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Performance evaluation and grain yield stability of released upland rice (*Oryza sativa L.*) varieties at Southwestern part of Ethiopia, Jimma Zone

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Abstract

In Ethiopia, rice is one of the most important strategic food security crops and it becomes the source of income. In Southwestern part of Ethiopia, especially in Jimma zone, lack of high yielding, biotic and abiotic stress tolerant upland rice varieties were major problem for the reduction of yield. The objective of the present study was to estimate the magnitude of GEI and to identify high yielding and stable upland rice varieties for Jimma zone and to recommend for large scale planting. A total of seven (including one check) rice genotypes were evaluated in randomized complete block design (RCBD) with three replications at Southwestern Ethiopia, Jimma zone of Melko, Shebe and Kersa under main season conditions for two main seasons (2021 to 2022). The combined ANOVA revealed significant variation among G, E and GEI for mean grain yield of seven upland rice genotypes. The relative contribution of E, G, and GEI indicated that environment was the most important source of variation for grain yield performance. E, explained 68.14% of total sum of square (SS) of grain yield, while GEI accounted for 20.73% and G contributed 4.98%. The first 2 principal components (PC1 and PC2) were used to create a 2-dimensional GGE bi-plot and explained 55.36 and 26.36 % of GGE sum of squares, respectively with a total of 81.72% for yield variation. The GGE biplot identified three rice growing mega-environments. The first mega environment consisted of environments Melko 2022 (M22),Melko 2021 (M21) and Kersa 2021 with the vertex genotype of Shaga (SHG) and Second mega environment consists of Kersa 2022 (K22) with the vertex genotype of Nerica-4 (NE) and third mega environment consists of Shebe 2021 and Shebe 2022 with the vertex genotype of Wanzaye (WZ).Melko 2022 was ideal environment for rice evaluation and rice variety,Shaga was found to be benchmark/ideal genotype and could be used as check to evaluate the performance of other genotypes and also can be recommended for wider cultivation in the tested locations and similar agro-ecologies.

Keywords: GGE, Genotype by environment, Performance**,** Rice, Southwestern

Introduction

Rice (*Oryza sativa L.*) belongs to the family *poaceae*. Among cereal crops after wheat, rice (*Oryza sativa* L.) ranks second and is a staple food of more than 50% world's population. Asia dominates both in rice production and consumption *i.e.* about 90%. The remaining 10% rice area is scattered in different parts of the world. It is expected that world population may reach the figure of 8 billion up to year 2025. Increasing population demands for increase both in area and per unit production. Keeping the present consumption pattern in view, 35 to 40% more rice production will be needed in 2025 to cater public demands. China and India are major rice growing countries in the world. According to WARDA (2004) rice is grown and consumed in about 39 countries of Africa.

The cultivation of rice in Ethiopia is of a recent history. However, its use as food and cash crop is well recognized. Rice in Ethiopia is one of the food security commodities and its expansion is also linearly increasing in different parts of the country (MoA, 2010). The country is endowed with a range of agro- ecological zones that suit to rice production with an estimated potential of more than 20 million hectares. The total area under rice production has increased from about 29,866 ha in 2011 to over 57,576 ha in 2020, and the production during the same period has increased from 90,412 tons to over 170,630 tons (CSA, 2020). The productivity of rice has also reached close to 3 t/ha in 2020 from 1.8 t/ha in 2005. The proliferation of improved rice production technologies over the last three decades is believed to have contributed to productivity growth. Low rice productivity in Ethiopia is attributed to shortage of high yielding varieties, terminal water deficit, low soil fertility and environmental fluctuations (MoA, 2010).

Genotype by environment interaction (GEI) refers to the different response of genotypes in a wide range of environments. It is known by researchers who are active in the field of crop breeding as it affects breeding progress and makes it difficult to evaluate and select superior genotypes. Quantitative traits such as yield, which are economically and agronomically important, can be significantly affected by GEI. These force breeders to be more careful in evaluating and releasing genotypes and choose the best genotypes in terms of yield and adaptability in target environment. On the other hand, GEI may also provide opportunities for breeders to select genotypes that interact positively with a particular location (specific adaptation) or perform well in most environments (general adaptation). This can be achieved by cultivating genotypes in different environments, recording their response, and finally selecting a superior and stable genotype (Fasahat *et al*., 2016) [5].

The production and productivity of upland rice varieties was highly reduced at Jimma zone due to lack of high yielding varieties, diseases and low temperature during germination and flowering. Identifying of high yielding and stable upland rice varieties for large scale production is major aim of the study. Therefore, present study was undertaken to understand the nature and magnitude of GEI and to evaluate seven (including one check) released upland rice varieties for yield and yield related traits at Southwestern part of Ethiopia, Jimma zone and to identify high yielding and stress (biotic and abiotic) tolerant upland rice varieties for large scale planting.

Materials and Methods

1. Experimental materials

A multi-environment trial was conducted using seven upland rice varieties (one check) (Table 1) for each location. The trial was conducted during the 2021 and 2022 main cropping seasons at Shebe, Melko and Kersa. Average weather of the test sites are presented in table 2. Seven nationally released rice varieties were included in the study (Table 1). The materials were obtained from Fogera Agricultural Research Center.

Table 1: Descriptions of experimental materials

Rice varieties	Year of release	Released center
Nerica-4	2006	Pawe
Check	-	-
Ediget	2011	Adet
Wanzaye	2017	Fogera
Yun31	2020	Fogera
Shaga	2017	Fogera
Chewaqa	2013	Bako

2. Description of experimental site

Table 2: Descriptions of testing sites

Sites	Altitude (m.a.s.l)	Soil type	Rainfall (mm)	Temp (^{0}C)
Kersa	>1780	Nitosols	2000	20.3
Melko	1753	Nitosols	1639	22
Shebe	1370	Nitosols	1400	22

3. Experimental Design and Trial management

The experiment was laid out in randomized complete block design (RCBD) with three replications. The experimental plot for each variety consisted of six rows (four rows harvested) of 2.5m. Spacing between rows, plots and replications 25cm, 30cm and 1.5m respectively. The seed rate was 80kg/ha. In addition; other relevant field trial management practices were carried out uniformly for all experimental units. Data were taken for days to 50% heading, effective tillers, plant height, disease, days to 90% maturity, grain yield and others based on the standard evaluation system developed by International Rice Research Institute (IRRI, 2002) but, only plot yield data converted to t/ha was subjected to statistical analysis.

4. Data Analysis

4.1 Individual and Combined ANOVA

An analysis of variance was conducted for individual environments to plot the residuals and identify outliers; the homogeneity of residuals variance was determined using Bartlett’s homogeneity test. Comparison of treatment means was done using Fischer’s least significant difference (LSD) test at 5% probability levels. In performing the combined analysis of variance genotypes were assumed to be fixed, while environments were assumed random. The analysis of variance (ANOVA) for each location and combined analysis of variance over locations was used as suggested by Gomez and Gomez (1984). The model employed in the analysis was;

$$Yijk = \mu + Gi + Ej + Bk + Geij + \varepsilon ijk$$

where: Yijk is the observed mean of the ith genotype (Gi) in the jth environment (Ej), in the kth block (Bk); μ is the overall mean; Gi is effect of the ith genotype; Ej is effect of the jth environment; Bk is block effect of the ith genotype in the jth environment; Geij is the interaction effects of the ith genotype and the jth environment; and εijk is the error term.

Result and Discussion

1. Mean grain yield performances of the genotypes across the testing locations

The mean grain yield of the seven released rice genotypes (including one local check) showed a wide range of variations in the different environments (P<0.005) (Table 3). The mean grain yield of varieties ranged from 20.4 to 30.6qt/ha with mean yield of 26.9qt/ha. The mean grain yield of local check was 27.4 and it was performed well compared to some of rice varieties. The testing environments Melko2021, Kersa2021, Melko2022, Kersa2022 were gave grain yield below the average and Shebe2021 and Shebe2022 were high yielding environments (Table 3). Rice genotypes showed different performance across tested locations and this rank change of genotypes showed presence of qualitative (crossover) GEI.

Table 3: Mean performance of grain yield (qt/ha) of seven rice genotypes tested across locations

Rice varieties	Locations							
	Melko 2021	Kersa 2021	Shebe 2021	Melko 2022	Kersa 2022	Shebe 2022	Overall mean	Rank
Nerica- 4	17.3	7.4	40.3	22.7	30.0	38.0	26.0	5
check	18.8	17.6	35.6	29.3	16.0	47.0	27.4	4
Ediget	17.9	18.8	53.8	22.7	23.3	47.3	30.6	1
Wanzaye	10.3	14.4	47.4	3.0	16.7	53.3	24.2	6
Yng31	17.7	33.0	41.5	26.7	8.3	47.0	29.0	3
Shaga	17.7	35.1	45.3	36.0	12.7	35.3	30.4	2
Chewaqa	12.9	10.1	44.3	8.7	5.3	41.3	20.4	7
Mean	16.1	19.5	44.0	21.3	16.1	44.2	26.9	
F test	0.025	<.0001	0.0068	<.0001	0.0002	0.0106		
LSD at (5%)	17.9	17.4	9.8	10.6	7.22	8.8312		
CV (%)	16.1	6.0	7.7	4.0	25.3	11.23		

Where=coefficient of variation, LSD =least significant difference

2. Combined Analysis of Variance

The combined analysis of variance (ANOVA) revealed significant variation among genotypes (G), environments (E) and GEI for mean grain yield of seven upland rice (including one check) genotypes (Table 4). The relative contribution of environment, genotype and GEI indicated that environment was the most important source of variation for grain yield performance. Environment explained 68.14% of total sum of square (SS) of grain yield, while GEI accounted for 20.73% and the least was by the genotype 4.98% (Table 4). This large yield variation explained by environments indicated that the environments were diverse and the major part of variation in grain yield could be attributed to environmental changes. Tadesse *et al*. (2021) also reported high contribution of environments for grain yield variation. Similarly, Zemede and Mekbib (2021) [17] reported highly significant variations among genotypes, environments and their interactions on grain yield and the largest variation was accounted by environments (60.6%), followed by GEI (20.6%) and then genotypes (18.2%). In contrary to our report, Bose *et al*. (2014) [2] and Akter *et al*. (2014) [1] found out that larger portion of variation in grain yield was attributed to the genotypes, followed by GEI and the least to the environments. On the other hand, Sharifi *et al*. (2017) [10] reported that 41% of the total sum of squares was explained by GEI effects, environmental effects (29%), and genotype effects (30%) using nine promising rice genotypes. Similarly, Huang *et al*. (2021) reported that the highest variation in grain yield of rice genotypes was attributed to GEI (37.1%), followed by genotype (35.6%) and environments (16.5%). They further explained that the significances variation by GEI effect revealed that the genotypes had variable performance in the tested environments, i.e., a change in the average rank of the genotypes was observed among the environments which suggested running a more refined analysis to understand the magnitude and pattern of GEI.

Table 4: Combined ANOVA for yield and the percentage sum of squares of the seven rice genotypes tested at three environments over a period of two years (2021 and 2022)

Source of variation	df	SS	MS	F value	%TSS
Environments	5	19167.9	3833.59	270.98***	68.14
Genotypes	6	1403.5	233.9	16.53***	4.98
GEI	30	5833.4	194.4		20.73
Error	72	1018.6	14.14		3.62
Total	125	28127.3			

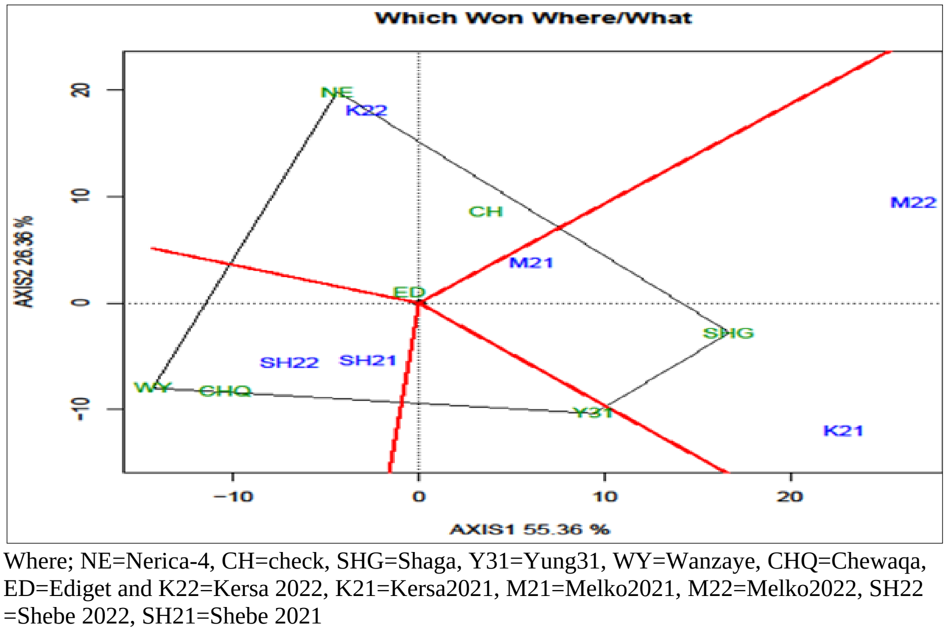
Where: Df=degrees of freedom, SS=sum squares, MS=mean square, TSS=total sum square explained in percentage and *** very highly significant, GEI=genotype by environment interaction

3. Genotype Main Effect and Genotype by Environment Interaction (GGE) Bi-Plot Stability Analysis

The GGE (genotype main effect (G) and genotype-by-environment interaction (GEI) concept is based on the understanding that genotype main effect (G) and GEI are the two sources of variation that are relevant to genotype evaluation and that they must be considered simultaneously for appropriate genotype evaluation (Yan, 2001) [16]. The graphical method was employed to investigate environmental variation and interpret GEI. The partitioning of GEI through GGE bi-plot analysis showed that IPCA-1 and IPCA-2 accounted for 55.36% and 26.36% of sum of squares, respectively, with a total of 81.72% variation for grain yield.

3.1 Which won where/What view of GGE-bi-plot

The GGE bi-plot showed four vertex genotypes were, Shaga (SHG), Nerica-4 (NE), Wanzaye (WZ) and Yung 31 (Y31). The vertex genotypes of each sector is the one that gave the highest grain yield in the environments which fell within that sector (Figure 1). The GGE bi-plot identified three rice growing mega-environments. The first mega environment consisted of environments Melko2022 (M22), Melko 2021 (M21) and Kersa2021 with the vertex genotype of Shaga (SHG) and Second mega environment consists of Kersa2022 (K22) with the vertex genotype of Nerica-4 (NE) and third mega environment consists of Shebe2021 and Shebe2022 with the vertex genotype of Wanzaye (WZ). It was also noted that no mega-environments fell into sectors where Yung 31 (Y31) was the vertex genotype (Fig1).

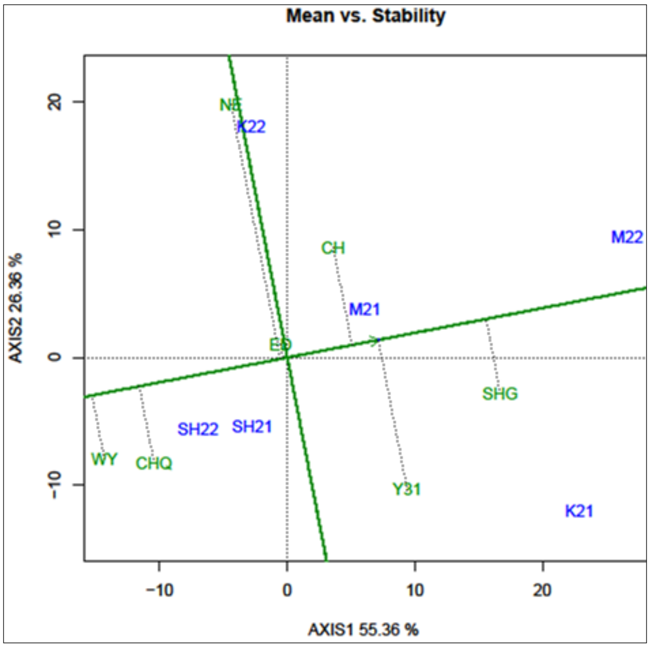


Where; NE=Nerica-4, CH=check, SHG=Shaga, Y31=Yung31, WY=Wanzaye, CHQ=Chewaqa, ED=Ediget and K22=Kersa 2022, K21=Kersa2021, M21=Melko2021, M22=Melko2022, SH22 =Shebe 2022, SH21=Shebe 2021

Fig 1: The polygon view of GGE biplot to the identification of winning genotypes and their related Mega environments

3.2 Mean and Stability of Genotypes

In GGE biplot methodology, the estimation of grain yield and stability of genotypes was done using the average environment (tester) coordinate (AEC) methods (Yan and Hunt, 2002) [14]. The line passing through the bi-plot origin is called the average environment (tester) coordinate (AEC), which is defined by the average PC1 and PC2 scores for all environments. The rice genotypes Ediget (ED), Shaga (SHG) and Yung31 (Y31) were high yielders and the rice variety Chewaqa (CHQ) and Wanzaye (WZ) were low yielders at tested locations. The line, which passes through the origin and is perpendicular to the AEC, represents the stability of genotypes. Either direction away from the bi-plot origin, on the axis, indicates greater GEI and reduced stability. For selection, the ideal genotypes are those with both high mean grain yield and high stability. In the bi-plot, they are close to the origin and have the shortest vector from the AEC. A longer projection to the AEC, regardless of direction, represents a greater tendency of the GEI of a genotype that means less stability across environments. The rice genotypes Ediget (ED) and Shaga (SHG) were high yielders and the most stable, genotype Wanzaye (WZ) and Chewaqa) were stable but, low yielders, while Nerica-4 (NE) and Yung31 (Y31) were the most unstable genotypes (Fig 2).

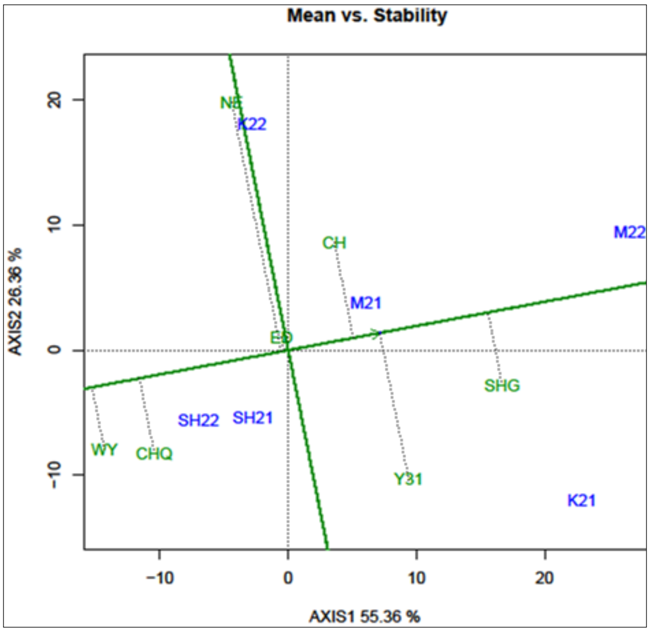


Where: NE=Nerica-4, CH=check, SHG=Shaga, Y31=Yung31, WY=Wanzaye, CHQ=Chewaqa, ED=Ediget and K22=Kersa 2022, K21=Kersa2021, M21=Melko2021, M22=Melko2022, SH22=Shebe 2022, SH21=Shebe 2021

Fig 2: GGE biplot visualization of the genotypes ranking for both yield and stability performance over environments

3.3 Ranking of Genotypes

An ideal genotype is expected to have the highest mean grain yield performance and stability in performance across environments (Farshadfar *et al*., 2012) [6]. Though such an ideal genotype may not exist in reality, it can be regarded as a reference for genotype evaluation (Kaya *et al*., 2006) [8]. The ideal genotype is located in the first concentric circle in the bi-plot. Genotypes found closer to the ideal genotypes are desirable genotypes and those found far from the ideal genotype are considered as undesirable genotypes. Thus, the ideal genotype can be used as a benchmark for selection. Genotypes that are far away from the ideal genotype can be rejected in early breeding cycles, while genotypes that are close to it can be considered in further tests (Yan and Kang, 2003) [15]. Accordingly, genotypes placed near to the first concentric circle, Shaga (SHG) and Yung 31 (Y31) were found to be benchmarks for evaluation of upland rice genotypes (Figure 3). Undesirable genotypes were those distantly located from the first concentric circle, namely, Wanzaye (WY) and Chewaqa (CHQ) (Fig3).

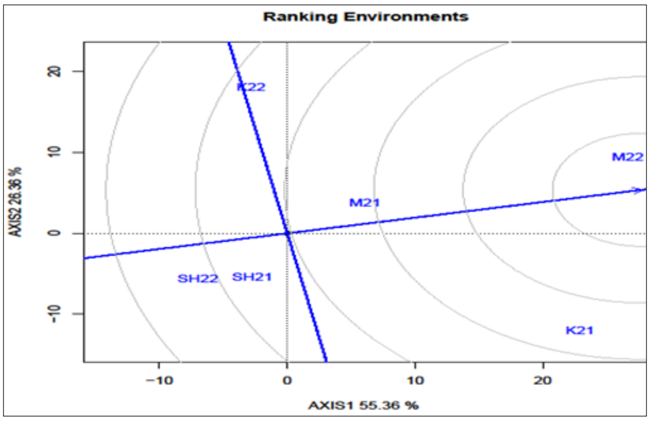


Where: NE=Nerica-4, CH=check, SHG=Shaga, Y31=Yung31, WY=Wanzaye, CHQ=Chewaqa, ED=Ediget and K22=Kersa 2022, K21=Kersa2021, M21=Melko2021, M22=Melko2022, SH22=Shebe 2022, SH21=Shebe 2021

Fig 3: GGE biplot of ideal genotypes and comparison of the genotypes with respect to the ideal genotype

3.4 Ranking of Environments

Discriminating ability and representativeness are important properties of a test environment. An ideal environment should be differentiating the tested genotypes and at the same time be a representative of the target agro-ecology (Yan, 2001 [13]; Yan and Kang, 2003) [15]. Similar to ideal genotype, an ideal environment is defined and shown by the small circle. Meaning that the environment is more desirable and discriminating when located closer to the center of a circle or to an ideal environment. Yan *et al*. (2001) [13] suggested that favorable test environments should have large PC1 scores (more discriminating of the genotypes) and near zero PC2 scores (more representative of an average environment). Accordingly, M22 (Melko2022), which had the longest vector which fell into the center of concentric circles, was considered as an ideal environment in terms of being the most representative of the overall environments and the most powerful to discriminate rice genotypes. Thus, K21 (Kersa 2021) was an ideal environment which could be used as a benchmark to evaluate the remaining environments. M21 (Melko 2021) was closer to the ideal environment, thus, it was regarded as the most desirable environment to select widely adapted rice genotypes (Figure 4). Conversely environments K22 (Kersa2022), SH21 (Shebe2021) and SH22 (Shebe2022) were located far from the ideal environment, thus were considered as less powerful to discriminate the rice genotypes (Fig4).



Where: K22=Kersa 2022, K21=Kersa2021, M21=Melko2021, M22=Melko2022, SH22=Shebe 2022, SH21=Shebe 2021

Fig 4: GGE biplot of ideal environments and comparison of the environments with respect to the ideal environment

Conclusion

The results of this study indicated that rice grain yield performances were highly influenced by environmental effect followed by the magnitude of GEI and genotype contributed the least effect. The magnitude of GEI effect was about more than four times that of genotype. Rice genotypes showed cross over GEI across environment and among genotypes tested, there were desirable genotypes in terms of mean yield and stability. The upland rice variety, Shaga showed good performance in both mean grain yield and stability and thus recommended for large scale production. Regarding testing environments, there exist three possible mega environments (Mega-1, 2 and 3) in Southwestern (Jimma zone) part of Ethiopia. Thus, rice breeding program of Fogera, should consider these three different mega environments separately to maximize yield potential of upland rice through exploitation of positive GEI. Beside this, additional rice yield trials may be launched to better clearly identify the magnitude of GEI and the causes of GEI by considering necessary environmental and biological variables.

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G: Genotype
E: Environment
GEI: Genotype by Environment Interaction
PC: Principal component

Conflict of interest

The authors have not declared any conflict of interests.

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