

Statistical Evaluation of Grain Yield in Millet Trials Using Principal Component Analysis

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Abstract - Production in Pearl Millet has turn down in the past due mainly to the poor varieties used, matching millet varieties with its production environment and poor environmental condition by famers which in turn lead to shortage of food production, farmers' income, poor commercialization and trade, among others. This study is aimed at providing substantial evidence by applying AMMI technique, GGE biplots and ranking method in assessing the stability and adaptability of genotypes and environment with a view to evaluate and identifying the high yielding pearl millet varieties. The combined ANOVA and AMMI analysis for grain yield of forty (40) millet genotypes at 4 environments showed that environments, genotype and Gx E interaction revealed highly significant ($P < 0.001$) variations. The first two PCA axes (PCA1, PCA2) were significant ($P < 0.001$) cumulatively contributed to 93.29% of the total GE interaction. Graphical display of genotype by environment interaction (GGE-biplot) was depicted in order to detect the locations of genotypes. Results indicated that genotypes ICMV IS 89305, CIVT, SoSank and SoSat C-88 are superior and high yielding based on graph and ranking method, three stable yielding genotypes (99-72, 01MisoNCD2-NE, and T454). Genotype ICMV IS 89305, CIVT, and NKK, had specific adaptation to E2 and E4, and E1 and E3 are unfavorable environment. Variety ICMV IS 89305 can thus be used as a reference genotype in cultivar evaluation follow by Variety SoSat C-88, CIVT, SoSank, Gwagwa as superior variety in this study.

Key Words - (AMMI) Additive main effects and multiplicative interactions, (GEI) genotype by environment interaction, (PCA) principal component analysis, Pearl Millet.

1. INTRODUCTION

Globally, Millet is an important cereal crop which receives the most needed attention in low production of West African region. However, its production is limited by the adverse environmental conditions. Meanwhile, genotype by environment interaction (GEI) refers to the differential responses of different genotypes across a range of environments [16].

Commercial markets for the traditional cereals of Africa will change as regional demand grows for processed foods and as consumption habits change from grains to animal products. Advances in food processing technology and an increasing demand for feed should lead to greater price stability for domestically produced grain. [27]

One challenge to increasing the commercial potential of Pearl Millet is the ability of growers to provide reliable products that meets market standard. [27] Farmers identified lack of suitable Pearl Millet varieties and poor soil as a major constraint to production of this crop.

Pearl millet genotypes with high yield stability, adaptable to suitable environmental condition are an integral part of meeting this challenge and genotypes improvement remains a goal of both national and international agencies [27].

Statistical theory and agricultural experiment in analysis of yield trial data have proven the effectiveness of the PCA. The AMMI model combines regular analysis of variance (ANOVA) for additive main effects with principal component analysis (PCA) for multiplicative structure within the interaction [35].

The purpose of this research was to apply GGE biplot, ranking method and PCA to assess genotypic yield prediction from homogeneous subgroups of environments and genotypes as well as identify stable and high yielding genotypes in millet; to graphically display means, adaptability and stability of millet genotypes and environments.

2. GENOTYPE BY ENVIRONMENT

The yield variation due to changing environment is commonly referred to as genotype \times environment interaction ($G \times E$). $G \times E$ usually complicates the process of selecting superior genotypes. Consequently, multi-environment trials (METs) are widely used by plant breeders for evaluating the relative performance of genotypes over the target environments [6]. A wide array of statistical techniques have been developed to study and reveal the nature of $G \times E$ interaction, e.g., joint regression [8]-[7], additive main effects and multiplicative interaction (AMMI) [10], and type B genetic correlation [4]. These methods are commonly used to analyze MET data and have also been applied in $G \times E$ interaction studies in many crops.

In genotype variation, E explains most of the variation, and G and $G \times E$ are usually small [28]. However, only G and $G \times E$ interaction are relevant to variety evaluation, particularly when $G \times E$ interaction is determined as repeatable. Hence, [32] deliberately put the two together and referred to the combination as GGE. Following the proposal of [9], the biplot technique was also used to display the GGE of MET data, and is referred to as a GGE biplot [28]-[32]. The GGE biplot is in fact a data visualization tool that graphically displays $G \times E$ interaction in a two way table [32]. The GGE biplot is an effective tool for the following applications: 1) Mega-environment analysis (e.g.; “which won-where” pattern), whereby specific genotypes can be recommended for specific mega environments [34]. 2) Genotype evaluation (mean performance and stability), and. 3) Environmental evaluation (to discriminate among genotypes in target environments). GGE biplot analysis is increasingly being used in $G \times E$ interaction studies in agricultural research.

3. AMMI TECHNIQUE

AMMI is a multivariate technique for assessing the stability and adaptability of genotypes [20]. This method partitions the overall variation into G, E and $G \times E$. The data structure that AMMI and GGE biplot analyses require is a two-way data matrix, such as number of genotypes tested in a number of environments. The experiment may or may not be replicated. These analyses combine two statistical procedures: analysis of variance (ANOVA) and principal component analysis (PCA)[12].

The permutation of analysis of variance and PCA in the AMMI model together with forecast assessment is an important approach for better understanding GEI and obtaining better yield estimates [23]. The interaction is explained in the form of a biplot display where, PCA scores are plotted against each other and it provides visual inspection and interpretation of the GEI components [24].

4. MULTI – LOCATIONAL TRIALS

Multilocal trials are mainly conducted to test and assess superior genotype from different environmental locations. They are used to ascertain which entries, if any, are superior to existing ones and to determine the stability of performance across sites and years. The data are also used to establish the area of adaptation in which the genotype will be recommended for cultivation [25].

Selecting the superior, high yielding and good quality genotypes as well as more stable genotypes are very important for researchers [12]. The superior genotypes to deal with unpredictable environmental factors have been studied in MET. In most cases, GE interaction is observed, complicating selection for improved millets due to the effect of the environmental factors such as soil type, weather conditions etc,[1].

Data on yield trials for studying genotypes are conducted in several locations for many years, Data of such trials may have three principle tasks, to;

- Evaluate accurately and to predict the yield on the basis of limited experimental data;
- Determine stability and explain variability in the response of genotype across locations;
- Be a good guide for the selection of the best genotype [3].

5. MATERIAL AND METHODS

The genotypes used in this study is based on preliminary trial, the $G \times E$ trials was conducted at four locations with forty genotype. They were Sadore local, Kapielga, Toronia, Zatib, Zongo, HKP, CIVT, SoSan C-88, Taram, SoSank, ICMV IS 89305, ICMV IS 90311, Synthetic 1-2000, NKO x TC1, Guefoue 16, Indaina 05, NKK, Bongo short head, Manga Nara, Arrow, Tongo Yellow, PT732B, P1449-2, $\frac{3}{4}$ Ex-Borno, $\frac{3}{4}$ HK, $\frac{3}{4}$ Souna, Gwagwa, LCIC 9702, DMR 15, DMR 68, DMR 72, GB 8735, 99-72, TG102, T99B, T454, IBMV8401Mx68A4R4w, 01MisoNCD2-NE, 68Ax086R, and 99M59043Mw x 68A4R4MIB05. The varieties used in this study were obtained from researchers at national and international programs. In 2003, field trials were grown in Ghana, Mali, Senegal and Nigeria; Randomized complete block design were used for the experiment with four replications in each environment. The data has already been used for other purpose, it is a secondary data.

6. STATISTICAL ANALYSIS

Reference to [10]-[11] has encouraged the use of AMMI analysis for yield trials experiment, [11]-[34] compared the performance of AMMI analysis together with the ANOVA approach and regression method and from that ANOVA fail to detect a significant interaction component and the regression method accounts only a small portion of the interaction sum of squares only when the pattern fits a specific regression model. The combined AMMI and ANOVA technique was used in this study.

The AMMI model for G genotype and E environment is

$$Y_{ij} = \mu + \alpha_i + \beta_j + \sum_{k=1}^m \delta_{ik} \theta_k \gamma_{jk} + \varepsilon_{ij} \dots (i)$$

$$\varepsilon_{ij} \sim N(0, \sigma^2) \quad i = 1, 2, \dots, G, \quad J = 1, 2, \dots, E$$

Where y_{ij} is the yield of the i^{th} genotype in the j^{th} environment, μ is the grand mean, α_i and β_j are the genotype and environment deviations from the grand mean respectively, θ_k is the Eigen value of the IPC analysis axis n ; δ_{ik} and γ_{jk} are the genotype and environment Eigen vectors for axis n ; n is the number

of principal components retained in the model and ε_{ij} is the error term.

In this modified AMMI stability parameter, all significant IPCs were used. [5] pointed out three main purposes of AMMI models: (i) model diagnosis — AMMI is more appropriate in the initial statistical analysis of yield trials because it provides an analytical tool for diagnosing other models as subclasses when these are better for a particular data set [2]; (ii) to clarify GEI — AMMI models summarize patterns and relations of genotypes and environments [18]-[35]-[5], and (iii) to improve the accuracy of yield estimates — gains have been obtained in the accuracy of yield estimates that are equivalent to increasing the number of replicates by a factor of two to five [35]; [5] which can be used to reduce the costs by reducing the number of replications, to include more treatments in the experiment, or to improve efficiency in selecting the best genotypes.

7. PRINCIPAL COMPONENT ANALYSIS

Principal component analysis is the most frequently used multivariate method [5]; [22]. Its aim is to transform the data from one set of coordinate axes to another, which preserves, as much as possible, the original arrangement of the set of points and concentrates most of the data structure in the first principal component axis. Various limitations have been noted for this technique [21]-[26]-[35].

It was observed that the linear regression method use only one statistic to describe the pattern of response of a genotype across environments and most of the information is wasted as a result of accounting for deviation. Principal component analysis (PCA) is a generalization of linear regression that overcomes this difficulty by giving more than one statistic, the score on the principal component axes to describe the response of a genotype.

The model

$$Y_{ij} = \mu + \alpha_i + \beta_j + \sum_{k=1}^m \delta_{ik} \theta_k \gamma_{jk} + \varepsilon_{ij} \dots \text{(iii)}$$

Where θ_k is the Eigen value of the PCA analysis k; δ_{ik} and γ_{jk} are the genotype and environment principal component scores for axis k; n is the number of principal component retained in the model and ε_j is the error term.

GGE-biplot approach, which is composed of 2 concepts, the biplot concept [9], and the GGE concept [32], was used to visually analyze the METs data. This approach uses a biplot to show the factors (G and GE) that are important in genotype evaluation and that are also the source of variation in GEI analysis of METs data [32]-[30]. The GGE-biplot shows the first 2 principal components derived from subjecting environment centered yield data (yield variation due to GGE) to

singular value decomposition [32]. In the current study, genotype-focused scaling was used in visualizing for genotypic comparison, with environment-focused scaling for environmental comparison. The statistical analysis was carry out using GenStat 16th edition.

8. RESULT AND DISCUSSION

The combine ANOVA and AMMI analysis for grain yield show that environments, genotype and GxE interaction revealed highly significant ($P < 0.001$) variations. The analysis also show that millet grain yield was significantly affected by environment E, which explained 33.20% of the total treatment (G+E+GE) variation, whereas the genotype G and GEI were significant accounted for 22.72% and 44.01% respectively.

In additive variance, the portioning of (GE) SS data matrix by using AMMI analysis indicates that the two PCAs were significant ($P < 0.001$). The first IPCA axis (IPCA1) accounted for 62.58% of the GxE interaction sum of squares, using 41 degree of freedom. The second IPCA axis (IPCA2) accounted for 30.71% of the interaction sum of squares using 39 degree of freedom. Both represent a total of 93.29% variation.

The yield variation explained by environment indicated that the environments were not diverse, there are not large differences between environments, but it can also contributing to the variation in grain yield. In Table 2 the environments showed much variability in both main effect and interaction.

Table 1: ANOVA table for AMMI model

Source of variation	Degree of freedom	Sum of squares	Mean sum of squares	F ratio
Treatments	159	199140547	1252456	<0.001
Genotypes	39	45239963	1159999	<0.001
Environment	3	66126020	22042007	<0.001
Block	8	200	25	0.3407
Interactions	117	87774564	750210	<0.001
IPCA 1	41	54927370	1339692	<0.001
IPCA 2	39	26955839	691175	<0.001
Residuals	37	5891355	159226	<0.001
Error	312	6895	22	
Total	479	199147643	415757	

Table 2: the first four AMMI selections per environment

Number	Environment	Mean	Score	1	2	3	4
2	E2	1442.6	52.05	G16	G11	G2	G14
4	E4	928.3	2.24	G11	G7	G8	G27
1	E1	487.1	-20.38	G19	G37	G18	G14
3	E3	599.3	-33.91	G19	G18	G37	G7

Table 2 shows the best environment and the most stable and high yielding genotypes in each location, its shows that E2 is favourable to G11, G2, G16 and G14 which also correspond to the results obtained in figure 5 and figure 1, both shows that the highest yielders are G16 and G11 which is the first two genotypes in table 5.

It also shows that G11, G7, G8, G27 are the most yielding and adaptable to E4 which also explained by the “which won where” pattern, the result indicate that E4 has winning genotype of G7, G8, G11 and G27. Figure 1. In table 5, G11 occurred in both E2 and E4 which clearly shows that G11 as the best and adaptable genotype in both environments.

Table 3 (a), (b): Sorted stability coefficients, five most stable genotype

NO	VARIETY	CULTIVAR SUPERIORITY	MEANS
1)	8	204065	1402
2)	7	216787	1430
3)	10	272681	1287
4)	11	277846	1446
5)	6	304102	1237

NO	VARIETY	STATIC STABILITY	MEANS
1)	33	13379	204.7
2)	38	24912	628.6
3)	36	26587	277.9
4)	24	33433	673.2
5)	35	33820	244

Table 3 (a) illustrate the five most superior genotype, in the analysis it was confirm that G8, G7, G10, G11 and G6. This has also identified in figure 2, 3 and 4. Table 3 (b) demonstrate different results with the biplots. Figure 1 shows that G35, G33, and G18 had no environments in their sector, figure 4 also list G33, G35, G25 and G38 as below average mean as they have to be discarded. Figure 5 which ranks the genotypes based on performance shows in E2 genotypes G20, G33, G35 and G34 has lower average yield, it also shows G35 as the lowest yielder. Therefore we should resort to our results in biplots graphs and conclude that G35, G33, G34 are not stable genotype.

The “which-won-where” pattern of the GGE biplot [32] is the most suitable tool for mega-environments analysis in variety trials [33]. The “which-won-where” pattern of MET data is represented by a polygon formed by connecting

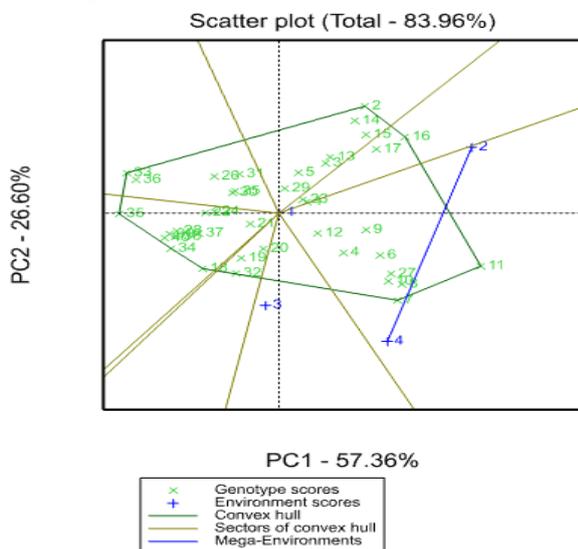


Figure 1. GGE biplot showing “which-won-where” the environment indicated by + and genotype by × respectively.

The markers of genotypes that are further from a biplot origin, and a set of lines drawn from the biplot origin perpendicular to each side of the polygon. The perpendicular lines to the polygon sides divide the polygon sectors, each having its own winning cultivar which is the vertex genotype for that sector [32]. Seven out of the forty genotypes located in the vertex formed a seven-sided polygon having seven possible sectors (Figure1). The vertex genotype for each sector is the one that yielded the highest for the environments filling within that sector. Five of the sectors had no environments. The four environments fell into two sectors delineated by different winning genotypes. With the present figure G2, G6, G11, G7, G16, G35, G33 expressed a high interactive behavior (positive or negative). Whereas the environment E1 exhibited low interaction, E2 stood as intermediate between the three Genotype G16, G11 and G7 sectors indicating the existence of one mega location, according to this biplot, G16, G11 and G7 are expected to give the same yield at E2. Genotype G11 was the winning genotype at E4, although G7 is expected to give the same yield in E4.

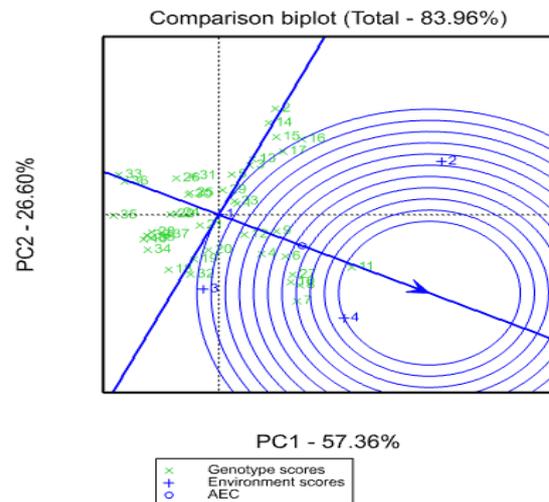


Figure 2. GGE biplot based on genotype focused scaling for comparison the genotypes with the ideal environment.

The vertex genotypes G18, G35, G33, G2 and G16 had no environment in their sector. The five genotypes were not the highest yielding ones at any of the test environments. G23 and G21 are located near to the plot origin and hence were less responsive than the vertex genotypes. The genotypes within the polygon and located nearer to plot origin are less responsive than vertex genotypes [30]. E2 and E4 have the best genotype as G11; so G11 is adaptable in both environments. The MET indicate the presence of different mega-environments, which is defined as the group of locations

that consistently share the most suitable set of genotypes across years.

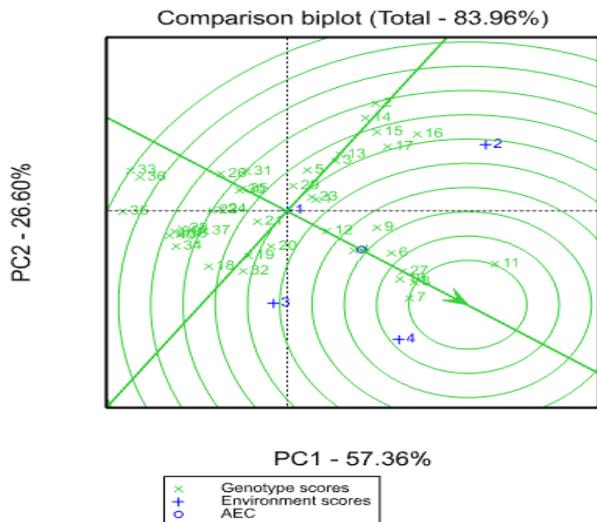


Figure 1. GGE biplot base on the comparison of environment relative to an ideal genotype.

An ideal genotype is defined as one that is the highest yielding across test environments and it's absolutely stable in performance that ranks the highest in all test environments [33] it should also possess both high mean performance and high stability within a mega-environment [33]. Although such an ideal genotype may not exist in reality, it could be used as reference for genotype evaluation[19].

In Figure 3, a genotype is more desirable if it is located closer to ideal genotype [17], the closer the genotype are G7, G8 and G11. Favorable genotypes are G10, G27, and G6. The ideal test environment should have large PC1 scores and small PC2 scores. Thus, using the ideal environment as the center, concentric circles were drawn to help visualize the distance between each environment as the ideal environment. [32].

Figure 3. Indicated that E4 which fell near the center of concentric circles was an ideal test environment in terms of being the most representative of the overall environment and the most powerful to discriminate genotypes. Favorable environment is E2, while unfavorable environment is E1 and E3.

Yield performance and stability of genotypes were evaluated by an average environment coordination (AEC) method [28]-[29]-[31]. In this method, an average environment is defined by the average PC1 and PC2 scores of all environments, represented by a small circle (Figure 4). A line is then drawn to pass through this average environment and the biplot origin; this line is called the average environment axis and serves as the abscissa of the AEC. The ordinate of the AEC is the line that passes through the origin and is perpendicular to the AEC abscissa (Figure 4). Unlike the AEC abscissa, which has one direction, with the arrow pointing to greater genotype main effect, the AEC ordinate is

indicated by a thick line or double arrows, and either direction away from the biplot origin indicates greater GEI effect and reduced stability. The AEC ordinate separates genotypes with below-average means from those with above-average means. Furthermore, the average yield of genotypes is approximated by the projections of their markers to the AEC abscissa. Figure give genotypes with above-average means were from G11 to G15, while genotypes below-average means were from G1 to G33. The length of the average environment vector (the distance from biplot origin and the average environment marker), relative to the biplot size, is a measure of the relative importance of genotype main effect vs. GEI. The longer it is, the more important is the genotype main effect, and the more meaningful the selection based on mean performance. For this study, the length of the average environment vector was sufficient to select genotypes based on yield mean performances. Genotypes with above-average means (i.e. from G11 to G15) could be selected, whereas the rest were discarded. On the other hand, genotype stability is very important, in addition to genotype yield mean. A longer projection to the AEC ordinate, regardless of the direction, represents a greater tendency of the GEI of a genotype, which means it is more variable and less stable across environments or vice versa. For instance, genotypes G11, G7, G10 and G8 were more stable as well as high yielding. Conversely, G32, G15 and G16 were more variable, but high yielding. An ideal genotype should have the highest mean performance and be absolutely stable (i.e. perform the best in all environments). Such an ideal genotype is defined by having the greatest vector length of the high yielding genotypes and with zero GEI, as represented by an arrow pointing to it (Figure 4). Although such an ideal genotype may not exist in reality, it can be used as a reference for genotype evaluation. A genotype is more desirable if it is located closer to the ideal genotype. Thus, using the ideal genotype as the center, concentric circles were drawn to help visualize the distance between each genotype and the ideal genotype.

To rank the genotypes based on their performance in an environment, a line is drawn that passes through the biplot origin and the environment. This line is called the axis for this environment, and along it is the ranking of the genotypes. Figure 5 ranks the genotypes based on performance in E2. Genotypes G20 to G35 had lower than average yield, G27, G7, G8, G10 and G11 had near average yield, and all others had higher than average yields. The highest yielder in E2 was G16 and G11, and the lowest yielder G35.

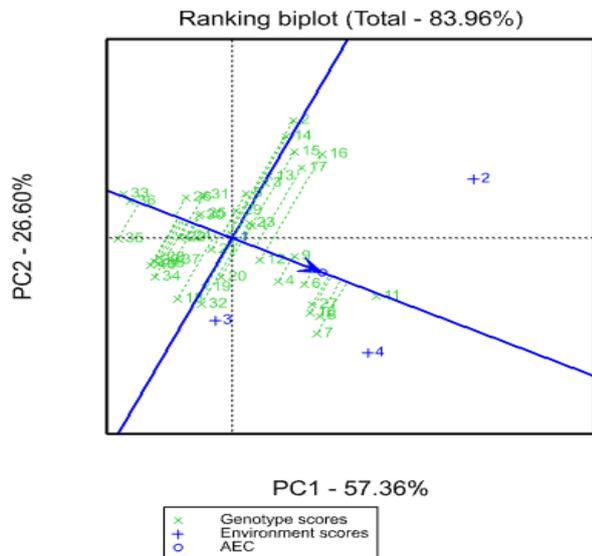


Figure 2. Environment focused scaling

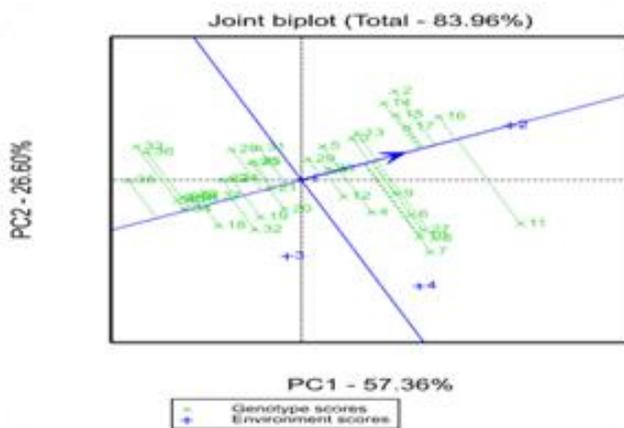


Figure 3. Genotype focused scaling.

9. CONCLUSION AND RECOMMENDATION

The application of AMMI and GGE biplot to millet multi-environmental grain yield trial facilitated the visual comparison and identification of the winning genotype in relation to the test environment. Based on the two analysis AMMI and GGE-biplot models, the genotype evaluated; G8, G7, G10, G11, G6 were the 5 top superior with high yielding performance and G33, G38, G36, G24, G35 were the genotypes that are stable in performance. Hence these genotypes can be considered as varieties for commercial production.

The GGE biplot analyses provided results in terms of stability and performance of the 40 pearl millet varieties. Based on the results of the present study, G11, G7, G10 and G8 were the highest yielding and most stable genotypes. They were the closest to the ideal genotype and may be considered as the best genotypes, but G11 is the closest of all, so G11 is the ideal genotype. Three genotype G11, G7 and G17 had specific adaptation to E2 and E4; they have the potential for production in Mali and

Senegal and other locations within the same agro-ecological zones. G33, G38 and G36 were low yielding and the most stable. This indicated that the performance of this genotype would be predictable in less favorable environments.

10. RECOMMENDATIONS

This study should be repeated in other major millet growing semi-arid zones of West African countries for two or more years to confirm yield stability and the pattern of response of the 40 millet varieties across locations. To save resources, the less superior genotypes should be excluded from future testing in other locations. The high yielding and stable genotypes with superior performances should be tested extensively in on-farm trials and promoted for adoption and commercialization in West Africa.

Nevertheless, these genotypes are to be recommended for specific planting at Mali and Senegal for their best shoot tips yield. Agriculturalist, policy makers have to search for genotypes that are stable and adaptable to E1 and E3.

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