



## Additive Main Effects and Multiplicative Interactions (AMMI) and genotype by environment interaction (GGE) biplot analyses aid selection of high yielding and adapted finger millet varieties

\*Dagnachew Lule<sup>1,2</sup>, Masresha Fetene<sup>3</sup>, Santie de Villiers<sup>4</sup> and Kassahun Tesfaye<sup>1</sup>

<sup>1</sup>Department of Microbial, Cellular & Molecular Biology, Addis Ababa University, Tel (+251)-911813638, \*E-mail: [hawinok@gmail.com](mailto:hawinok@gmail.com).

<sup>2</sup>Bako Agricultural Research Centre, Bako, Ethiopia

<sup>3</sup>Department of Plant Biology and Biodiversity Management, Addis Ababa University;

<sup>4</sup>Department of Chemistry and Biochemistry, Pwani University, Kenya

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### ABSTRACT

*Background and justification:* Lack of stable high yielding cultivars is one of the major bottlenecks for production and productivity of finger millets in Ethiopia. Identification of adaptable, stable and high yielding genotypes under varying environmental conditions prior to release as a cultivar is the first and foremost steps for plant breeding and this has direct bearing on the adoption of the variety, its productivity and total production of the crop.

*Objective:* The major objectives of the present study were to (i) assess the stability and yield performance of advanced finger millet genotypes evaluated in multiple environments, and (ii) identify stable high yielding candidate cultivar (s) for possible release using different statistical tools.

*Material and methods:* A total of 30 advanced finger millet genotypes were evaluated against two standard checks (Gute and Taddese) across four locations (Arsi Negele, Assosa, Bako and Gute) in 2012 and 2013 main cropping seasons. The trial was arranged in a randomized complete block design (RCBD) replicated three times.

*Summary result and application of the study:* Additive Main effect and Multiplicative Interaction (AMMI), Genotype and Genotype by Environment interaction (GGE) biplot analysis and, Eberhart and Russell model revealed that Acc. 203544 is stable high yielding (3.16 ton ha<sup>-1</sup>) with a yield advantage of 13.7% over the best standard check, Gute (2.78 ton ha<sup>-1</sup>), and thus should be recommended for possible release with wider environmental adaptability. Acc. 242111 (3.08 ton ha<sup>-1</sup>), Acc. BKFM0051 (3.07 ton ha<sup>-1</sup>) and Acc.229738 (2.99 ton ha<sup>-1</sup>) were also high yielding, but showed narrow stability and thus should be recommended for verification and possible release for specific environments.

**Key words/phrases:** Additive main effect and multiplicative interaction (AMMI), Finger millet (*Eleusine coracana* subsp. *coracana*), Genotype by Environment Interaction (GEI)

## INTRODUCTION

Finger millet (*Eleusine coracana* subsp. *coracana*) represents one of the critical plant genetic resources for the agriculture and food security of farmers inhabiting arid, infertile and marginal lands (Barbeau and Hilu, 1993). It has excellent nutritional value as its seeds contain 7 – 14% protein (Barbeau and Hilu, 1993) and is rich in calcium, iron, methionine, phosphorus, carbohydrate and other nutrients (Leung *et al.*, 1968). In general, breeding efforts in finger millet has been limited and farmers are growing unimproved and low yielding cultivars (Dida *et al.*, 2007; Neves, 2011). In Ethiopia, it occupies diversified agro-ecologies with a vast range of genetic variability and its utilization is deep-rooted in the culture of the people (Kebede and Menkir, 1986). The area allotted to the crop is increasing yearly (CSA, 2013). However, the current national average productivity is 1.5 tons ha<sup>-1</sup> (CSA, 2013); half of the potential productivity (3 tons ha<sup>-1</sup>) (Tadesse *et al.*, 1995). The lower productivity could be attributed mainly due to lack of stable high yielding and adaptable improved varieties, poor management practices and other biotic and abiotic factors (Kebede and Menkir, 1986; Bezawuletaw *et al.*, 2006). This necessitates development of stable high yielding cultivars with additional desirable traits. Evaluating genotypes under varying environmental conditions to recommend a new varieties for release as cultivars is fundamental and this has direct bearing on the adoption of a variety, productivity and total production of the crop (Flores *et al.*, 1998;

Showemimo *et al.*, 2000; Mustapha *et al.*, 2001). Genotypes exhibit fluctuating yields when grown in different environments or agro-climatic zones. This complicates demonstrating the superiority of a particular variety. Multi- environment yield trials are crucial to identify adaptable high yielding cultivars and discover sites that best represent the target environment (Yan *et al.*, 2000). Adaptability is the result of genotype, environment and genotype by environment interaction and generally falls into two classes: (1) the ability to perform at an acceptable level in a range of environments, referred to as general adaptability, and (2) the ability to perform well only in desirable environments, known as specific adaptability (Farshadfar and Sutka, 2006). Combined analysis of variance can quantify G x E interactions and describe the main effects but does not explain the interaction effect (Yuksel *et al.*, 2002; Asnake *et al.*, 2013). AMMI model and GGE biplot analysis are the most commonly used analytical and statistical tools to determine the pattern of genotypic responses across environments (Gauch and Zobel, 1996; Yan *et al.*, 2000; Yuksel *et al.*, 2002). The goal of the present study was, therefore, to determine the stability and yield performance of advanced finger millet genotypes at multiple locations using GGE biplot analysis, AMMI and the Eberhart and Russell model in order to identify stable high yielding candidate cultivar(s) recommend for possible release in the test environments and similar agro ecologies.

## MATERIALS AND METHODS

Thirty advanced finger millet genotypes were evaluated against the standard checks (Gute and Tadesse) at 4 locations - Arsi Negele (1947 m.a.s.l., 07°19, N, 38°39, E), Assosa (1417 m.a.s.l., 10°04, N, 34°31,E), Bako (1650 m.a.s.l., 07°17, N, 038°25,E) and Gute (1906 m.a.s.l., 09°00, N, 36°38, E) in the 2012 and 2013 main cropping season. The trial was arranged in a randomized complete block design (RCBD), replicated three times. Important agronomic traits, such as days to 50% heading, days to 50% maturity, plant height (cm), productive tiller number, ear length (cm), finger number per main ear and grain yield per plot (g) were recorded

following the finger millet descriptor (IBPGR, 1985). However, since grain yield is the central parameters for measurement of varietal adaptability and stability, data analysis and interpretation was done for grain yield alone.

### Data analysis

**Analysis using Eberhart and Russell model:** Yield stability was determined by regression of the mean grain yield of individual genotypes on environmental index and calculating the deviation from the regression according to Eberhart and Russell (1966) as:

$$Y_{ij} = \mu_i + b_i l_j + S^2 d_{ij};$$

Where  $Y_{ij}$  was the mean performance of  $i^{\text{th}}$  variety in  $j^{\text{th}}$  environment,  $\mu_i$  was the mean of  $i^{\text{th}}$  variety over all environments;  $b_i$  is the regression coefficient which measured the response of  $i^{\text{th}}$  variety to varying environment;  $S^2 d_{ij}$  was deviation from regression of  $i^{\text{th}}$  variety in the  $j^{\text{th}}$  environment, and  $l_j$  was the environmental index of  $j^{\text{th}}$  environment. Regression coefficient ( $b_i$ ) was considered as an indication of the response of the genotype to varying environment. If the regression coefficient was close to one ( $b_i = 1.0$ ), the genotype was adapted in all environments, genotypes with  $b_i > 1.0$  were more responsive or adapted to high yielding environments, whereas any genotype with  $b_i$  significantly lower than 1.0 was adapted to low yielding environments (Eberhart and Russell, 1966). Both AMMI and Eberhart and Russell models were computed using Agrobases software (Agrobases, 2000).

**Additive mean effect and multiplicative interaction model:** The AMMI model:

$$Y_{ger} = \mu + \alpha_g + \beta_e + \sum_n \lambda_n \gamma_{gn} \delta_{en} + \epsilon_{ger} + \rho_{ge};$$

where  $Y_{ger}$  was the observed yield of genotype ( $g$ ) in environment ( $e$ ) for replication ( $r$ );

**Additive parameters:**  $\mu$  was the grand mean;  $\alpha_g$  is the deviation of genotype  $g$  from the grand mean,  $\beta_e$  is the deviation of the environment  $e$ ;

**Multiplicative parameters:**  $\lambda_n$  was the singular value for interaction principal component axis (IPCA)  $n$ ,  $\gamma_{gn}$  was the genotype eigenvector for axis  $n$ , and  $\delta_{en}$  is the environment eigenvector;  $\epsilon_{ger}$  is the error term and  $\rho_{ge}$  are PCA residuals. Accordingly, genotypes with low (regardless of the sign) IPCA scores showed general or wider adaptability, while those with high IPCA scores showed specific adaptability (Gauch and Zobel, 1996).

**AMMI Stability Value (ASV):** The ASV is the distance from the coordinate point to the origin in a two-dimensional plot of IPCA1 scores against IPCA2 scores in the AMMI model (Purchase, 1997). Because the IPCA1 score contributes more to the  $G \times E$  interaction sum of squares, a weighted value is needed. This was calculated for each genotype and each environment according to the relative contribution of IPCA1 to IPCA2 as follows:

$$ASV = \sqrt{[(SS_{IPCA1} \div SS_{IPCA2})(IPCA1score)]^2 + (IPCA2score)^2}$$

Where  $SS_{IPCA1} / SS_{IPCA2}$  was the weight given to the IPCA1-value by dividing the IPCA1 sum of squares by the IPCA2 sum of squares. The larger the ASV value, either negative or positive, the more specifically adapted a genotype was to certain environments. A

smaller ASV value indicated a more stable genotype across environments (Purchase, 1997).

**Genotype and Genotype by Environment Interaction biplot analysis:** Genotype and Genotype by Environment Interaction biplot analysis was conducted using GenStat Release 15.1 computer software.

## RESULT AND DISCUSSION

**Analysis based on Eberhart and Russell regression model:** Results from Eberhart and Russell model revealed that the best yielding accession, 203544 (G6) showed regression coefficient ( $b_i$ ) closer to one (1.08), suggesting that it was relatively stable and widely adapted candidate cultivar as compared to the rest of cultivars, though its deviation from regression was quite different from zero (0.42) (Table 1; Fig 1). Eberhart and Russell (1996) noted that cultivars with high yield and regression coefficients closer to one, but squared deviation from regression ( $S^2 d_i$ ) different from zero

should be considered stable and adaptable to wider environments. The other three relatively stable and high yielding accessions, Acc. 242111 (G2), Acc. BKFM0051 (G10) and Acc. 229738 (G9) recorded regression coefficient higher than one (1.40, 1.41 and 1.32, respectively) and squared deviation from regression different from zero (0.54, 0.27 and 1.40, respectively). This implied that those genotypes were highly responsive for the changes in environmental conditions and hence can be recommended for favourable growing conditions with appropriate

agronomic practices. On the other hand, Acc. 230104 (G1), Acc. BKFM0028 (G23) and Acc. BKFM0042 (G24) gave grain yield below the average and regression coefficient lower than one (0.58, 0.47 and 0.51, respectively) indicating that they were adapted to low yielding environments (Table 1; Fig 1). Generally, the regression coefficient ( $b_i$ ) ranged from 0.37 to 1.48

in the present study, indicating wider deviation from the ideal or stable genotypes. On the contrary, though the number of test genotypes was small, Dogan, *et al.* (2011) reported that regression coefficient ( $b_i$ ) ranged from 0.824 to 1.180 for 8 triticale genotypes, showing narrow deviation from ideal regression.

**Table 1:** Mean grain yield (ton ha<sup>-1</sup>) per location, AMMI and regression analysis parameters

G#	Acc. name	Mean grain yield over locations (ton ha <sup>-1</sup> )									b <sub>i</sub>	s <sup>2</sup> di	ASV	IPCA1	IPCA2
		AN12	AS12	BK12	GT12	AN13	AS13	BK13	GT13	Mean					
1	230104	1.23	3.60	1.40	2.93	3.67	2.13	2.07	0.99	2.25	0.56	0.64	5.35	-0.77	0.05
2	<b>242111</b>	<b>3.97</b>	<b>2.00</b>	<b>2.33</b>	<b>2.90</b>	<b>7.00</b>	<b>1.87</b>	<b>2.50</b>	<b>2.03</b>	<b>3.08</b>	<b>1.40</b>	<b>0.54</b>	<b>4.91</b>	<b>0.70</b>	<b>0.09</b>
3	203360	3.43	1.90	1.57	2.10	6.63	1.93	2.23	0.76	2.57	1.30	0.45	3.52	0.51	0.28
4	229722	2.47	1.57	1.77	2.67	5.20	1.47	0.99	1.77	2.24	0.96	0.18	0.95	0.13	-0.22
5	242120	2.53	2.20	1.80	3.10	6.23	1.43	1.53	1.13	2.49	1.26	0.01	1.23	0.22	-0.08
6	<b>203544</b>	<b>3.30</b>	<b>3.43</b>	<b>2.03</b>	<b>4.73</b>	<b>5.50</b>	<b>2.07</b>	<b>2.27</b>	<b>2.00</b>	<b>3.16</b>	<b>1.08</b>	<b>0.42</b>	<b>1.18</b>	<b>-0.15</b>	<b>-0.53</b>
7	238346	4.23	1.70	2.50	1.60	7.00	0.94	2.40	1.53	2.76	1.32	1.17	5.88	0.84	0.41
8	214993	3.13	1.00	1.93	3.23	7.00	1.20	1.57	1.70	2.60	1.40	0.61	4.62	0.66	-0.28
9	<b>229738</b>	<b>5.40</b>	<b>1.40</b>	<b>2.43</b>	<b>3.37</b>	<b>6.67</b>	<b>1.70</b>	<b>1.67</b>	<b>1.20</b>	<b>2.99</b>	<b>1.32</b>	<b>1.40</b>	<b>5.97</b>	<b>0.85</b>	<b>-0.57</b>
10	<b>BKFM0051</b>	<b>3.23</b>	<b>2.43</b>	<b>2.63</b>	<b>2.70</b>	<b>7.60</b>	<b>1.83</b>	<b>2.30</b>	<b>1.80</b>	<b>3.07</b>	<b>1.41</b>	<b>0.27</b>	<b>3.66</b>	<b>0.52</b>	<b>0.37</b>
11	AAUFM-33	3.77	1.07	3.10	2.37	5.63	1.27	1.17	0.46	2.36	1.12	1.03	4.26	0.61	-0.22
12	229730	3.87	0.90	2.07	3.50	5.03	0.79	1.77	1.05	2.37	0.99	0.97	3.36	0.47	-0.81
13	BKFM0047	2.37	3.17	2.10	2.00	6.07	2.10	2.00	1.40	2.65	1.07	0.23	0.59	-0.01	0.59
14	203545	3.07	2.20	2.70	1.63	6.17	1.43	2.33	1.73	2.66	1.05	0.53	2.67	0.37	0.53
15	243636	2.63	1.87	2.20	2.83	7.53	1.53	1.53	1.80	2.74	1.48	0.31	3.69	0.53	0.19
16	230103	2.43	3.97	2.67	1.97	4.40	2.27	2.27	1.30	2.66	0.61	0.49	3.17	-0.45	0.53
17	203546	2.10	2.07	1.07	3.30	4.00	1.43	1.50	1.80	2.16	0.68	0.24	2.11	-0.29	-0.51
18	242617	2.30	2.60	1.73	2.03	5.40	1.57	1.70	0.70	2.25	1.05	0.08	0.34	0.02	0.32
19	214995	1.37	3.27	1.90	3.50	3.93	2.17	0.83	1.43	2.30	0.65	0.64	4.70	-0.67	-0.29
20	BKFM0005	2.70	3.50	1.93	3.17	4.37	2.10	1.63	2.30	2.71	0.63	0.18	3.03	-0.43	-0.16
21	214988	1.40	3.67	2.17	2.13	4.13	2.03	1.60	0.88	2.25	0.67	0.54	4.11	-0.58	0.41
22	BKFM0034	2.43	3.27	1.70	1.97	5.33	1.73	1.97	1.77	2.52	0.90	0.20	1.08	-0.14	0.45
23	BKFM0028	0.92	3.83	0.60	3.40	2.87	2.20	0.79	1.30	1.99	0.47	1.41	7.42	-1.06	-0.34
24	BKFM0042	1.67	4.20	1.77	3.10	3.77	1.90	1.97	1.90	2.54	0.51	0.64	5.58	-0.79	0.04
25	BKFM0043	1.90	3.83	1.70	3.73	4.60	2.10	2.00	1.50	2.67	0.76	0.49	4.11	-0.59	-0.16
26	BKFM0010	1.30	3.33	2.77	3.33	3.70	2.87	2.10	1.80	2.65	0.37	0.53	5.46	-0.78	-0.04
27	214990	1.83	3.90	1.77	2.67	5.63	1.77	1.37	1.30	2.53	1.08	0.38	2.23	-0.31	0.36
28	237443	4.40	0.75	2.20	2.10	6.63	0.44	1.06	0.61	2.27	1.47	1.34	7.05	1.01	-0.19
29	214989	1.47	2.50	1.73	3.77	5.20	1.83	1.12	1.43	2.38	0.99	0.39	1.95	-0.27	-0.33
30	203362	3.10	3.20	1.11	3.93	6.17	1.93	2.23	1.10	2.85	1.23	0.31	0.27	-0.00	-0.26
31	<b>GUTE</b>	<b>2.23</b>	<b>3.07</b>	<b>2.13</b>	<b>3.53</b>	<b>5.79</b>	<b>1.97</b>	<b>2.07</b>	<b>1.73</b>	<b>2.78</b>	<b>1.02</b>	<b>0.09</b>	<b>1.02</b>	<b>-0.15</b>	<b>-0.03</b>
32	TADESSE	2.07	2.77	1.13	2.23	6.37	1.97	1.53	2.13	2.53	1.17	0.38	0.68	0.03	0.43
	<b>MEAN</b>	<b>2.63</b>	<b>2.64</b>	<b>1.96</b>	<b>2.86</b>	<b>5.50</b>	<b>1.72</b>	<b>1.75</b>	<b>1.44</b>	<b>2.56</b>	<b>0.99</b>	<b>0.53</b>	<b>3.32</b>	<b>0.001</b>	<b>0.001</b>

G# = Genotype number, AN = Arsi Negelle, AS = Assosa, BK = Bako, GT = Gute, the number following each location indicates the year (12 = 2012, 13 = 2013), IPCA = Interaction Principal Component Axis, CV = Coefficient of variation, LSD = Least Significance difference, GEI = Genotype by Environment Interaction, Cumu.Int = cumulative interaction, b<sub>i</sub> = Regression coefficient, s<sup>2</sup>di = Squared deviation from regression, ASV = AMMI Stability Value, IPCA = Interaction Principal Component Axis

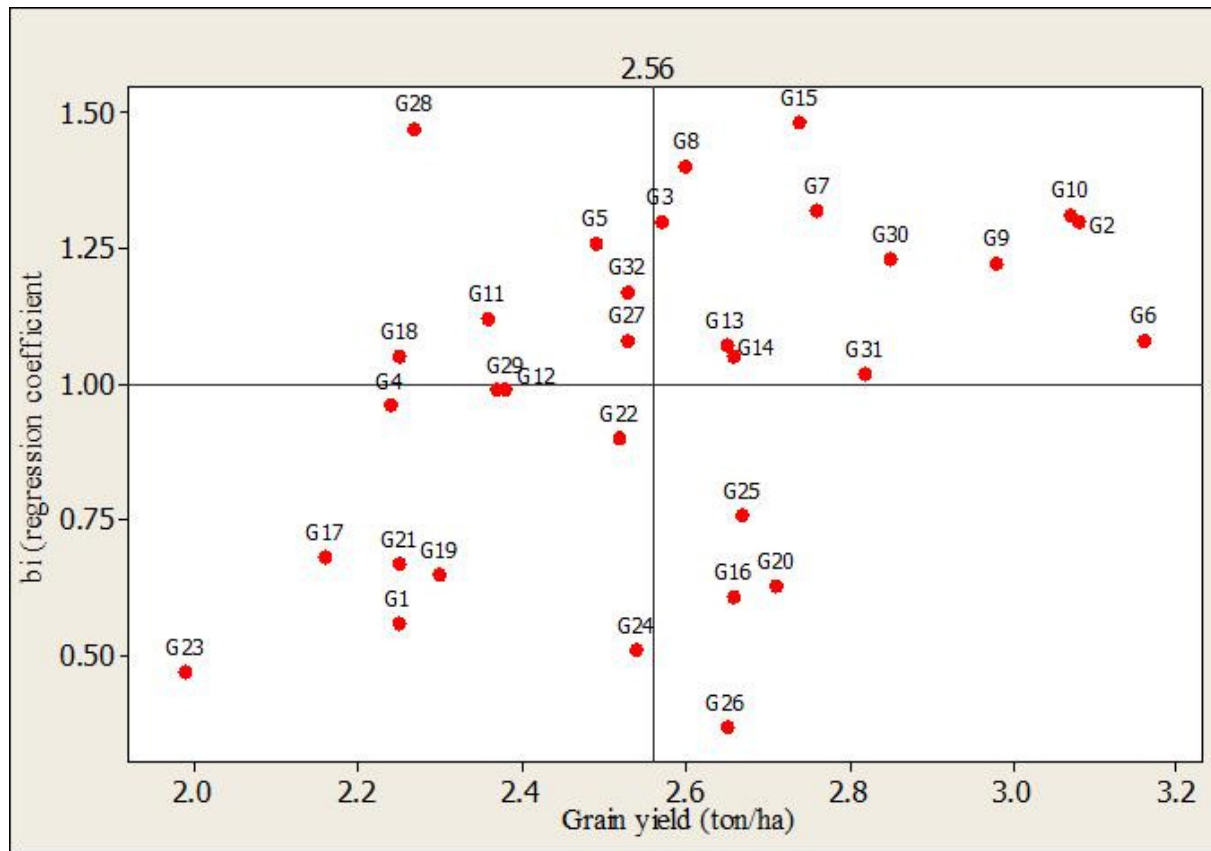


Fig 1: Matrix plot of genotypes mean grain yield (ton/ha) versus regression coefficient (b) indicating stability and yield performance of the test genotypes

**Additive Main Effects and Multiple Interaction (AMMI) model:**

Combined analysis of variance revealed highly significant ( $P \leq 0.01$ ) variations among environments, genotype x environment interaction and IPCAs (Table 2). This result revealed that there was a differential yield performance among the finger millet genotypes across testing environments and the presence of strong genotype by environment (G X E) interaction. As G x E interaction was significant, further calculation of genotype stability is possible. Similarly, Farshadfar (2008) evaluated 20 bread wheat genotypes for four years under two different conditions and reported that significant variations among genotypes, environments and environment G X E interaction were recorded and thus necessitate stability analysis. Several authors also reported significant G x E interaction and thus stability analysis for bread wheat (Sial *et al.*, 2000), rice (Panwar *et al.*, 2008) and finger

millet (Misra *et al.*, 2009). Substantial percentage of G x E interaction was explained by IPCA-1 (66.05%) followed by IPCA-2 (12.81%) and IPCA-3 (9.46%) (Table 2). The remaining five IPCAs axes contributed only 11.67% to G x E interaction. Because of their maximum, the first two principal components (IPCA-1 and IPCA-2) were used to plot a 2-dimensional GGE biplot. Gauch and Zobel (1996) suggested that the most accurate model for AMMI can be predicted by using the first two IPCAs. Several authors took the first two IPCAs for GGE biplot analysis since because the greater percentage of genotype by environment interaction (GEI), in most cases, were explained by the first IPCA such as for maize (Wonde and Labuschagne, 2005), bread wheat (Yuksel *et al.*, 2002; Farshadfar, 2008; Asnake *et al.*, 2013), common bean (Abeya *et al.*, 2008), for finger millet (Misra *et al.*, 2009) and field pea (Girma *et al.*, 2011).

**Table 2:** Analysis of variance for grain yield using AMMI model

Source	df	SS	MS	Eigenvalue	% G x E interaction	% cumulative interaction
Environments	7	1126.965	160.99**			
Genotype	31	59.542	1.921*			
G x E interaction	217	433.914	2.00**			
IPCA 1	37	286.61	7.75**	95.53552	66.05	66.05
IPCA II	35	55.5	1.6**	18.52138	12.81	78.86
IPCA III	33	41.1	1.244**	13.68863	9.46	88.32
Residual	496	32.523	0.065			

\*, \*\* significant at 0.05 and 0.01 probability levels, respectively.

df= degree of freedom, SS=sum of squares, MS= mean squares, IPCA=Interaction Principal Component Axis

Acc. 203544 (G6) produced the best average yield (3.16 ton ha<sup>-1</sup>) and attained an IPCA-1 value relatively close to zero (-0.15) indicating that it was a stable and widely adaptable cultivar (Table 1, Fig 2). Genotypic stability is crucial in addition to grain yield (Naroui *et al.*, 2013). Acc. 203362 (G30) attained the lowest IPCA-1 score (-0.0002) and medium grain yield (2.85 ton ha<sup>-1</sup>) (Table 1, Fig 2). Genotypes with below average yield, such as Acc. 242617, Tadesse, Acc. 229722 and Acc. BKFM0034 also showed IPCA-1 close to zero, indicating consistence in yield performance across locations. Acc. 242111 (3.08 ton ha<sup>-1</sup>), BKFM0051 (3.07

ton ha<sup>-1</sup>) and Acc. 229738 (2.99 ton ha<sup>-1</sup>) yielded better than Gute (2.82 ton ha<sup>-1</sup>) but attained relatively high IPCA-1 scores (0.70, 0.52 and 0.85, respectively) (Table 1, Fig. 2). Although these results indicated inconsistent yield performance across years and locations, they demonstrated site specific adaptability for these accessions. Acc. BKFM0028 (G23) yielded the least grain (1.99 ton ha<sup>-1</sup>) and attained the highest IPCA-1 score (-1.06) implying that it was not adaptable (Fig 2; Table 1). Besides, Acc. 203546 (G17), Acc. 229722 (G4) and Acc. 230104 (G1) are among the low yielding genotypes (Table 2).

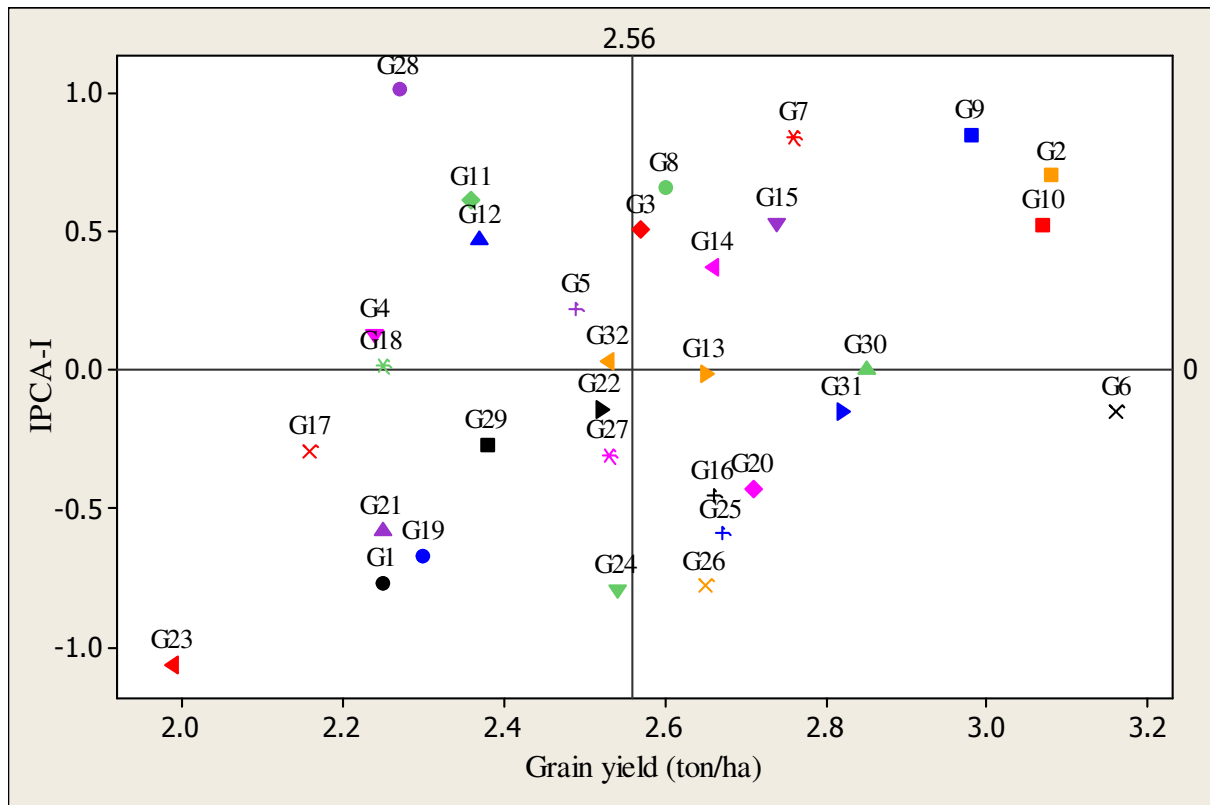
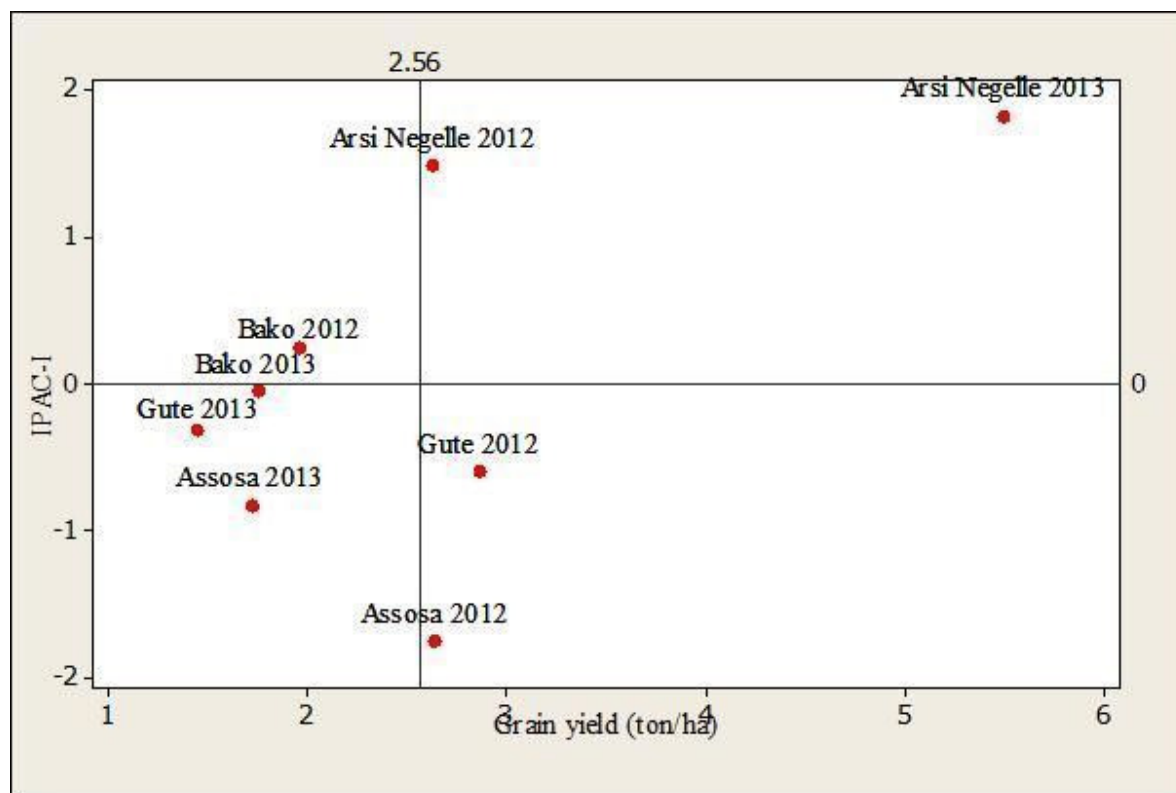


Fig 2: Matrix plot of genotypes mean grain yield (ton ha<sup>-1</sup>) versus IPCA-1.

Except for Bako, all test environments exhibited fluctuating mean grain yields and IPCA scores in 2012 and 2013 (Fig 3). For instance, the overall mean grain yield at Arsi Negele during 2012 crop growing season was 2.63 ton ha<sup>-1</sup>, while the mean grain yield at the

same location during 2013 cropping season was 5.5 ton ha<sup>-1</sup> (Fig 3; Table 1). The variation in weather conditions, experimental plots and other edaphic factors could be the possible reason behind these fluctuations.





**Fig 3:** Matrix plot of Environment focused mean grain yield versus Interaction Principal Component Axis (IPCA-1) scores.

**AMMI Stability Value (ASV) :** AMMI Stability Value aids selection of relatively stable high yielding genotypes. An ideal genotype should have high mean grain yield and small ASV. Accordingly, Acc. 203362 (G30), an introduced accession from Zimbabwe, showed the lowest ASV (0.266) and moderate grain yield (2.85 ton ha<sup>-1</sup>). Furthermore, Acc. 203544 (G6), an introduced accession from Kenya, was the highest yielding genotype (3.16 ton ha<sup>-1</sup>) with relatively lower ASV (1.18) (Table 1). These results revealed that those accessions are showing relatively better stability than the rest of accessions. However, stability needs to be considered in combination with yield (Farshadfar, 2008). Thus, Acc. 242111, Acc. BKFM0051 and Acc. 229738 had better grain yield (3.08 ton ha<sup>-1</sup>, 3.07 ton ha<sup>-1</sup> and 2.99 ton ha<sup>-1</sup>, respectively) but with high ASV (4.91, 3.66 and 5.97, respectively) were identified as good genotypes to validate for yield performance and specific adaptability. The results of ASV further confirmed that Acc. BKFM0028 was unstable and not adaptable and that Acc. 242617 and a released variety Tadesse were consistent low yielders across locations and years. Odewale *et al.*, 2013 reported that two out of the five coconut genotypes grown across nine

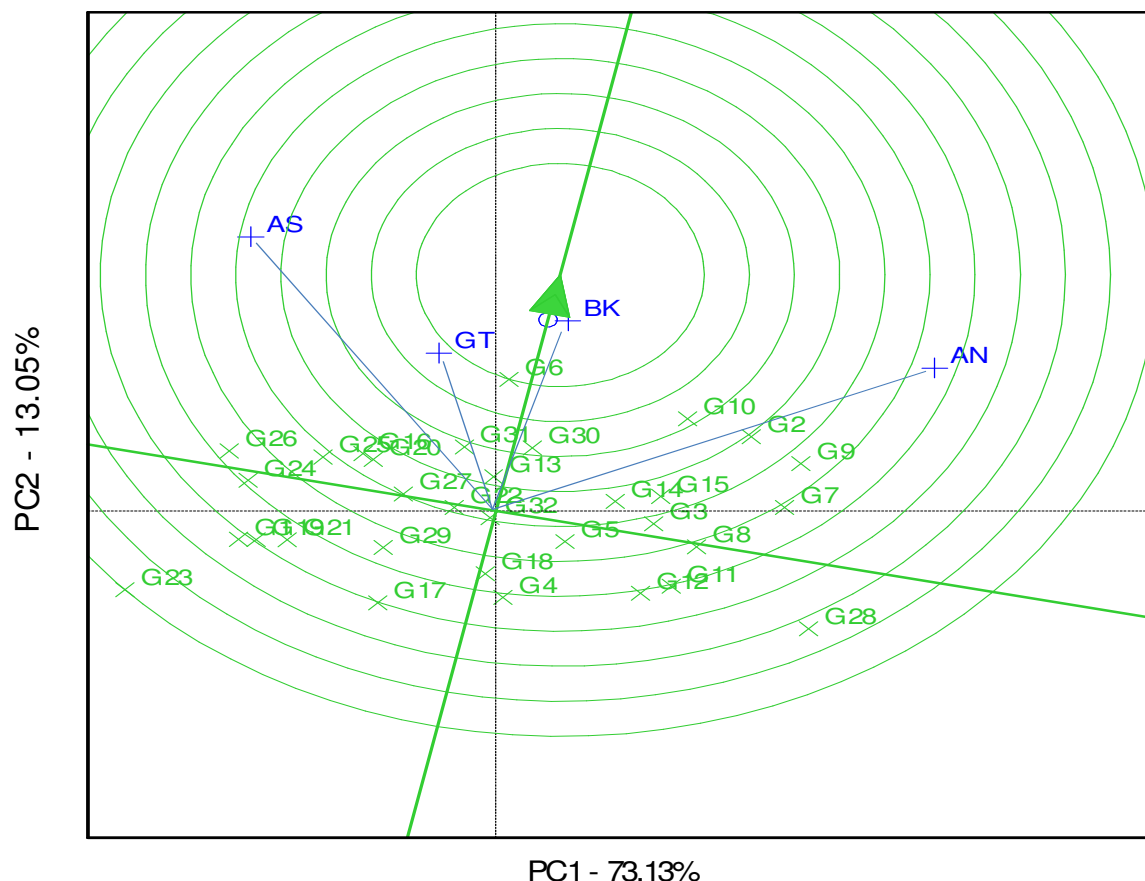
environments in southern Nigeria showed smaller ASV and thus better stability. Farshadfar (2008) noted three out of the 20 bread wheat genotypes evaluated gave smaller ASV and higher grain yield than the grand mean and thus better relative stability.

**Genotype and Genotype by Environment interaction (GGE) biplot analysis**

**Relationship among test environments:** Mean grain yield data of both years were used to assess the relationships between the different test environments and this was visualized by the line connecting each environment to the biplot origin or environment vectors (Fig 4). The cosine of the angle between two environments was used to calculate the correlation between them (Dehghani *et al.*, 2009; Kaya *et al.*, 2006). Environments, Bako (BK) and Gute (GT), correlated positively (acute angle), Assosa (AS) and Arsi Negele (AN) correlated negatively (obtuse angle), whereas AN and GT did not correlate (right angle). According to Yan and Tinker (2006), a strong negative correlation indicated high cross-over or GEI. Tukamuhabwa *et al* (2012) and Choukan (2010) reported that if two test locations correlated consistently across years, one could be dropped without significant

loss of information about the genotypes. In the current study, variable environmental conditions among sites as well as within a given site from year to year resulted in inconsistent correlations between the test locations

(Fig. 3). This type of relationship was depicted by Gute and Bako, where positive correlation was observed in 2013, but negatively correlated in 2012.



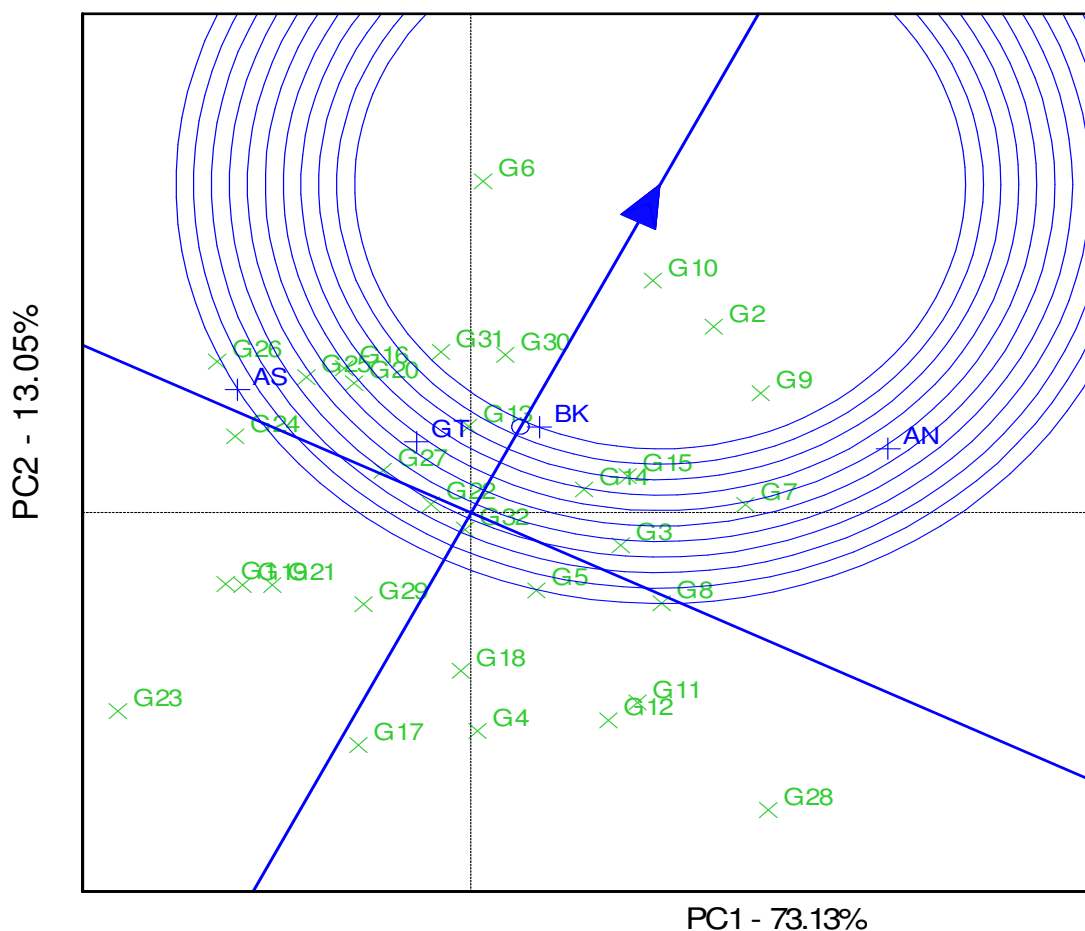
**Figure 4:** GGE biplot based on test environments-focused comparison for their relationships

**Discriminating ability of the test environment and genotype stability :** The concentric circles on the biplot help to visualize the length of the environment vectors, which are proportional to the standard deviation within the respective environments and is a measure of the discriminating ability of the environments (Asnake *et al.*, 2013). Environments and genotypes that fall in the central (concentric) circle are considered ideal environments and stable genotypes, respectively (Yan, 2002). An environment is more desirable and discriminating when located closer to the centre circle or to an ideal environment (Naroui *et al.*, 2013). The Average-Environment Axis (AEA) or Average-Tester-Axis (ATA) is the line that passes through the average environment and the biplot origin (Yan, 2002). A test environment with a small angle with the AEA is more representative than other

environments (Yan, 2002; Asnake *et al.*, 2013). In the present study, Bako was the most discriminating environment followed by Gute (Fig. 4). Arsi Negele and Assosa were non-discriminating and less representative sites although the former was high yielding and the latter a poor yielding environment (Fig. 3 and 4; Table 1). This implied that, varietal stability could be challenged not only due to the change in the test environment but also due to change in growing season per environment. Similarly, Odewale *et al.* (2013) reported that only one environment was stable, representative and discriminating among nine environments for the performance of 5 coconut genotypes evaluated in southern Nigeria. Ranking based on the genotype-focused scaling assumed that stability and mean yield were equally important (Yan, 2002). The best candidate genotypes

were expected to have high mean grain yield with stable performance across all test locations. In practice, such genotypes are very rarely to be found. Therefore, high yielding and relatively stable genotypes can be considered as references for genotype evaluation (Yan and Tinker, 2006). Both environments-focused biplot and genotype-focused comparison of genotypes revealed that Acc. 203544 (G6) fell in the central circle indicating its high yield potential and relative stability compared to the rest of genotypes evaluated in this study (Figs. 4 and 5). Besides, Acc.242111 (G2) and

BKFM0051 (G10) fell close to the ideal genotype or around the center of concentric circle, suggesting their potential for specific adaptability with better grain yield performances. Among the genotypes, Acc. 203544 (G6), Acc.242111 (G2) and BKFM0051 (G10) were the top performing pipeline cultivars with 13.7%, 10.8% and 10.43%, yield advantages, respectively, over Gute (G31), and hence recommended for further verification and possible release. The GGE biplot analysis result also supported those obtained using AMMI and the Eberhart and Russell model.



**Figure 5:** GGE biplot based on genotype-focused scaling for comparison of genotypes for their yield potential and stability.

**CONCLUSION AND RECOMMENDATION**

Combined analysis of variance depicted highly significant variation for all characters between genotype, environments and GEI. GGE biplot analysis, AMMI and Eberhart and Russell model revealed that Acc. 203544 is a stable, high yielding (3.16 ton ha<sup>-1</sup>) variety with yield advantage of 13.7% over the best

standard check, Gute (2.78 ton ha<sup>-1</sup>), thus should be recommended for release with wider environmental adaptability in Ethiopia. Acc. 242111 (3.08 ton ha<sup>-1</sup>), Acc. BKFM0051 (3.07 ton ha<sup>-1</sup>) and Acc.229738 (2.99 ton ha<sup>-1</sup>) were also high yielding, but inconsistent and thus should be recommended for verification and

possible release for adaptation in specific environments. With regards to the test environments, about 66.05% of GEI was explained by IPCA-I and a total of 88.33% GGE interaction by the first three IPCAs. GGE biplot based analysis on test environments-focused comparison for their consistence

revealed that, except at Bako, the test environments were inconsistent for mean grain yield and IPCA scores during 2012 and 2013. This observed instability might have been due to variation in weather conditions, soil and other uncontrolled edaphic factors.

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