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GGE bi-plot Analysis of Genotype by Environment Interaction in Finger Millet (*Eleusine coracana* (L.) Gaertn.) varieties in different Locations of Southwestern Ethiopia

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Abstract

The objectives of the study were to evaluate the yield performance of each genotype in relation to each environment, to examine the possible existence of different mega environments and to identify the winning genotype for each mega environment using GGE bi-plot method. Ten finger millet varieties which were for the experiment. The experiment was laid out using randomized complete block design with four replications in all testing sites. The plot size was four harvestable rows and spacing between rows was 40cm with the length of 5m long. All management practices such as cultivation, fertilization and weeding were done based on the recommendations for each test sites. Data for all relevant agronomic traits were collected, but only plot yield data converted to qt/ha was subjected to statistical analysis. The mean grain yield of the varieties was ranged from 18.9qt/ha to 15.3qt/ha. The highest mean was harvested from the variety Gudetu (18.9qt/ha) and the lowest from variety Meba (15.3qt/ha).Out of ten varieties, six varieties had grain yield below the average. Among the environments, the LM2017 and GM2019 had below the mean average yields. The highest yield were recorded in the environment BD2018 and BD2017 with mean yields of 25.6 and 24.5qt/ha respectively. A combined analysis of variance indicated that genotype, environment and GEI showed significant ($P<0.001$) differences among finger millet varieities. This result showed that finger millet yields were significantly influenced by environment, which accounted 78.7% of the total yield variation, while genotype and GEI explained 1.55 and 9.86% of the variation respectively. The partitioning of GGE through GGE biplot analysis showed that PC1 and PC2 accounted 46.3 and 27.2% of GGE sum of squares, respectively, explaining a total of 73.5% variation. GGE biplot identified G7 and BD19 as ideal genotype and environment respectively.

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Keywords

GGE, genotype by environment interaction, finger millet varieties.

Introduction

Finger millet (*Eleusine coracana* (L.) Gaertn.) is an allotetraploid ($2n = 4X = 36$, AABB) belonging to the Family *Poaceae* and the genus *Eleusine*. The genome size of finger millet is 1,593 Mb and is a self-pollinated crop (Goron and Raizada, 2015). It is an annual herbaceous cereal crop widely grown and consumed by poor people in Africa and Asia. The major attributes of finger millet are its adaptability to adverse agro-ecological conditions with minimal inputs, tolerance to moisture stress, productivity on marginal land where other crops cannot perform and tolerance to acidic soil (Upadhyaya *et al.*, 2007). Since it is rich in calcium, iron and other important nutrients, finger millet serves as a main staple food for rural populations in developing tropical countries where calcium deficiency and anemia are widespread (Babu *et al.*, 2007). In Ethiopia, finger millet occupies diverse agro-ecologies with a vast range of genetic variability and is intensively *cultivated* in mid and lower altitude regions of Tigray, Gojam, Gonder and Wollega where it constitutes 10 to 20 % of the total cereal production (Kebede and Menkir, 1986).

The yield potential of finger millet reported is more than 3.0 tons ha-1 (Mulatu and Kebede 1993), the current national average is only limited to 1.7 tons ha-1 (CSA, 2013). This could be mainly due to the lack of widely adaptable improved varieties, blast disease infection, limited management recommendations and other biotic and abiotic factors (Bezawuletaw *et al.*, 2006). Moreover, breeding efforts in finger millet has been limited, in general, and majority of farmers are generally growing unimproved and low yielding cultivars (Dida *et al.*, 2007).Identifying adaptable and stable high yielding genotypes with other desirable traits under varying environmental conditions to recommend new varieties for release as cultivar(s) is fundamental and this has direct bearing on the adoption of a variety, productivity and total production of the crop (Flores *et al.*, 1998).

Multi-Environment Yield Trials (MEYT) are conducted for different crops throughout the world (Yan and Rajcan, 2002) not only to identify high yielding cultivars but also to identify sites that best represent the target environment (Yan *et al.*, 2000). As usual in MEYT a number of genotypes are tested over a number of sites and years to see adaptation of the crop. But, it is often difficult to determine the pattern of genotypic responses across environments without the use of appropriate analytical tools such as GGE biplot (Yan *et al.*, 2001) for graphical display of data. The measured yield of each cultivar in each test environment is a result of genotype main effect (G), an environment main effect (E) and genotype x environment (GE) interaction (Yan and Kang, 2003). Though, E is accountable for about 80% of the total yield variation; however, it is only G and GE interaction that are relevant to cultivar evaluation and mega environment classification (Yan *et al.*, 2000; Yan and Rajcan, 2002; Kaya *et al.*, 2006).

GEI is related to component of yield variation across environments for a genotype that cannot be explained either by G or E alone (Yan and Hunt, 2001). GEI reduces the genetic progress in plant breeding programs through minimizing the association between phenotype and genotype (Comstock and Moll, 1963). Hence, GEI must be either exploited by selecting superior genotype for each a specific target environment or avoided by selecting widely adapted and stable genotype across wide range of environments (Ceccarelli, 1989). GEI is used to determine if a genotype is widely adapted for a wide range of environmental conditions or selected for different sub environments. The objective of the study was to evaluate the yield performance of each genotype in relation to each environment, to examine the possible existence of different mega environments and to identify the winning genotype for each mega environment using GGE bi-plot method

Materials and Methods

Experimental materials and Testing locations

Ten finger millet varieties which were obtained from Melkassa and Bako (regional) Agricultural Research Center (Table 1) were evaluated at different location of jimma and Illuababora zones of southwestern Ethiopia (Table 2).The experiment was laid out using randomized complete block design (RCBD) with four replication in all testing sites.

Statistical analysis

The grain yield data for ten finger millet in six environments were used to combined analysis of variance (ANOVA) to determine the effects of environment (E), genotype (G) and their interactions. The data were graphically analyzed for interpreting GE interaction using the GGE biplot software (Yan, 2001). 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 finger millet MET data. This methodology uses a biplot to show the factors (G and GE) that are important in genotype evaluation and that are also the sources of variation in GEI analysis of MET data (Yan, 2001). The graphs were generated based on (i) The polygon view of GGE biplot to identification of winning genotypes and their mega environments by 'which-won-where' pattern, (ii) Ranking of genotypes based on yield and stability performance, (iii) Evaluation of genotypes related to an ideal genotypes, (iv) Evaluation of environments related to ideal environments, (v) Relationship among environments and (Vi) Discriminativeness vs Representativeness of environments.

Results and Discussion

A separate analysis of variance (ANOVA) was computed for each locations and the mean grain yield of the varieties is in Table 3.The mean grain yield of the varieties was ranged from 18.9qt/ha to 15.3qt/ha.The highest mean was harvested from the variety Gudetu (18.9qt/ha) and the lowest from variety Meba (15.3qt/ha).Out of ten varieties, six varieties had grain yield below the average. Among the environments, the LM2017 and GM2019 had below the mean average yields. The highest yield were recorded in the environment BD2018 and BD2017 with mean yields of 25.6 and 24.5qt/ha respectively.

The combined analysis of variance was presented in Table 4.A combined analysis of variance indicated that genotype, environment and GEI showed significant ($P<0.001$) differences among finger millet varieities. This result showed that finger millet yields were significantly influenced by environment, which accounted 78.7% of the total yield variation, while genotype and GEI explained 1.55 and 9.86% of the variation respectively. The effect of GEI is more than six times that of G effect. The magnitude of GEI as compared to G suggested the possible existence of different mega environments. The partitioning of GGE through GGE biplot analysis showed that PC1 and PC2 accounted 46.3 and 27.2% of GGE sum of squares, respectively, explaining a total of 73.5% variation. This result revealed that there was a differential yield performance among finger millet varieties across testing environments due to the presence of GEI. The presence of GEI complicates the selection process as GEI reduces the usefulness of genotypes by confounding their yield performance (Pham and Kang, 1988) through minimizing the association between genotype and phenotype (Comstock and Moll, 1963).

Polygon view of GGE biplot analysis of MET data

The polygon view of GGE biplot (Figure. 1). Visualization of the won where pattern of MEYT data is necessary for studying the possible existence of different mega environments in the target environment (Yan *et al.*, 2000). 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 GEI which is helpful in estimating the possible existence of different mega environments (Gauch and Zobel, 1997). The polygon is formed by connecting the markers of genotypes that are further away from the biplot origin such that all genotypes are contained in the polygon (Kaya *et al.*, 2006).

The genotypes which are located on vertices of the polygon formed are either the best or poorest in one or more environments (Yan *et al.*, 2000). The vertex genotypes in each sector is also the best genotype for sites whose markers fell in to the respective sector so that sites within the same sector share the same winning genotype (Yan *et al.*, 2000). On the biplot, rays or lines that are drawn perpendicular to the sides of the polygon divide it in to sectors.

The vertex genotypes were G1, G2, G4,G5 and G9 having the largest distance from the origin. These genotypes are the best or poorest in some or all environments because they are farthest from the origin of biplot (Yan and Kang, 2003), which were more responsive to environmental change and are considered as specially adapted genotypes. The presence of cross over GEI shows the existence of different mega environment in which different winning genotypes can be selected. The GGE biplot identified three finger millet growing environments. The first mega environment consisted of OM19 and BD17 with winning genotype G5, the second mega environment included BD19, GM19 and BD18 with winning genotypes of G1 and G4 and third mega environment consisted of LM17 with the winning genotypes of G9 and G2 (Figure 1).

Ranking of genotypes based on mean yield and stability performance

In GGE biplot methodology, the estimation of yield and stability of genotypes (Figure.2) were done by using the average environment (tester) coordinate (AEC) methods (Yan, 2001). The line passing through the biplot origin is called the average environment (tester) coordinate (AEC), which is defined by the average PC1 and PC2 scores for all environments (Yan and Kang, 2003). The single arrowed line is the AEC abscissa which points to higher mean yield across environments or to greater genotype main effect.

In this study, the highest grain yielder genotypes were G1,G7 and G4 and lowers were G2 and G9.Stability of the genotypes depends on their distances from average environment coordinate abscissa. Genotypes closer to abscissa are more stable than others. In this study, the most stable and high yielding was G7.

Table.1 Finger millet varieties evaluated across different locations

Common name	Variety name	Year of release	Altitude (m.a.s.l.)	Maturity date
Boneya	(KNE#411)	2002	1400-1600	145
Bareda	(BRC-356-1)	2009	1200-1900	146-169
Tessema	ACC#229469	2014	1600 -1900	145-150
Wama	(KNE#392)	2007	1400-1900	145-150
Padet	KNE #409	1999	1600-1900	NA
Tadesse	(KNE #1098)	1999	1600-1900	NA
Gudetu	(Acc.215990)	2014	1400-1900	145-150
Addis 01	Acc. 203544)	2015	1400-2200	145-155
Axum	NA	NA	NA	NA
Meba	NA	NA	NA	NA

NA=not available

Table.2 Environmental sites, Altitude, Rainfall and Temperature.

No.	Environments	Env.code	Altitude (m.a.s.l.)	Rainfall (mm)	Temp (0C)
1.	Bedele	#BD	2087	1700	18
2.	Omonada	#ON	1975	1600	20
3.	Limu kosa	#LK	NA	NA	NA
4.	Gooma	#GM	1,560	1764	19.7

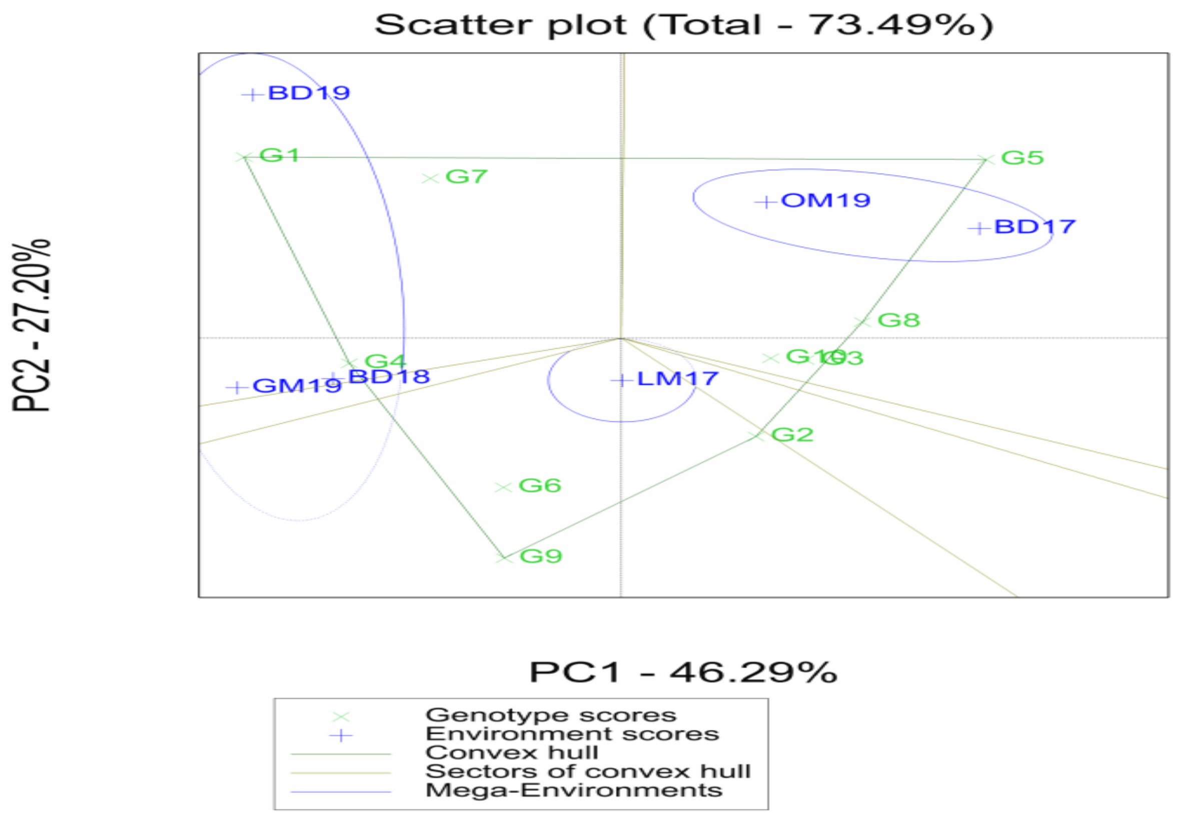
NA=not available

Table.3 Mean grain yield (qt/ha) of ten finger millet varieties across different locations and years.

	Locations and years							
Varieties	**BD 2017**	**BD 2018**	**BD 2019**	**LK 2017**	**GM 2019**	**ON 2019**	**Overall Mean**	**Overall Rank**
Boneya	20.4	25.8	25.8	6.6	12.1	19.1	18.3	2
Bareda	25	20.9	14.5	9.4	10.4	16.6	16.1	9
Tesema	24.5	24.9	15.15	6.8	5.8	19.7	16.1	8
Wama	22	27.9	20	7.5	12.5	16.2	17.7	3
Padet	33.3	23.7	17.9	6.5	5	19.3	17.6	4
Tadesse	24.5	29.2	16.6	7.2	9.6	11.6	16.5	7
Gudetu	26.2	28.5	22.9	6.2	10.8	18.5	18.9	1
Addis01	26.5	23.6	15.4	7.6	5.8	20	16.5	6
Axum	22.1	28.9	13.3	7.2	12.1	15.8	16.6	5
Meba	22.5	22.5	15.8	5.6	6	19.1	15.3	10
Mean	**24.5**	**25.6**	**17.7**	**7.1**	**9**	**17.6**	**16.9**	
CV (%)	**15.5**	**10.7**	**14.9**	**13.6**	**13.3**	**11.6**		
LSD at 5%	**5.5**	**4**	**3.8**	**1.4**	**1.7**	**2.9**		

Where, BD=Bedele, LK=Limu kosa, GM=Gooma, ON=Omonada

Fig.1 Polygon view of GGE bi plot based on symmetrical scaling for the which won where pattern of genotypes and environment



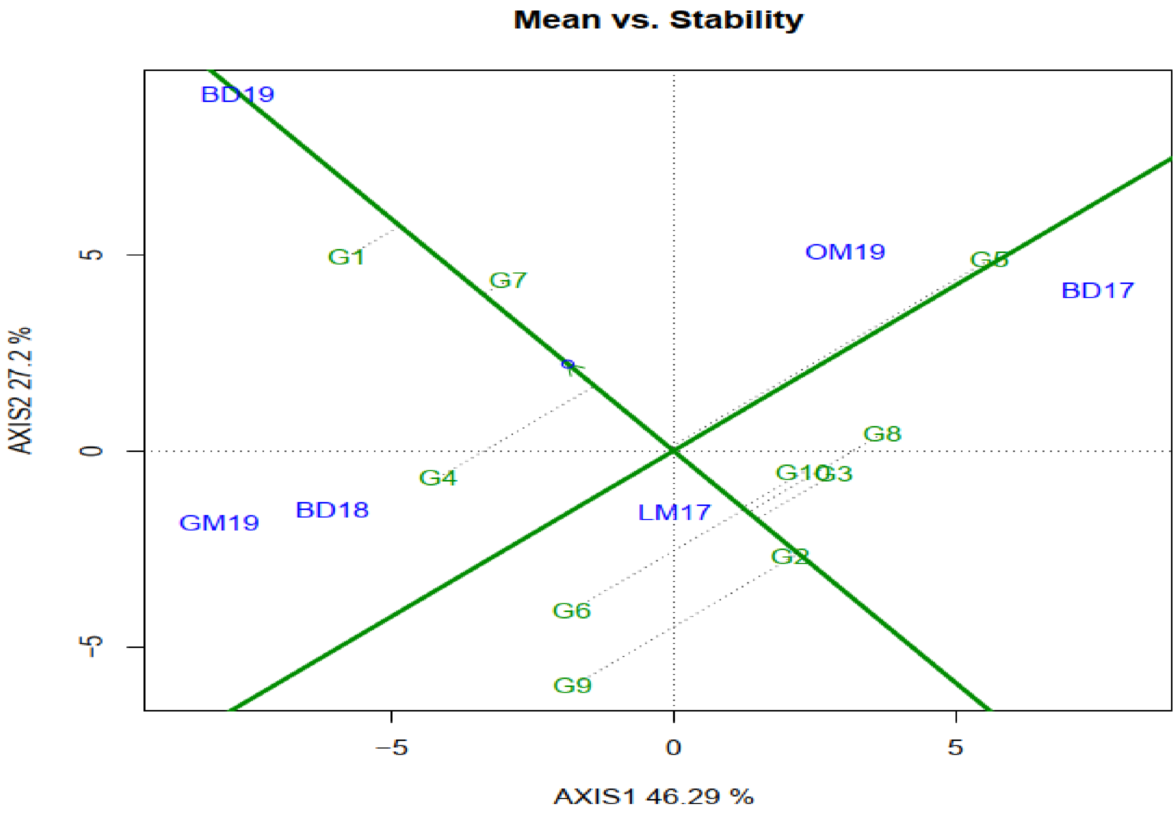
BD=Bedele,OM=Omonada,LM=Limukosa,G=Gooma,G1=Boneya,G2=Bareda,G3=Tesema,G4=Wama,G5=Padet, G6=Tadesse,G7=Gudetu,G8=Addis 01,G9=Axum and G10=Meba

Table.4 Combined ANOVA for grain yield (Qt/ha) and the percentage sum of squares of the 10 finger millet varieties tested at different locations during 2017 to 2019 cropping season

Source of variation	d.f	SS	%SS	MS
Environment	5	13032.8	78.77	2606.56**
Genotype	9	256.6	1.55	28.5**
Rep (location)	18	217.3	1.31	12.1
Interaction	45	1631.6	9.86	36.2**
Residuals	162	1407.9	8.51	8.7
Total	239	16546.4		
CV (%) = 14.4			**R^2= 0.93**	

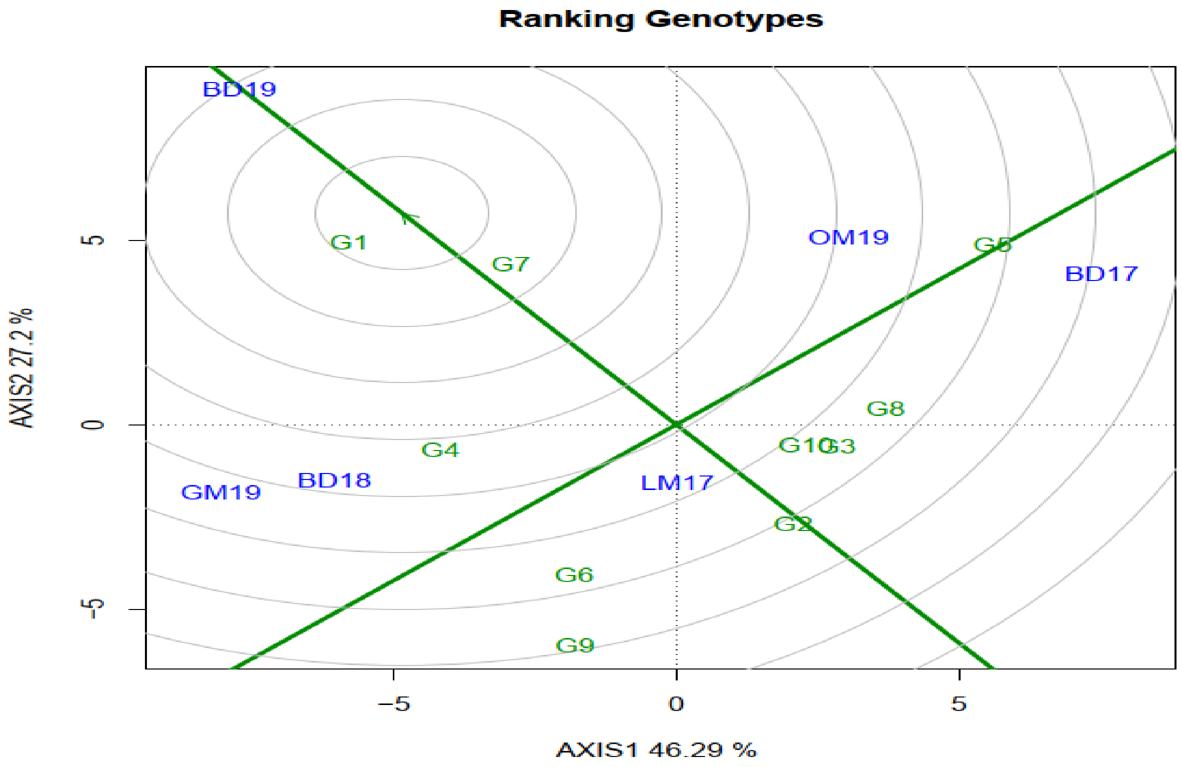
**,* Significant difference at p<0.01 and p<0.05 respectively, df= degree of freedom, SS = sum square, MS=mean square

Fig.2 Mean and Stability of the GGE biplot



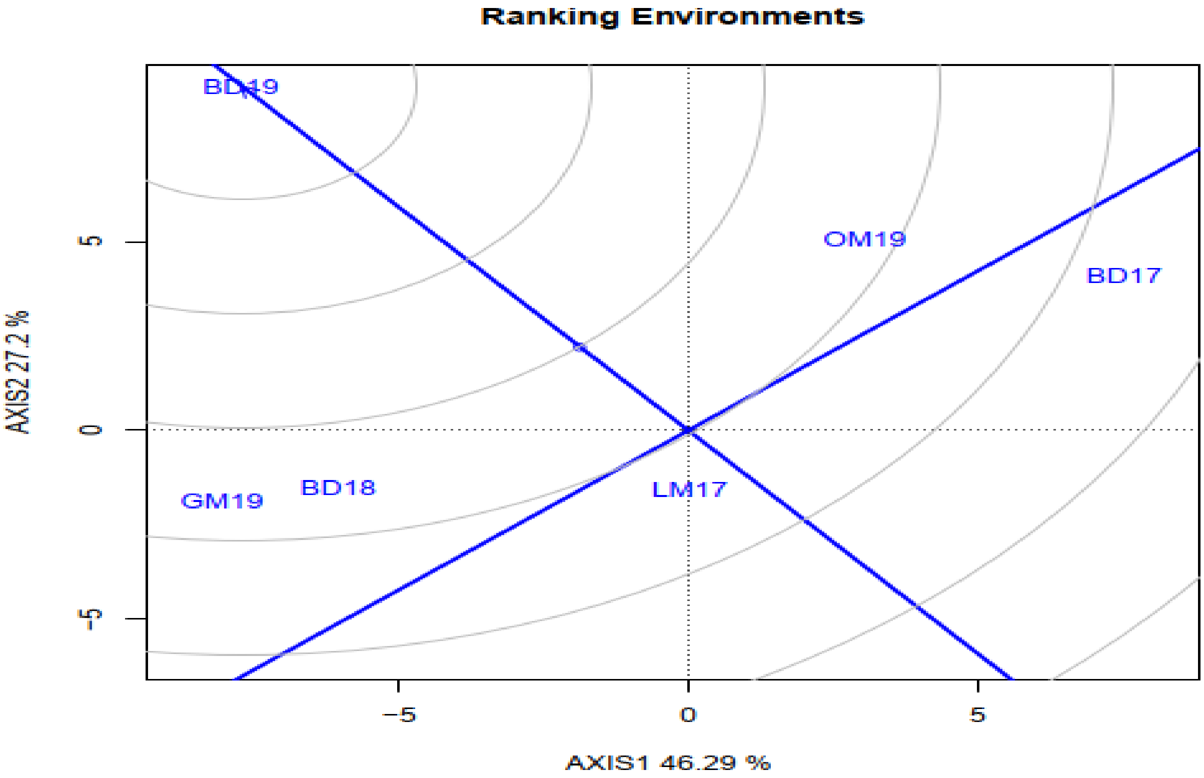
BD=Bedele,OM=Omonada,LM=Limukosa,G=Gooma,G1=Boneya,G2=Bareda,G3=Tesema,G4=Wama,G5=Padet, G6=Tadesse,G7=Gudetu,G8=Addis 01,G9=Axum and G10=Meba

Fig.3 Evaluation genotypes based on ideal genotype



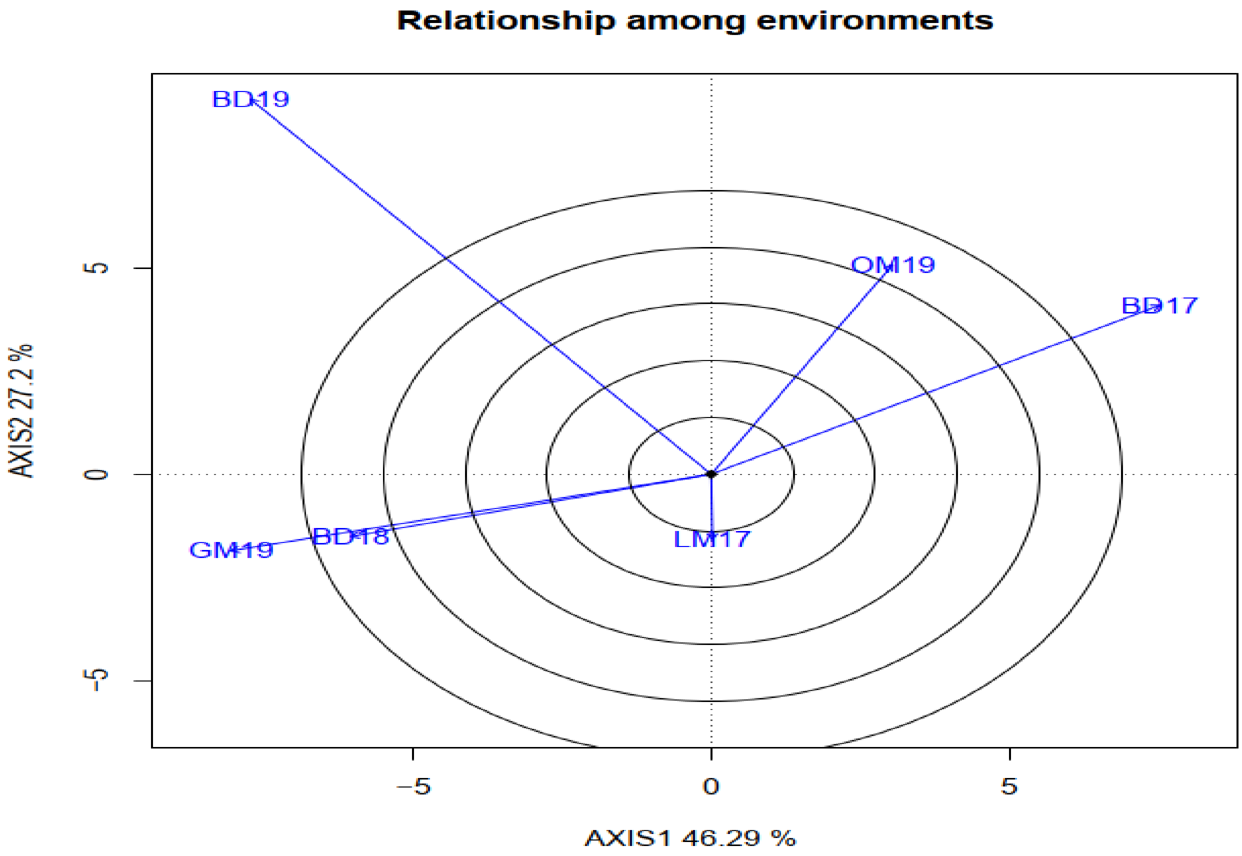
BD=Bedele,OM=Omonada,LM=Limukosa,G=Gooma,G1=Boneya,G2=Bareda,G3=Tesema,G4=Wama,G5=Padet, G6=Tadesse,G7=Gudetu,G8=Addis 01,G9=Axum and G10=Meba

Fig.4 Evaluation of environments based on ideal environment



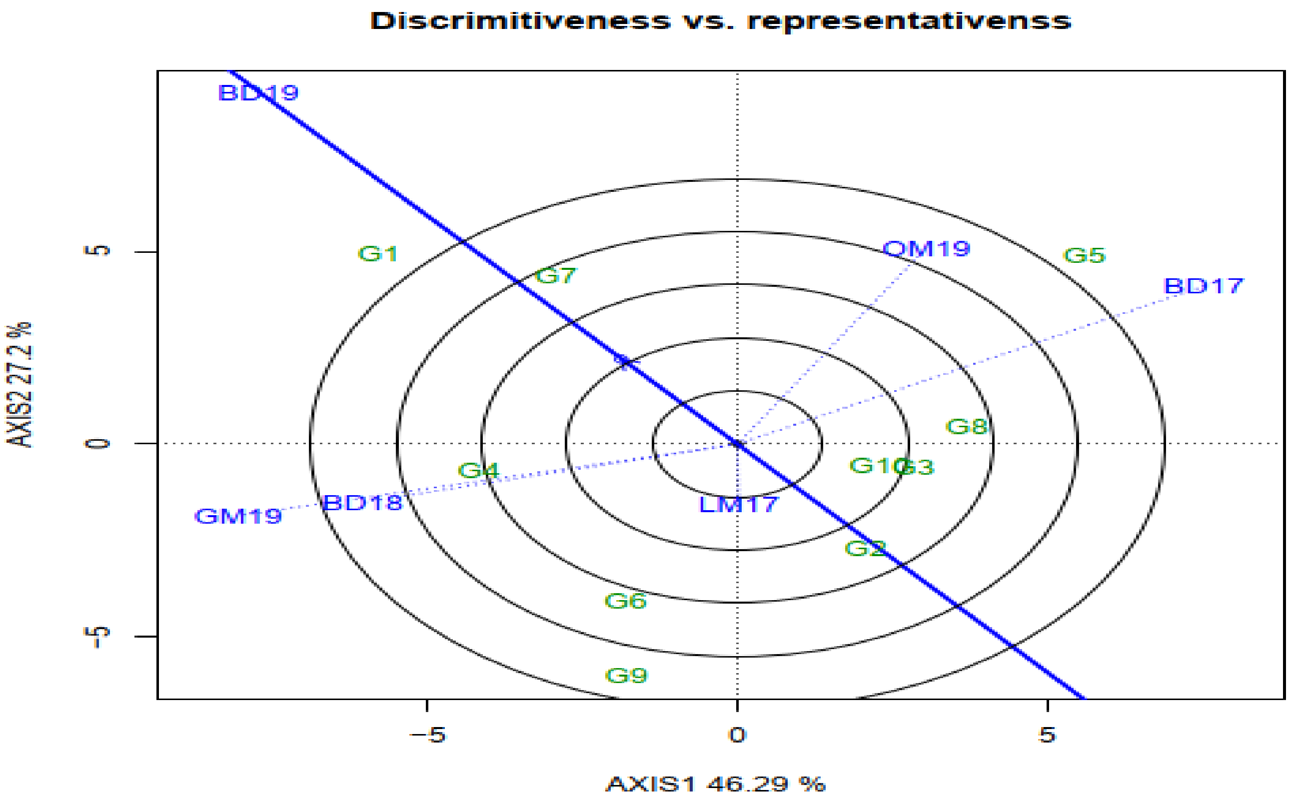
BD=Bedele, OM=Omonada, LM=Limukosa, G=Gooma

Fig.5 Relationship among environments



BD=Bedele, OM=Omonada, LM=Limukosa, G=Gooma

Fig.6 Discriminativeness vs Representativeness of the GGE biplot



BD=Bedele,OM=Omonada,LM=Limukosa,G=Gooma,G1=Boneya,G2=Bareda,G3=Tesema,G4=Wama,G5=Padet, G6=Tadesse,G7=Gudetu,G8=Addis 01,G9=Axum and G10=Meba

Ranking of genotypes based on ideal genotypes

Evaluation of genotypes relative to ideal genotypes was presented in figure 3. The ideal genotype as virtual genotype is one that has both high mean yield across test environments and is absolutely stable in performance (Yan and Kang, 2003). This genotype has large PC1 scores (high mean yield) and small (absolute) PC2 scores (high stability).

Although such an ‘ideal’ genotype may not exist in reality, it could be used as a reference for genotype evaluation (Mitrovic *et al.,* 2012). A genotype is more desirable if it is closer to ‘ideal’ genotype (Kaya *et al.*, 2006 and Mitrovic *et al.*, 2012).In the study, to use ideal genotype as the measurement center, concentric circles were drawn in the bi-plot to graphically determine the distance between the test genotypes and the ideal one. According to GGE bi-plot a genotype that is located at the center of the circles or is the genotype with high grain yield and stability. Hence, G1 was in the small circle and considered ideal genotype and G7 and G4 were closest to ideal genotype and were more desirable.G9 and G2 were positioned far away from it and thus not in the ideal group.

Ranking of environments based on ideal environment

The GGE biplot was way of measuring representativeness is to define an average environment and use is as a reference or benchmark. The average environment is indicated by small circle (Figure 4).The ideal environment, represented by the small circle with an arrow pointing to it. Therefore, BD19 was the most desirable test environment followed by GM19 and BD18.

Relationship among environments

The summary of the interrelationships among the environments was on figure 5. To visualize the relationship between environments, lines are drawn to connect the test environments to the biplot origin known as environment vectors. The cosine of the angle between the two environments is used to approximate the relation between them (Kaya *et al.,* 2006).According to the angles between test location vectors, the six locations were grouped into three major groups. The first group includes OM19 and BD17,the second group includes BD19,GM19,BD18 and third was LM17. The smallest angle between OM19 with BD17 and BD19 with GM19 and BD18 implying that there is very high correlation between them, suggesting that the locations provide redundant information. Obtaining suitable tool to analyze this kind of similar information by using fewer test environments generally reduces the cost of testing and increases breeding efficiency. In addition, in the vector view of the biplot, the length of the location vectors estimates the standard deviation within each location, which is a measure of their discriminating ability.

Discriminativeness vs Representativeness of the GGE biplot

The discriminating power and representativeness of the GGE biplot was shown in figure 6.The test environment BD19 with the longest projection from the biplot origin were found to be the environment with more discriminating power that provide more information about the difference among genotypes. On the other hand, LM17,with the shortest vector from the origin, was found less discriminating of the test genotypes. Test environment OM19, BD18 and BD19 were found to be more representative of the test environments due to the fact that they have smaller angles with the average environment axis (AEA). An ideal location should be highly differentiating (discriminating) for the tested genotypes and at the same time be representative of the target locations (Yan and Kang,2003).The ideal environment is representative and has the highest discriminating power (Yan and Tinker 2006).BD19 was therefore identified as ideal environment that both discriminating abilities of genotypes and representative of the other test environments. Thus BD19,can be used to effectively select superior finger millet varieties that can perform consistently across environments.

Signficant GEI affects the performance of finger millet yield across locations.The combined ANOVA revelaed that the genotype,enviornment and interaction effects were highly significant at $p<0.01$.GGE biplot identified G7 and BD19 as ideal genotype and enviornmnet respectively. Mean yield and stability performance over enviornmnets of each genotypes is explored by using Average enviornmnet coordinate (AEC).The method identified the genotypes G1 and G7 had higher mean yield while G7 had highest stability.

Acknowledments

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Conflict of Interest

The authors have not declared any conflict of interests

Abbreviations

GGE = Genotype Main Effect and Genotype by Environment Interaction, GEI= genotype by environment interaction, PCA=Principal component analysis, MEYT= Multi-Environment Yield Trials

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