualization of the GGE Biplot "means vs stability" for the productivity of five upland rice genotypes in five different environments.

mega-environments. The genotypes located below the average were the ones that obtained the lowest performance, where G5 is close to the average. Genotypes G3 and G5 were the most stable, this does not mean that these genotypes had good yields relative to the other genotypes but rather indicates that their ranking was highly consistent across all environments within this mega-environment (Yan et al., 2007). Thus, G2 was highly unstable while G3 was highly stable. The highlight was given to the genotype G4, which combined with good stability obtained productivity well above average, with 4.9 t/ha.

Visualization of GGE biplot "discrmimitiveness vs. Representativeness

In the GGE Biplot visualization "discrmimitiveness vs. representativeness" (Figure 3), environments with the longest vectors are the most discriminatory and those with the shortest vectors are the least discriminatory, providing little or no information about the genotypes and can be discarded as a test environment (Yan and Tinker, 2006).

The most representative environments are those that form a smaller angle between their vector (discontinuous blue line) and AEA (continuous blue line) (Yan and Tinker, 2006). Environments are ranked based on their distance from the ideal environment (Yan and Kang, 2002). Thus, the environment that most discriminated the genotypes for productivity was E3 (Nampula, harvest 2021/2022), being the most suitable to test the genotypes. The most representative environments were E3 (Nampula, harvest 2021/2022) and E2 (Nampula, harvest 2020/2021). The ideal test environment should be the most discriminating (informative) and also most representative of the target environment (Yan and Tinker 2006; Rad et al., 2013), to identify and select superior genotypes. Environment E3 (Nampula, harvest 2021/2022) is the ideal environment for selecting adapted genotypes since it unites these two characteristics, discriminating and representative, while E4 was the poorest for selecting cultivars adapted to the entire region.

Figure 3: Visualization of the GGE Biplot "Discrmimiteness vs. Representativeness" of five upland rice genotypes in five environments.

The visualization of ranking genotypes

The visualization of the GGE Biplot, shows (Figure 4), that the performance of the genotypes for the productivity character in these sets of environments, is based on the proximity of the genotypes to the center of the concentric circles. Thus, the genotypes closest to the center of the circle are the closest to the optimal line (AEC) and thus are the most desired. In this case, according to Yan and Hunt (2002), only one mega-environment is considered, where genotypes are considered stable if they are in the AEC line and are productive if the CP is high and positive.

An ideal genotype should have both high productivity and high stability in all environments, which is defined by the center of the concentric circles (Rad et al., 2013; Yamamoto et al., 2021). Consequently, it can be inferred that genotypes G4, G5, and G2 are the closest to the genotype considered ideal, with the genotype G4 being distinguished where it was assigned in the fifth concentric circle, which combines high productivity and good phenotypic stability, with 4.9 t/ha.

Conclusions

Genotypes G4 and G2 were superior to the general average for productivity and genotype G3 showed high stability.

Genotype G4 can be recommended for the mega-environment (Nampula district) and genotype G2 can be recommended for the mega-environment (Namapa district), being candidates for launching as new cultivars.

The genotype G4 can be recommended for all mega-environments, for presenting good adaptability and phenotypic stability.

Acknowledgments
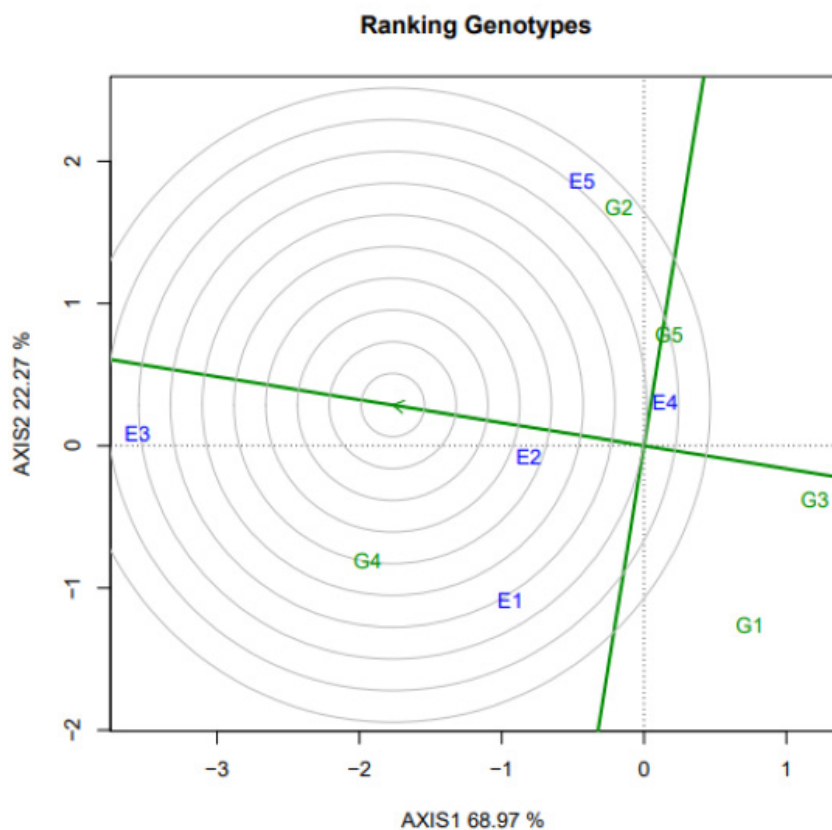
Figure 4: Visualization of the GGE Biplot "Ranking Genotypes" performance of the five upland rice genotypes in five environments.

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