



## Performance of Rain Fed Lowland Rice Genotypes in Multi Environment Trials as Analyzed Using Ggebiplot

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### Abstract:

Twenty rainfed lowland rice genotypes were evaluated at four locations of ten environments in western and north western part of Ethiopia from 2009 to 2011 to identify stable and high yielding genotypes for possible release and to determine mega environments. Randomized complete block design with three replications was used. GGE (G= genotype plus GE= genotype-by-environment interaction) biplot methodology was used for graphically display of grain yield data. The combined analysis of variance revealed that environment (E) accounted for 43.3% of the total variation while G and GEI captured 10.3% and 25.8%, respectively. The first 2 principal components (PC1 and PC2) were used to create a 2-dimensional GGE biplot and explained 34.7% and 22.9% of GGE sum of squares (SS), respectively. Genotypic PC1 scores >0 detected the adaptable and/or higher-yielding genotypes, while PC1 scores <0 discriminated the non-adaptable and/or lower-yielding ones. Unlike genotypic PC1 scores, near-zero PC2 scores identified stable genotypes, whereas absolute larger PC2 scores detected the unstable ones. On the other hand, environmental PC1 scores were related to non-crossover type GEIs and the PC2 scores to the crossover type. Of the tested genotypes, G17, G11, G9, and G20 were found to be desirable in terms of high yielding ability and stability. Based on GGEbiplot analysis, the test environments were classified into three mega-environments (Mega-1, Mega-2 and Mega-3). Mega -1 included environments such as WO-1, WO-4 and WO-7 (all are representing Woreta) with genotype 4 as a winner; Mega-2 constituted environments such as AZ-2, AZ-10 (Addis Zemen) and AS-5 and AS-10 (Assosa) with genotype 17 as a winner and Mega-3 contained environments including PA-3, PA-6 and PA-9 (all are representing Pawe) with genotype 2 as winner. The two testing locations (Addis Zemen and Assosa) were found to be combined in Mega environment-2 and highly correlated, indicating as there is no need to conduct variety trial at both locations as the result in one can represent the other. By doing so research cost can be reduced. The result of this study can be used as a driving force for the national rice breeding program to design breeding strategy that can address the request of different stakeholders for improved varieties through either exploiting or avoiding the effect of GEI. Among the tested genotypes in this study, three candidate genotypes including genotype 17, 11 and 9 were selected and verified. Of which, considering their performance in terms of grain yield, stability, farmers' preferences and other desirable agronomic traits, genotype 9 has been officially released as wide adaptable variety with better performance for large scale production with the vernacular name "HIBER" meaning unity.

*Key words: Multi-Environment Trials, GGE biplot, analysis, G × E interaction, lowland rice*

### INTRODUCTION:

Plant breeders perform multi-environment trials (MET) to evaluate genotypes across several locations and over years before a specific genotype is officially released for large scale production. In such experiments, genotype × environment (GE) interaction is commonly observed (Yan *et al.*, 2007). A GE interaction refers to differential ranking of genotypes across environments and may complicate the selection process and recommendation of a genotype for a target environment (Ebdon and Gauch, 2002; Gauch, 2006). It may also reduce the selection efficiency in different breeding programs because in a GE interaction, measured traits are less predictable and cannot be interpreted using main effects (genotype or environment) and need more analysis (Gauch *et al.*, 2008). GE interaction is also one of

the most important reasons for the failure or decreased efficiency of breeding efforts to serve small resource-poor farmers (Ceccarelli, 1996). Gauch and Zobel (1996) explained the importance of GEI as: "Were there no interaction, a single variety of any crop would yield the most the world over, and furthermore the variety trial need to be conducted at only one location to provide universal results". Hence, GE interaction must be either exploited by selecting superior genotype for each specific target environment or avoided by selecting widely adapted and stable genotype across wide range of environments (Ceccarelli, 1996). This can be materialized by analyzing the genotype-by-environment data from multi environment trials which has been an important component of plant breeding and cultivar recommendation (Yan, 2011).



Different statistical models are used to describe GE interaction and facilitate genotype recommendations in MET. These models have been classified as univariate *versus* multivariate approaches (Flores *et al.*, 1998). Multivariate statistical approaches explore multi-directional aspects of GE interaction and attempt to extract more information from GE interaction components (Gauch and Zobel, 1996; Gauch *et al.*, 2008). Several multivariate procedures have been proposed to explore GE interaction including principal component analysis (PCA), additive main effects and multiplicative interactions (AMMI) and genotype plus GE interaction biplot (GGE biplot) analysis (Yan *et al.*, 2000; Zobel *et al.*, 1988). Of which GGE biplot analysis is a new technique for graphical display of GE interaction pattern of MET data with many advantages (Yan *et al.*, 2000).

GGE biplot analysis considers both genotype (G) and GE interaction effects and graphically displays GE interaction in a two way table (Yan *et al.*, 2000). GGE biplot is an effective method based on principal component analysis (PCA) to fully explore MET data. It allows visual examination of the relationships among the test environments, genotypes and the GE interactions. It is an effective tool for: (i) mega-environment analysis (e.g. “which-won-where” pattern), where by specific genotypes can be recommended to specific mega-environments (Yan and Kang, 2003; Yan and Tinker, 2006), (ii) genotype evaluation (the mean performance and stability), and (iii) environmental evaluation (the power to discriminate among genotypes in target environments) (Ding *et al.*, 2007). It has been proposed that GGE biplot analysis was a useful method for the analysis of GE interactions and had been exploited in the variety evaluation of wheat (Yan and Hunt 2001; Yan *et al.*, 2000), Maize (Fan *et al.*, 2007), soybean (Yan and Rajcan, 2002) and rice (Balestre *et al.*, 2010).

Among the target commodities that have received due attention in promotion of agricultural production, rice is considered as the “millennium crop” expected to contribute in ensuring food security in Ethiopia (MoARD, 2010). Though introduced recently, the importance of rice is being well recognized both by the Government and different stakeholders as the crop is treated as one of the major national research projects and the trend of area coverage and total production is on the increase. As a result, the demand for improved varieties is increasing which has to be addressed through developing different varieties for different situations. However, this needs to understand the

genotype by environment interaction which is a prerequisite to design demand driven breeding strategies through conducting multi environment yield trials and analyzing the data using appropriate statistical software. Therefore, the objectives of this research activity were:

- To interpret the magnitude and causes of genotype (G), environment (E) and GE interaction on grain yield performances of 20 lowland rice genotypes tested across 10 environments,
- To evaluate rice genotypes for their yield performance and stability and select and release genotypes with high grain yield, stability and other desirable agronomic traits
- To examine the possible existence of different mega environments and the winning genotype for each mega environment

## MATERIALS AND METHODS

Planting materials and trial management Nineteen rainfed lowland rice genotypes plus one standard check (Table 1) were evaluated from 2009 to 2011 at four locations of ten environments including, Woreta (WO-1, WO-4 and WO-7) Addis Zemen (AZ-2 and AZ-8), Pawe (PA-3, PA-6 and PA-9) and Asosa (AS-5 and AS-10) in western and north western part of Ethiopia. The locations where the experiment was conducted differ in soil type, altitude, temperature, rainfall received per annum (Table 2). The experiment was laid out in randomized complete block design (RCBD) with three replications. Each plot had six rows of 5 m length and spaced 0.2 m apart. Fertilizer (UREA and DAP) was applied as per the recommendation of each respective location. Total DAP was applied at planting while urea was applied one third at planting, one third at tillering and the remaining one third at panicle initiation. Dry seed rate of 60 kg ha<sup>-1</sup> was used and seeds were drilled in a row. Plantings were done in the main cropping season (rainy season) following the optimal dates in each respective location. All relevant agronomic practices were applied when deemed necessary. Data on grain yield and some other yield components were collected (Table 1). However, this paper is reporting mainly on grain yield data (t ha<sup>-1</sup> at 14% moisture level and estimated on the basis of four central harvestable rows).



**STATISTICAL ANALYSIS**

Analysis of variance was done using system analysis software (SAS, 2004). Before grain yield data analysis, homogeneity of variance was determined by Bartlett's test (Gomez and Gomez, 1984). The data were found to be homogenous and subjected to combined analysis of variance (ANOVA) to determine the effects of environment (E), genotype (G), and their interactions. The data were also graphically analyzed for interpreting GE interaction using the GGEbiplot software (GGEbiplot, 2009). GGE biplot methodology, which is composed of two concepts, the biplot concept (Gabriel, 1971) and the GGE concept (Yan *et al.*,

2000), was used to visually analyze the lowland rice genotypes MET data. This methodology uses a biplot to show the factors (G and GE) that are important in genotype evaluation and also the sources of variation in GE interaction analysis of MET data (Yan, 2001). The graphs were generated based on (i) "which-won-where" pattern, (ii) ranking of genotypes on the basis of yield and stability, (iii) comparison of genotypes to an ideal genotype, (iv) genotype –environment relationships (v) relationships between testing environments based on the angles between the vectors of the environments and (vi) discriminating ability and representativeness of the test environments.

Name of Genotype	Geno type code	Days to maturity	Panicle length (cm)	Plant height (cm)	% effective tillers/plant	No. of grains/panicle	% fertile grains/panicle	Thousand grain wt (gm)	Grain yield (t ha <sup>-1</sup> )
FKRS	1	136.2 <sup>fgh</sup>	27.7 <sup>ef</sup>	71.8 <sup>ef</sup>	85.3	114.8 <sup>bcd</sup>	88.5 <sup>def</sup>	34.3 <sup>a</sup>	2.9 <sup>de</sup>
IR75502-5-1-1-B	2	141.1 <sup>bc</sup>	28.7 <sup>def</sup>	74.8 <sup>de</sup>	84.7	126.2 <sup>ab</sup>	91 <sup>abcde</sup>	25.2 <sup>ef</sup>	3.5 <sup>bc</sup>
IR72022-7-6-3-2-3	3	140.3 <sup>cd</sup>	27.8 <sup>ef</sup>	66.3 <sup>f</sup>	86.3	108.5 <sup>de</sup>	85.2 <sup>g</sup>	21.4 <sup>ij</sup>	2.8 <sup>fg</sup>
ROJOMENA271/10	4	139.2 <sup>de</sup>	37 <sup>a</sup>	96.2 <sup>a</sup>	89.5	125.7 <sup>ab</sup>	92.1 <sup>ab</sup>	25.6 <sup>e</sup>	4.2 <sup>a</sup>
IR75517-23-1-1-B	5	134.2 <sup>ij</sup>	29.3 <sup>cdef</sup>	80.8 <sup>bcd</sup>	85.7	110.1 <sup>cde</sup>	91 <sup>abcde</sup>	29.8 <sup>cd</sup>	2.8 <sup>efg</sup>
IR71730-51-2	6	138.8 <sup>de</sup>	27.9 <sup>ef</sup>	71.5 <sup>ef</sup>	86.1	104.3 <sup>e</sup>	86 <sup>fg</sup>	24.5 <sup>efg</sup>	2.4 <sup>g</sup>
WAB272-B-B-5-H4	7	131.4 <sup>r</sup>	29 <sup>bcdef</sup>	83.5 <sup>bc</sup>	87.4	109.9 <sup>cde</sup>	90 <sup>abcde</sup>	31.9 <sup>b</sup>	2.8 <sup>def</sup>
IRGA370-38-1-1F-B1-1	8	132.4 <sup>jk</sup>	28.2 <sup>ef</sup>	76.9 <sup>cde</sup>	88.1	104 <sup>e</sup>	93.2 <sup>a</sup>	30.3 <sup>cd</sup>	3.7 <sup>b</sup>
WAB95-B-B-40-HB	9	135.1 <sup>ghi</sup>	33.8 <sup>abcd</sup>	95.3 <sup>a</sup>	87.0	111 <sup>cde</sup>	91 <sup>abcde</sup>	30.1 <sup>cd</sup>	3.3 <sup>cd</sup>
IR76999-52-1-3-2	10	142 <sup>abc</sup>	26.6 <sup>f</sup>	71.3 <sup>ef</sup>	84.8	110.3 <sup>cde</sup>	88.8 <sup>cde</sup>	24.2 <sup>fg</sup>	3.1 <sup>def</sup>
WAB502-8-5-1	11	135 <sup>fghi</sup>	34.1 <sup>abc</sup>	91.3 <sup>a</sup>	84.6	121 <sup>abcd</sup>	90 <sup>abcde</sup>	29.9 <sup>cd</sup>	3.7 <sup>b</sup>
WAB368-B-HI-HB	12	136.5 <sup>fg</sup>	32 <sup>abcde</sup>	84 <sup>b</sup>	85.3	120 <sup>abcd</sup>	91 <sup>abcde</sup>	30.5 <sup>c</sup>	3.1 <sup>cd</sup>



IR74052-184-3-3	13	142.4 <sup>ab</sup>	25.1 <sup>f</sup>	70.9 <sup>ef</sup>	85.1	121 <sup>abcd</sup>	85.2 <sup>g</sup>	22.6 <sup>hi</sup>	2.7 <sup>g</sup>
WABC165{IAC165}	14	134.6 <sup>hi</sup>	33.7 <sup>abcd</sup>	92.2 <sup>a</sup>	84.6	116.2 <sup>bcd</sup>	91.2 <sup>abc</sup>	30.4 <sup>cd</sup>	3.2 <sup>cd</sup>
PSBRC44	15	143.6 <sup>a</sup>	29.1 <sup>cdef</sup>	75.5 <sup>de</sup>	84.8	116.3 <sup>bcd</sup>	90 <sup>bcde</sup>	23.3 <sup>gh</sup>	3.0 <sup>de</sup>
PSBRC46	16	141.9 <sup>abc</sup>	29 <sup>bcdef</sup>	80.1 <sup>bcd</sup>	84.2	122.8 <sup>abc</sup>	89.5 <sup>bcd</sup>	21.9 <sup>i</sup>	2.8 <sup>de</sup>
PSBRC92	17	137.6 <sup>ef</sup>	34.7 <sup>ab</sup>	93.2 <sup>a</sup>	89.7	133.6 <sup>a</sup>	91.8 <sup>abc</sup>	20.4 <sup>j</sup>	4.0 <sup>a</sup>
WAB376-B-10-H3	18	135 <sup>efghi</sup>	33.8 <sup>abcd</sup>	91.3 <sup>a</sup>	84.2	116.9 <sup>bcd</sup>	89.9 <sup>bcd</sup>	29.1 <sup>d</sup>	3.2 <sup>cde</sup>
PSBRC50	19	142.1 <sup>abc</sup>	28.3 <sup>ef</sup>	73.1 <sup>ef</sup>	84.9	111.6 <sup>cde</sup>	91 <sup>abcde</sup>	24.5 <sup>efg</sup>	3.0 <sup>de</sup>
GUMARA{Check}	20	135 <sup>efghi</sup>	35.3 <sup>a</sup>	97 <sup>a</sup>	84	115 <sup>bcde</sup>	88 <sup>efg</sup>	29.3 <sup>cd</sup>	2.9 <sup>def</sup>
Mean		137.8	30.7	81.9	85.8	116.0	89.6	27.0	3.2
CV (%)		2.5	33.6	16.3	21.9	22.3	6.8	9.7	26.4
Genotype (GEN)		**	**	**	NS	**	**	**	**
Environment (ENV)		**	**	**	**	**	**	**	**
GEN*ENV		**	NS	**	NS	NS	**	**	**

**Table 1.** List of testing genotypes and their mean performance for grainyield and for some agronomic traits tested at four locations from 2009 to 2011

\*\* Significant at  $p < 0.01$  probability level; NS= non -significant

**Table 2.** Description of experimental locations

Agro ecological character	Locations			
	Woreta	Addis Zemen	Pawe	Assosa
Latitude	11 <sup>o</sup> 58'N	11 <sup>o</sup> 92 'N	11 <sup>o</sup> 9'N	10 <sup>o</sup> 03'N
Longitude	37 <sup>o</sup> 41' E	37 <sup>o</sup> 7' E	36 <sup>o</sup> 3' E	34 <sup>o</sup> 59'E
Altitude (masl)	1810	1780	1050	1590
Annual rainfall(mm)	1300	1032	1457	1050



Mean maximum temp.(<sup>0</sup>C) 27.9 29.36 32.75 29

Mean minimum temp(<sup>0</sup>C) 11.5 11.31 17.17 14

Soil type Vertisol Fluvisol Cambisol Nitosol

Source: Agricultural development office of each respective location

## RESULTS AND DISCUSSION

### Analysis of variance

The combined analysis of variance showed significant difference among the tested genotypes in all measured parameters except % effective tillers /plant. (Table 1), The combined analysis of variance for grain yield is presented in Table 3. Genotype (G), environment (E) and genotype × environment interaction (GEI) were significant ( $P \leq 0.01$ ). Such statistical interaction resulted from the changes in the relative ranking of the genotypes from one environment to another. The significant genotype × environment interaction effects demonstrated that genotypes responded differently to the variation in environmental conditions indicating the necessity of testing rice varieties at multiple locations. This also shows the difficulties encountered by breeders in selecting new varieties for release. The factors explained (%) show that rice grain yield was affected by environment (43.3%), genotype (10.3%) and their interaction (25.8%).

Gauch and Zobel (1997) reported that, in normal MEYTs, E accounts for about 80% of the total variation, while G and GE each account for about 10%. However, it is G and GE that are relevant to cultivar evaluation (Yan *et al.* 2002). The large GE interaction, relative to G effect, in this study suggests the possible existence of different mega-environments (Yan and Kang, 2003).

It is commonly reported that MET data may constitute a mixture of cross over and non-cross over types of GE interaction. The former indicates the change in yield ranking of genotypes across environments and the later shows constant yield rankings of genotypes across environment (Yan and Hunt, 2001; Matus-Cadiz *et al.*, 2003). Accordingly, in this study inconsistency in grain yield ranking from environment to environment was observed (Table 4) indicating the presence of possible cross over GEI as described by Yan and hunt (2001) and Kaya *et al* (2006). The mean grain yield of the 20 genotypes ranged from 2.4 to 4.2 t ha<sup>-1</sup> and the highest grain yield was obtained from genotype 4 and the lowest from genotype 6 (Table 4).

Table 3. Combined analysis of variance of grain yield (t ha<sup>-1</sup>) of 20 lowland rice genotypes tested across 10 environments

Source of variation	Degree of freedom	Sum of squares	Mean squares	Explained variation (%)
Total	599	1475.9		
Replication	2	3.4		



<b>Genotype(G)</b>	19	152.1	8.0**	10.3
<b>Environment(E)</b>	9	639.8	71.0**	43.3
<b>G*E</b>	171	382.1	2.2**	25.8
<b>Error</b>	398	298.5		

\*\* Significant at  $P \leq 0.01$  probability level

Table 4. Mean grain yield ( $t\ ha^{-1}$ ) of 20 rainfed lowland rice genotypes evaluated at four locations from 2009 to 2011

Genotype		Woreta			Pawe			Addis Zemen		Assosa		Mean
Name	code	2009	2010	2011	2009	2010	2011	2009	2011	2010	2011	
FKRS	1	3.3	1.7	3.9	4.7	1.8	3.9	2.1	2.7	2.4	2.7	2.9 <sup>de</sup>
IR75502-5-1-1-B	2	3.1	1.7	5.1	4.9	3.1	4.2	2.4	3.6	3.0	3.9	3.5 <sup>bc</sup>
IR72022-7-6-3-2-3	3	3.4	2.3	3.8	3.6	1.7	5.3	2.8	1.8	2.3	1.2	2.8 <sup>fg</sup>
ROJOMENA271/10	4	7.9	5.8	8.9	3.1	1.3	3.9	1.5	3.7	2.6	3.7	4.2 <sup>a</sup>
IR75517-23-1-1-B	5	3.7	2.1	3.9	3.9	1.2	4.8	1.8	2.7	2.3	1.7	2.8 <sup>efg</sup>
IR71730-51-2	6	2.5	1.5	3.3	3.9	2.0	3.5	1.9	1.8	1.9	2.1	2.4 <sup>g</sup>
WAB272-B-B-5-H4	7	3.7	3.7	4.7	3.0	1.2	3.9	1.8	2.1	1.9	2.2	2.8 <sup>def</sup>
IRGA370-38-1-1F-B1-1	8	6.6	2.2	5.8	4.3	2.2	4.7	2.2	3.9	3.1	2.0	3.7 <sup>b</sup>
WAB95-B-B-40-HB	9	4.3	4.7	4.2	3.9	1.5	4.7	2.5	2.6	2.5	2.5	3.3 <sup>cd</sup>



IR76999-52-1-3-2	10	4.9	2.2	7.0	4.1	1.6	3.1	1.8	2.7	2.2	1.4	3.1 <sup>def</sup>
WAB502-8-5-1	11	5.4	2.9	6.1	3.4	2.1	4.6	2.0	4.5	3.2	2.7	3.7 <sup>b</sup>
WAB368-B-HI-HB	12	1.9	2.2	4.5	3.9	2.7	4.4	2.1	4.1	3.1	2.3	3.1 <sup>cd</sup>
IR74052-184-3-3	13	2.4	2.2	5.7	3.5	1.6	3.5	2.9	1.7	2.3	1.1	2.7 <sup>g</sup>
WABC165{IAC165}	14	4.5	2.1	5.3	3.4	1.7	4.0	2.4	3.6	3.0	2.1	3.2 <sup>cd</sup>
PSBRC44	15	3.4	2.5	5.2	4.3	1.5	3.2	2.6	2.4	2.5	1.9	3.0 <sup>de</sup>
PSBRC46	16	3.5	1.4	5.4	4.0	1.6	2.9	2.3	2.0	2.2	2.6	2.8 <sup>de</sup>
PSBRC92	17	5.6	3.8	6.5	4.9	2.4	4.3	1.9	4.6	3.2	3.0	4.0 <sup>a</sup>
WAB376-B-10-H3	18	3.5	1.4	4.6	4.0	2.0	4.2	1.9	4.6	3.2	2.2	3.2 <sup>cde</sup>
PSBRC50	19	3.0	2.2	5.6	3.5	2.1	5.2	2.7	1.2	2.0	2.6	3.0 <sup>de</sup>
GUMARA{Check}	20	4.8	1.0	4.8	3.1	2.2	3.0	2.2	3.3	2.8	1.7	2.9 <sup>def</sup>
Mean		4.1 <sup>b</sup>	2.5 <sup>de</sup>	5.2 <sup>a</sup>	3.9 <sup>b</sup>	1.9 <sup>f</sup>	4.1 <sup>b</sup>	2.2 <sup>e</sup>	3.0 <sup>c</sup>	2.6 <sup>d</sup>	2.3 <sup>e</sup>	

### Polygon view of GGE biplot analysis of MET data

The polygon view of a biplot is the best way to visualize the interaction patterns between genotypes and environments (Yan and Kang, 2003) to show the presence or absence of cross over GE interaction which is helpful in estimating the possible existence of different mega environments (Gauch and Zobel, 1997; Yan and Rajcan, 2002; Yan and Tinker, 2006). Visualization of the "which won where" pattern of MET data is necessary for studying the possible existence of different mega environments in the target environment (Gauch and Zobel, 1997; Yan *et al.*, 2000).

Fig. 1 represents a polygon view of lowland rice genotypes MET data in this investigation. In this biplot, a polygon was formed by connecting the vertex genotypes with straight lines and the rest of the genotypes placed within the

polygon. The vertex genotypes in this study were 4,17,2 6,7 and 13. These genotypes were the best or the poorest genotypes in some or all of the environments because they were farthest from the origin of the biplot (Yan and Kang, 2003). From the polygon view of biplot analysis of MET data, the genotypes fell in seven sections and the test environments fell in three sections. The first section contains the test environments WO-1.WO-4 and WO-7 which had the genotype 4 as the winner; the second section contains the environments AZ-2, AZ-8, AS-5 and AS-10 with genotype 17 as the best yielder; the third section contains the test environments PA-3, PA-6 and PA-9 with genotype 2 as the winner. This cross over GE suggests that the target environments may be divided in to three mega environments. No environments fell in to the sectors of vertex genotypes 6,7 and 13. This means that these

genotypes were not the winner in any of the environment, rather, they were likely to be the poorest genotypes in some or all of the environments as indicated in Table 4.

**Mean yield and stability performance of genotypes**

Yield performance and stability of genotypes were evaluated by an average environment coordination (AEC) method (Yan, 2001; Yan and Hunt, 2002; Yan, 2002). In this method, an average environment is defined by the average PC1 and PC2 scores of all environments, represented by a small circle (Figure 2). A line is then drawn to pass through this average environment and the biplot origin; which is called the average environment axis (AEA) 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 2). Unlike the AEC abscissa, which has one direction, with the arrow pointing to greater genotype main effect, the AEC ordinate is indicated by double arrows, and either direction away from the biplot origin indicates greater GEI effect and reduced stability. For selection, the ideal genotypes are those with both high mean yield and high stability. In the biplot, they are close to the origin and have the shortest vector from the AEC. Genotype 17 followed by 11 and 9 can be considered as genotypes with both high yield and stability performance. The other genotypes on the right side of the line with double arrows have yield performance greater than mean yield and the genotypes on the left side of this line had yields less than mean yield.

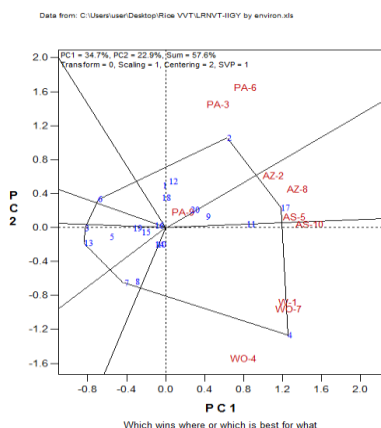


Fig.1 The which-won-where view of the GGE biplot

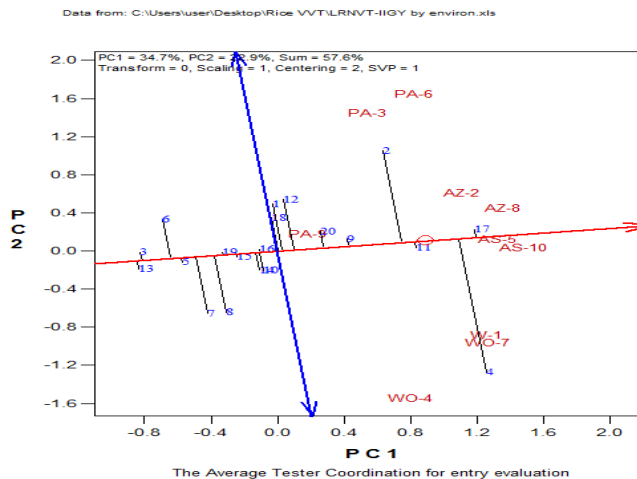


Fig. 2 GGE biplot showing the ranking of genotypes for both yield and stability performance over environments

Note: WO=Woreta, AZ=Addis Zemen, PA=Pawe, AS=Assosa

The genotypes with highest yielding performance but low stability were 4, 2 and 12 whereas the genotypes with low yield and low stability were 6,7and 8. Yan and Kang (2003) noted that based on their grain yield and stability performance genotypes are classified in to three categories: (1) generally adapted, genotypes with high yield and stability performance (2) specifically adapted,genotypes with high mean yield but low stability performance and (3) adapted nowhere, genotypes with low grain yield and low stability performance.

**Performance of rice genotypes in all environments**

To visualize the performance of each genotype in each environment both the genotype and environmental vectors are drawn (Fig 3). The performance of the genotype in an environment is better than average if the angle between its vector and the environment’s vector is less than 90°; if the angle is greater than 90° it is less than average and if the angle is about 90° it is near to average (Yan and Tinker, 2006). Accordingly, genotype 4 performed very well in environments WO-1, WO-4 and WO-7 than others. Similarly genotypes 2 and 17 showed better performance in environment PA-3, PA-6 and AZ-2, AZ-8, AS-5, AS-10,



respectively than other environments. On the contrary, genotypes 3,5, 6,13, showed poor performance in most of the environments. Different genotypes showed different responses in different environments. A genotype located nearer to the biplot origin has an average value in each of the environments. Such genotype has minimum contribution to both G and GE interaction. Besides, the length of genotype vector measures the contribution of the genotype to either G or GEI or both (Yan and Tinker, 2006). Thus, genotypes 2, 4, 6, 13, and 13 with the longest vector contributed to both G and GEI. On the other hand, genotype 14 having very short vector and nearer to the biplot origin has very minimum contribution to both G and GEI.

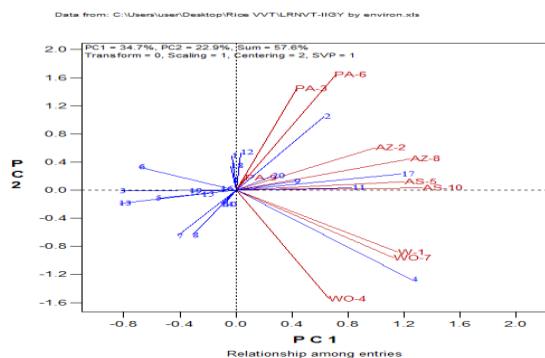


Fig. 3 The GGE biplot view showing the performance of each genotype in each environment

Note: WO=Woreta, AZ=Addis Zemen, PA=Pawe, AS=Assosa

### Evaluation of genotypes relative to an ideal genotype

An ideal genotype should have the highest mean performance and be absolutely stable (Yan and Kang, 2003). 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. Thus, using the ideal genotype as the center, concentric circles were drawn to help visualize the distance between each genotype and the ideal genotype. A genotype is more desirable if it is located closer to the ideal genotype. Thus, genotype 17 was located near to the ideal genotype and followed by genotypes 11, 9, 20, 2 and 4 in ascending order. On the other hand, genotypes 3,13,6,5,7,8,19,15, 16,10 and 14 were undesirable because they are far from the ideal genotype.

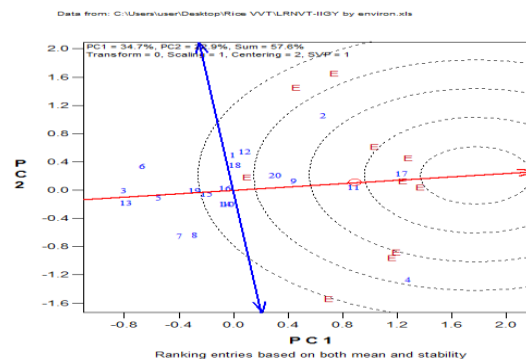


Fig. 4. GGE biplot of ideal genotype and comparison of the genotypes with the ideal genotype

Note: WO=Woreta, AZ=Addis Zemen, PA=Pawe, AS=Assosa

### RELATIONSHIPS AMONG TEST ENVIRONMENTS

Fig. 5 provides the summary of the interrelationships among the test environments. The lines that connect the biplot origin and the markers for the environments are called environment vectors. The angle between the vectors of two environments is related to the correlation coefficient between them. The cosine of the angle between the vectors of two environments approximates the correlation coefficient between them (Kroonenberg, 1995; Yan, 2002). Acute angles indicate a positive correlation, obtuse angles a negative correlation and right angles no correlation (Yan and Kang, 2003). Based on the angles between environment vectors, the ten environments fell in to three groups: WO-1, WO-4 and WO-7 (Woreta) formed group 1, AZ-2, AZ-8 (Addis Zemen) and AS-5 and AS-10 (Assosa) formed group two and PA-3, PA-6 and PA-9 (Pawe) formed group three. The smallest angle between Addis Zemen and Assosa implies that there was the highest correlation between them while the largest angle between Woreta and Pawe indicates the poor correlation between these locations (Figure 5). Yan and Tinker (2006) and Kaya *et al* (2006) reported that the presence of close associations between testing environments reveals that similar information about the genotype could be obtained from fewer test environments and hence this could be an opportunity to reduce testing cost under limited resources.

### Discriminating ability and representativeness of the test environments

Discriminating ability is an important measure of a test environment. A test environment which lacks discriminating ability provides no information about the cultivars and, therefore, it is useless (Yan and Kang, 2003). Another equally important measure of a test environment is its representativeness of the target environment. If a test environment is not representative of the target environment, it is not only useless but also misleading since it may provide biased information about the tested cultivars (Yan and Kang, 2003). GGE biplot discriminating ability of the genotypes and representativeness of the target environment is an important measure of the testing environments. The concentric circles on the biplot as shown in Fig. 6 help to visualize the length of the environment vectors, which is proportional to the standard deviation within the respective environments and is a measure of the discriminating ability of the environments. Therefore, among the ten testing environments, WO-4 and PA-6 were the most discriminating (informative) while PA-9 was the least discriminating one (Fig.6). Test environments that are consistently non-discriminating (non-informative) provide little information on the genotypes and, therefore, should not be used as test environments (Yan and Tinker, 2006). The average environment (represented by the small circle at the end of the arrow) has the average coordinates of all test environments, and Average-Environment Axis (AEA) is the line that passes through the average environment and the biplot origin (Yan, 2002). A test environment that has a smaller angle with the AEA is more representative of other test environments. Thus, AS-5 and AS-10 ( Assosa ) were the most representative environments whereas WO-1, WO-4,WO-7 (Woreta) and PA-3, PA-6(Pawe) were the least representative environments (Figure 6). Test environments (locations) that are both discriminating and representative are good test environments for selecting generally adaptable genotypes (Yan and Tinker, 2006). Hence, AS-5 and AS-10 (Assosa) were good test environments for selecting widely adapted genotypes. According to Yan and Tinker (2006) discriminating but non-representative test environments are useful for selecting specifically adaptable genotypes if the target environments can be divided into mega-environments or they are useful for culling unstable genotypes if the target environment is a single mega-environment. On the other hand, non-discriminating and non-representative environments are not useful. Thus, environments such as

WO-1, WO-4, WO-7 (Woreta) and PA-3, PA-6(Pawe) were used to select specifically adapted genotypes while PA-9 was not useful test environment.

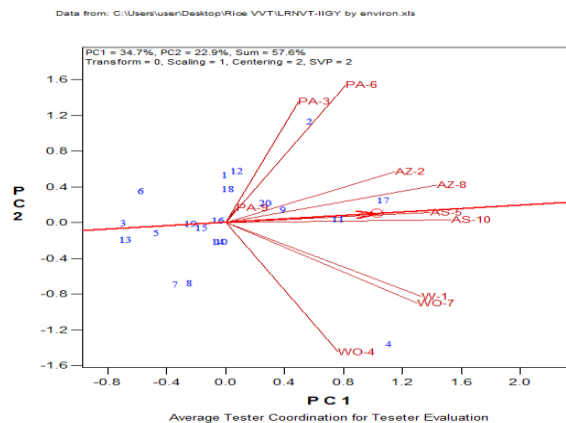


Fig. 5 GGE biplot on relationship among test environments

Note: WO=Woreta, AZ=Addis Zemen, PA=Pawe, AS=Assosa

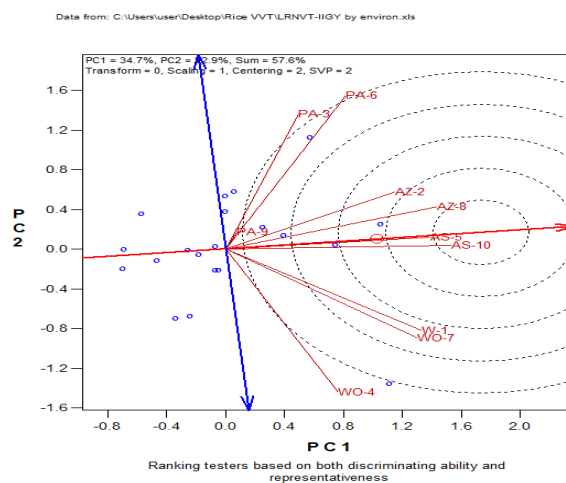


Fig. 6 Discriminating and representativeness view of the GGE biplot for the test environment

Note: WO=Woreta, AZ=Addis Zemen, PA=Pawe, AS=Assosa



## CONCLUSION

The result of this study indicated that lowland rice yield performance was highly influenced by the environment effect followed by GEI and genotype. The magnitude of GE interaction effect was about three times than that of the genotype effect. The tested genotypes exhibited crossover type of GEI revealed by their differential rankings across test environments. It was therefore, difficult to identify one superior genotype for all the environments.

GGE biplot analysis provides an easy and comprehensive solution to genotype by environment data analysis, which has been a challenge to plant breeders; It not only allows effective evaluation of the genotypes but also allows a comprehensive understanding of the target environment and the test environments. Specifically, biplot analysis can help one understand the target environment as a whole, i.e., whether it consists of a single or multiple mega-environments, which determines whether GE can be exploited or avoided. Within a single mega-environment, biplot analysis can help one understand the test environments: whether they are informative, representative, and unique in terms of genotype discrimination. At the same time, biplot analysis can help one evaluate genotypes in terms of both mean performance and stability across environments.

The 20 lowland rice genotypes showed very high variation for grain yield. In terms of mean grain yield and stability performance, there were desirable genotypes such as genotype 17; while there were also genotypes with high grain yield but low in stability such as genotype 4 and there were genotypes such as genotype 6 with poor performance. Regarding testing environments, there exist three possible mega-environments. The result of this study can be considered as a driving force for the national rice breeding program of the country to execute multi-location yield trials at a number of lowland rice potential growing areas of the country. So that demand driven breeding strategy can be designed and the effect of GEI can be either exploited or avoided as a result sustainable lowland rice production would be secured in the country.

Among the tested genotypes included in this study, three genotypes including genotype 17, 11 and 9 were selected and promoted to verification considering their better

performance in terms of grain yield, stability, farmers' preference and other desirable agronomic traits following the guideline for variety release of the country. Of which, genotype 9 has been officially released by the national variety release standing committee as a wider adaptable variety for large scale production with the vernacular name "HIBER" meaning unity.

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