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# Evaluation of adaptability and stability of tef (*Eragrostis tef* (Zucc.) Trotter) varieties using GGE bi-plot analysis in South and Southwestern Ethiopia

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## Abstract

This study was carried out to evaluate released tef varieties for yield stability using GGE biplot method and to identify high yielding and well adapted varieties for the South and Southwestern Ethiopia. The experiment was conducted using twenty-one tef varieties obtained from a tef breeding program based at Debre zeit Agricultural Research Center. The trial was laid out using randomized complete block design with three replications in six locations during the 2018 of main cropping season. Data was collected on days to heading, days to maturity, grain filling period, plant height, fertile tillers, panicle length,culm length, lodging index, thousand seed weight, above ground biomass, straw yield, harvest index and grain yield. The result of combined analysis for grain yield of twenty-one tef varieties tested across six environments showed that there is a highly significant difference among the environment, genotypes and genotype by environment interaction. Yield data were analyzed using the GGE (that is, G, genotype + GEI) biplot method. Environment explained 69.4% of the total sum of squares, and genotype and genotype x environment interaction explained 17.5 and 7.9%, correspondingly. The first 2 principal components (PC1 and PC2) were used to create a 2-dimensional GGE biplot and explained 48.07 and 18.6% of GGE sum of squares, respectively. The GGE biplot identified three tef growing mega-environments. The first mega environment consisted of environments Ambo,Bedele,Arjo and Areka with variety G11 and G15 as the winning variety and the second sector represents Melko with G2 as winning variety while the third section represents Omonada with G8 as the winner variety. The varieties Kena (G3),Felagot (G9) and Wellekomi (G12) were low yielding and unstable during the experimental year.The varieties Dukem (G15),Heber-1 (G11),Quncho (G1) and Abola (G7) were found to be the most stable varieties and with mean grain yield exceeding the grand mean. The varieties Dukem,Heber-1 and Quncho were found to be benchmark or ideal varieties and can be recommended for wider cultivation in the South and Southwestern Ethiopia.

**Keywords**: **Adaptability, GEI, GGE biplot, Mega-environment, Stability.**

## Introduction

Tef belongs to the grass family, *Poaceae*, sub-family Chloridoideae (Eragrostoideae), tribe Eragrostidae, sub-tribe Eragrostae, and genus *Eragrostis*. The genus *Eragrostis* comprises of about 350 species. Although the crop species have had several synonyms previously used by several authors, its presently most accepted binomial nomenclature is [*Eragrostis tef* (Zucc.) Trotter]. In cultivation as a cereal, tef is the only species in the genus *Eragrostis* and together with finger millet (*Eleusine crocana* L.) they constitute the sole two species in the sub-family Chloridoideae cultivated for human consumption of the grains (Watson and Dallawitz, 1992).

In Ethiopia, tef, maize, sorghum and wheat took up 24.02% (about 3,016,053.75 hectares),16.80% (about 2,110, 209.61 hectares), 14.58% (1,831,600.45 hectares) and 13.25% (1,663,837.58 hectares) of the grain crop area, respectively. As to production, maize, tef, wheat and sorghum made up 27.02% (7.84 million tons), 17.29% (5.02 million tons), 15.63% (4.54 million tons) and 16.36% (4.75 million tons) of the grain production, in the same order. Tef is cultivated annually on about 3.01 million hectares and occupies a premier position in areacoverage among the various food crops cultivated in the country. With regard to estimated crop yield, average national yield of tef is about 1.66-ton ha$^{-1}$ (CSA, 2017). This crop is the most important cereal crop in the country accounting for about 28% of the total acreage and 21% of the gross grain production of all cereals. It is grown by over 6.99 million farmers' households, and constitutes the major staple food grain for over 50 million Ethiopian people (CSA, 2017). This implies that tef is very important in the overall national food security of the country (Kebebew *et al*., 2013).

Multi-environment yield trials (MEYTs) are used in the final selection cycles to identify superior genotypes in plant breeding programs. This task is not generally easy due to the frequent presence of GEI. It attenuates the association between phenotype and genotype, reducing genetic progress in plant breeding programs. Means across environments are adequate indicators of genotypic performance only in the absence of GEI. If it is present, the use of means across environments ignores the fact that genotypes differ in relative performance over environments (Voltas *et al*., 2002). A significant GEI may be either (i) a non-crossover type where the ranking of genotypes remains constant across environments and the interaction is significant because of changes in the magnitude of the response, or (ii) a crossover type where a significant change in rank occurs from one environment to another. When selecting genotypes across a number of environments, plant breeders look for a non-crossover type of GEI or preferably the absence of a GEI for general adaptation (Matus *et al*., 2003), and a crossover type of GEI for specific adaptation.

MEYTs aim not only to identify superior genotypes for the target region, but also to determine if the target region can be subdivided into different MEs. Investigation of ME is a prerequisite for meaningful cultivar evaluation and recommendation (Yan *et al*., 2000). CIMMYT has introduced the concept of ME, defined as "a broad, not necessarily contiguous area, occurring in more than one country and frequently transcontinental, defined by similar biotic and abiotic stresses, cropping system requirements, consumer preferences, and, for convenience, by volume of production" (Braun *et al*.,1996).

Several statistical methods have been used for the analysis and interpretation of multi environment trial data (Crossa and Cornelius, 1997). Of these statistical tools, the two most frequently used are the additive main effects and multiplicative interaction (AMMI) model (Zobel *et al*., 1988) and the genotype main effect plus GEI (GGE) biplot methodology proposed by Yan *et al*. (2000).

The GGE biplot analysis is efficient because it enables predicting the mean genotype yield per specific environment, as well as helps identifying the most stable genotype for the region of interest (Santos *et al*. 2016). According to Badu *et a*. (2012), this analysis is more versatile and flexible than other models based on simple linear regression and on segmented linear regression, as well as than non-parametric methods, because it allows better understanding the GEI. Studies about the adaptability and stability of different cultures based on biplot graphics corroborate the efficiency of the analysis to recommend genotypes and to group favorable and unfavorable environments (Santos *et al*. 2016).The objective of present study was to evaluate released tef varieties for yield stability using GGE biplot method and to identify high yielding and well adapted varieties for the South and Southwestern Ethiopia

## Materials and Methods

**Description of Experimental sites:** The experiment was conducted during the main cropping season of 2018 in six locations (Table 1).

**Plant Materials Used:** Twenty one tef varieties obtained from national tef breeding program were evaluated at six locations of south and south western Ethiopia (Table 2).

**Table 1. The main cropping season of 2018 in six locations**

| Location | Geographic position |  | Altitude (m.a.s.l) | Soil type | Temp ($^0$C) | Rainfall (mm) |
|---|---|---|---|---|---|---|
|  | Latitude (N) | Longitude (E) |  |  |  |  |
| Ambo | $8^0$57′ | $38^0$07′ | 2175 | Vertisol | 18 | 1018 |
| Areka | $7^0$09′ | $37^0$41′ | 1830 | Alfisol | 27 | 1539 |
| Arjo | $8^0$74′ | $36^0$50′ | 2457 | Nitosol | 18 | 1850 |
| Bedele | $8^0$27′ | $36^0$21′ | 2087 | Nitosol | 18 | 1700 |
| Melko | $7^0$47′ | $36^0$ 47′ | 1753 | Nitosol | 22 | 1639 |
| Omonada | $7^0$41′ | $37^0$12′ | 1975 | Nitosol | 20 | 1600 |

**Table 2. Tef varieties obtained from national tef breeding program at six locations of south and south western Ethiopia**

| No. | Variety name | Common name | Released Center | Year of release |
|---|---|---|---|---|
| 1 | DZ-Cr-387 RIL355) | Quncho | DZARC | 2006 |
| 2 | DZ-01-1880 | Guduru | Bako | 2006 |
| 3 | 23-Tafi Adi-72 | Kena | Bako | 2008 |
| 4 | DZ-01-3186 | Etsub | Adet | 2008 |
| 5 | DZ-Cr-438 RIL133 B | Kora | DZARC | 2014 |
| 6 | DZ-Cr-438 RIL91A | Dagim | DZARC | 2016 |
| 7 | DZ-Cr- 438 RIL7 | Abola | Adet | 2016 |
| 8 | DZ-Cr-429 RIL125 | Negus | DZARC | 2017 |
| 9 | DZ-Cr-442 RIL77C | Felagot | DZARC | 2017 |
| 10 | DZ-Cr-457 RIL181 | Tesfa | DZARC | 2017 |
| 11 | DZ-Cr-419 (DZ-Cr-974 X PI 222988) | Heber -1 | Adet | 2017 |
| 12 | DZ-01-787 | Wellenkomi | DZARC | 1978 |
| 13 | DZ-Cr-255 | Gibe | DZARC | 1993 |
| 14 | DZ-01-99 | Asgori | DZARC | 1970 |
| 15 | DZ-01-974 | Dukem | DZARC | 1995 |
| 16 | DZ-01-1285 | Koye | DZARC | 2002 |
| 17 | DZ-01-2053 | Holetta Key | Holetta | 1998/99 |
| 18 | DZ-Cr-37 | Tsedey | DZARC | 1984 |
| 19 | DZ-CR-409 (sel. 50D) | Boset | DZARC | 2012 |
| 20 | DZ-01-196 | Magna | DZARC | 1970 |
| 21 | DZ-01-354 | Enatite | DZARC | 1970 |

**Experimental design and field management:** The treatments were laid out in randomized complete block design with three replications. Sowing was done manually in rows and the spacing between rows and plants was 20cm and 10cm, respectively. Spacing between plots was 1 m, whereas that between replications was 1.5 m and the total plot size was 2mx2m.Seed rates was based on the recommendation which was 15kg/ha. Planting was done on the onset of rain in the respective locations. As per the recommendations, plots were fertilized with 40 kg of N and 60 kg of $P_2O_5$per hectare for light soils and 60 kg N and 60kg $P_2O_5$ per hectare for black soils (Vertisols). All DAP was applied at planting, while urea was applied in split half at planting and the remaining half at tillering stage. All other relevant field trial management practices were carried out throughout the experimentation period across all locations as per the recommendations for the respective locations. Data were recorded from each plot on days to heading, days to maturity, days to grain filling period, grain yield, straw yield, above ground shoot biomass, harvest index, thousand seed weight, plant height, panicle length, culm length, lodging index and number of fertile tillers.

**Statistical Analysis:** Primary statistical analyses (such as an Anderson-Darling normality test and the Levine homogeneity test of variances) were performed. 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 analyses of variance genotypes were assumed to be fixed while environments were assumed random.

The following statistical model was used for combined analysis of variance over environments:

$Yijk = \mu + Gi + Ej + GEij + Bk(j) + \epsilon ijk$

where, Yijk, Observed value of genotype i in block k of environment (location) j; μ, grand mean; Gi, effect of genotype I; Ej, environment or location effect; GEij, the interaction effect of genotype i with environment j; Bk(j), The effect of block k in location (environment) j and ϵijk, error (residual) effect of genotype i in block k of environment j.The combined analysis of variance was carried out to estimate effects of environment (E), genotype (G) and GEI. Levels of significance of these variables were determined by using F-test.

**Genotype Main Effect and Genotype by Environment Interaction effect (GGE) biplot Analysis:** 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 tef varieties 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 GE interaction 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) Comparison between two genotypes. We will, thus, use this method to analyze the data. First, the combined analysis of variance was performed, with all effects fixed. The GGE biplot was built according to the formula given by Yan *et al*. (2000):

$$Y_{ij} - \mu - \beta_j = \lambda_1 \varepsilon_{i1} \eta_{j1} + \lambda_2 \varepsilon_{i2} \eta_{j2} + \varepsilon_{ij}$$

where, $Y_{ij}$, the performance of the ith genotype in the jth environment; $\mu$, The grand mean; $B_j$, the main effect of the environment j; $\lambda_l$ and $\lambda_2$, singular value for IPCA1 and IPCA2, respectively; $\varepsilon_{i1}$ and $\varepsilon_{i2}$, eigen vectors of genotype i IPCA1 and IPCA2, respectively; $\eta_{j1}$ and $\eta_{j2}$, eigen vectors of environment j for IPCA1 and IPCA2, respectively and $\varepsilon_{ij}$ = Residual associated with genotype i and environment j.

## Results and Discussion

The combined ANOVA showed that tef grain yield were significantly affected by E,which explained 69.4% of the total (G+E+GEI) variation, whereas G and GEI, which were significant ($P<0.001$),accounted for 7.9 and 17.5%,respectively (Table 4).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%.It is very common for MEYTs data to embody a mixture of crossover and non-crossover types of GEI.In this study, different varieties produced the highest grain yielder in different environments. The varieties G1 (Quncho),G8 (Negus) and G15 (Dukem) were high yields at Omonada and G2 (Guduru),G5 (Kora) and G3 (Kena) were high yielders at Melko (Table 3).These differential rankings of varieties across test environments revealed that there exists possible crossover GEI. However, GEI is not always the case.

**Table 3. Mean grain yield (kg/ha) of 21 tef varieties evaluated in the South and South western part of Ethiopia**

| Varieties | Locations | | | | | | | Overall rank |
|---|---|---|---|---|---|---|---|---|
| | Omonada | Melko | Bedele | Areka | Arjo | Ambo | Mean | |
| G1 | 1250 | 521 | 525 | 1330 | 608 | 1510 | 959.0 | 3 |
| G2 | 330 | 1013 | 580 | 1108 | 430 | 1120 | 765.9 | 15 |
| G3 | 500 | 740 | 390 | 1040 | 425 | 882 | 664.4 | 21 |
| G4 | 540 | 680 | 360 | 1330 | 540 | 1250 | 786.8 | 11 |
| G5 | 790 | 790 | 208 | 1220 | 580 | 1260 | 812.9 | 9 |
| G6 | 790 | 713 | 330 | 1340 | 660 | 1360 | 869.5 | 7 |
| G7 | 916 | 528 | 790 | 1330 | 560 | 1520 | 949.7 | 4 |
| G8 | 1250 | 420 | 225 | 1490 | 460 | 908 | 759.6 | 16 |
| G9 | 330 | 530 | 275 | 1140 | 940 | 1005 | 704.8 | 20 |
| G10 | 660 | 730 | 350 | 1130 | 350 | 1101 | 723.3 | 18 |
| G11 | 1000 | 720 | 580 | 1460 | 808 | 1625 | 1034.1 | 2 |
| G12 | 708 | 707 | 300 | 1060 | 330 | 1170 | 713.7 | 19 |
| G13 | 790 | 480 | 280 | 1080 | 416 | 1340 | 735.0 | 17 |
| G14 | 1083 | 574 | 508 | 1120 | 850 | 1250 | 899 | 5 |
| G15 | 1250 | 715 | 641 | 1420 | 790 | 1690 | 1086.3 | 1 |
| G16 | 958 | 658 | 675 | 1080 | 416 | 1250 | 841.5 | 8 |
| G17 | 875 | 460 | 340 | 1030 | 480 | 1520 | 787.2 | 10 |
| G18 | 916 | 520 | 625 | 1101 | 760 | 1310 | 874 | 6 |
| G19 | 958 | 678 | 625 | 1210 | 470 | 1170 | 774.5 | 13 |
| G20 | 1000 | 604 | 560 | 930 | 370 | 1210 | 781.6 | 12 |
| G21 | 830 | 679 | 480 | 968 | 540 | 1104 | 768.4 | 14 |
| **Mean** | **844** | **641** | **459.4** | **1187.6** | **561.1** | **1264.5** | | |
| **CV (%)** | **113** | **138** | **107** | **188** | **192** | **343** | | |
| **LSD at 5%** | **8.8** | **13** | **17.4** | **9.6** | **20.6** | **9.9** | | |

Where,G1=Quncho,G2=Guduru,G3=Kena,G4=Etsub,G5=Kora,G6=Dagim,G7=Abola,G8=Negus,G9=Felagot,G10= Tesfa,G11=Heber-1,G12=Wellenkomi,G13=,GibeG14=,Asgori,G15=Dukem,G16=Koye,G17=Holetta Key,G18=Tsedey,G19=Boset,G20=Magna and G21=Enatite, CV=Coefficient of Variation ,LSD= Least Significant difference

**Table 4: Combined analysis of variance for grain yield of 21 tef varieties tested in six locations**

| Source of Variation | DF | SS | %SS | MS | Pr > F |
|---|---|---|---|---|---|
| Environment | 5 | 36913429.26 | 69.4 | 7382685.85 | <.0001 |
| Replication within E (R/E) | 12 | 208288.87 | 0.391 | 17357.41 | 0.0646 |
| Genotype | 20 | 4223319.35 | 7.94 | 211165.97 | <.0001 |
| GEI | 100 | 9377492.99 | 17.5 | 93774.93 | <.0001 |
| Residuals | 240 | 2431273.26 | 4.57 | 10130.31 | |
| Total | 377 | 53153803.73 | | | |

**Mean = 824.2** **CV (%) =12.12**

**Genotype Main Effect and Genotype by Environment Interaction (GGE) biplot:** The graphical method was employed to investigate environmental variation and interpret GEI. The partitioning of GEI through GGE biplot analysis showed that IPCA1 and IPCA2 accounted for 48.1% and 18.6% of sum of squares, respectively, with a total of 66.67% variation for grain yield. This result suggests that biplot graphics explain most sums of squares and GEI in the genotype. This outcome made it possible to have a safe genotype selection based on the multivariate analysis (Yan, 2001).

**The polygon view of the GGE biplot ("which-won-where" pattern):** The polygon view of the GGE-biplot analysis helps one detect cross-over and non-cross-over genotype-by-environment interaction and possible mega environments in multi-location yield trials (Yan *et al.*,2007). The biplot polygon view has been used to identify "which-won-where" patterns in MET data analysis. In this graph, lines are drawn to connect the farthest genotypes in the biplot and then a line is drawn perpendicular to that side of the polygon so as to pass through the origin (Yan, 2002). The farthest genotype is the best performer in the environment/location included in that sector. The varieties G2 (Guduru),G11 (Heber-1),G15 (Dukem),G8 (Negus) and G3 (Kena) were vertex genotypes (Figure 1). They are best in the environment lying within their respective sector in the polygon view of the GGE-biplot (Yan and Tinker 2006); thus these genotypes are considered specifically adapted. Genotypes close to the origin of axes have wider adaptation (Abay and Bjornstand 2009).The GGE biplot identified three tef growing mega-environments. The first mega environment consisted of environments Ambo, Bedele, Arjo and Areka with variety G11 and G15 as the winning variety and the second sector represents Melko with G2 as winning variety while the third section represents Omonada with G8 as the winner variety. It was also noted that no mega-environments fell into sectors where genotype G3 (Kena) was the vertex variety, indicating that the variety was not suitable to any of the test environments.

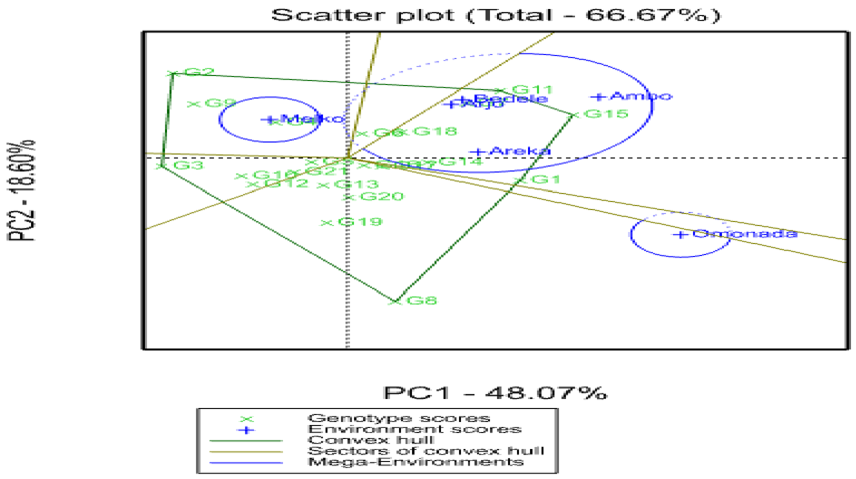

**Figure 1.Polygon view of the GGE biplot using symmetrical scaling for the which-won-where pattern of the genotypes environments**

Where,G1=Quncho,G2=Guduru,G3=Kena,G4=Etsub,G5=Kora,G6=Dagim,G7=Abola,G8=Negus,G9=Felagot,G10=Tesfa,G11=Heber1,G12=Wellenkomi,G13=,GibeG14=,Asgori,G15=Dukem,G16=Koye,G17=Holetta Key,G18=Tsedey,G19=Boset,G20=Magna and G21=Enatite

**Ranking of Varieties Based on Mean Grain Yield and Stability performance:** Yield performance and stability of genotypes were evaluated by an average environment coordination (AEC) method (Yan, 2001). 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). The average environment coordinates (AEC X-axis) or the performance line passes through the biplot origin with an arrow indicating the positive end of the axis. The AEC Y-axis or the stability axis passes the plot origin and perpendicular to the AEC X-axis. In order to evaluate the genotypes by ranking with reference to the mean value of the tested trait and trait stability, the AEC method can be used in the GGE bi-plot graph is presented in Figure 2.The length of the line segment between the origin and the orthogonal projection of the genotype location onto the AEC axis, is proportional to the mean genotype value and represents the main effect of the genotype G. Genotype ranking in descending order is as follows: G15 > G11 > G1 > G7 > G14 > G18 > G6 > G16 > Mean > G5 > G17 > G4 > G20 > G19 > G21 > G2 > G8 > G13 > G10 > G12> G9> G3.The length of the line segment between the genotype location and its orthogonal projection onto the AEC axis is a measure of genotype stability. In the present study, starting from the most stable, the genotypes G16, G6 and G1 showed the heights above the overall average and the highest stability. G21,G5 and G19 genotypes were also stable, but their height was below the overall average. The unstable genotypes can be determined in an analogous way: G11, G7, G18 and G14 and with the height above the overall average and G8, G2,G9 and G3 with the height below the overall average.

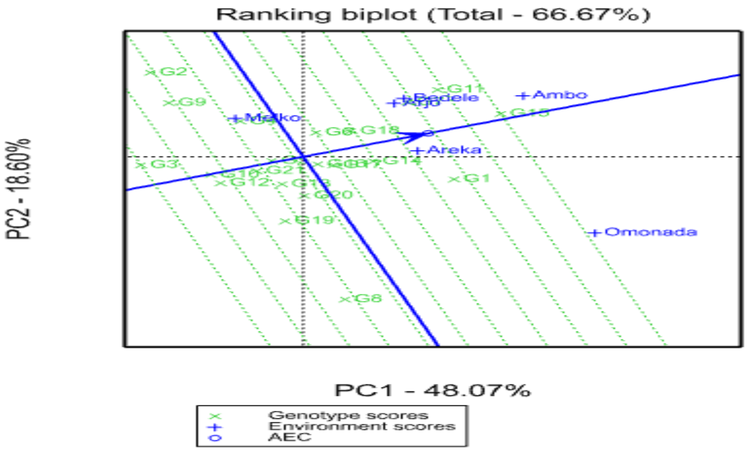

**Figure 2.Mean and stability performance of genotypes**

Where,G1=Quncho,G2=Guduru,G3=Kena,G4=Etsub,G5=Kora,G6=Dagim,G7=Abola,G8=Negus,G9=Felagot,G10= Tesfa,G11=Heber1,G12=Wellenkomi,G13=,GibeG14=,Asgori,G15=Dukem,G16=Koye,G17=Holetta Key,G18=Tsedey,G19=Boset,G20=Magna and G21=Enatite

**Ranking of genotypes based on relative to the ideal genotypes:** An interesting application of GGE biplot is the evaluation of genotype relative to an ideal genotype. 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 Rajcan, 2002). Such an ideal genotype is defined by having the greatest vector length of the high yielding genotypes with zero GEI, as represented by an arrow pointing to it (Figure.3).Although such an ideal genotype may not exist in reality, it can be used as a reference for genotype evaluation. A genotype is more desirable if it is located closer to the ideal genotype as the center, concentric circles were drawn to help visualize the distance between each genotype and ideal genotype. Therefore, G15 was closer to the 'ideal' genotype followed by G11 and G1 being more desirable than other genotypes (Figure.3). On the other hand, the low yielding genotypes (G9 and G3) were considered to be undesirable because they are placed far from the ideal genotypes. It seems that identification of ideal genotype through GGE biplot methodology is a proper tool for identifying most stable high yielding genotypes.

**Ranking of Environments Based on relative to ideal environment**: According to Yan (2001), discriminating ability and representativeness are the important properties of a test location. An ideal location should be highly differentiating for the tested genotypes and at the same time representative of the target location (Yan and Kang, 2003). Similar to ideal genotype, an ideal environment or location is defined and showed by the small circle with an arrow pointing to it. Figure 3 shows the environment Ambo as an 'ideal' environment. The ranking of other environments based on the ideal nature of environments were Bedele>Arjo>Areka >Omonada >Melko (Figure.3). The environment Ambo has large PC1 score and small PC2 score. Hence, this environment is more stable and suitable for all genotypes following Bedele. On the other hand, Melko is a discriminating environment because it has large PC2 score. The discriminating ability of a location is concerned with the composition of genotypes, but the presence of GE interaction complicates the identification of an ideal test location (Yan *et al.*, 2000). GGE methodology is interactions partioning them into their PCs. The test environments should have large PC1 scores in order to discriminate genotypes in terms of the genotypic main effect and absolute small PC2 scores in order to be more representative of the overall locations (Yan and Rajcan, 2002).

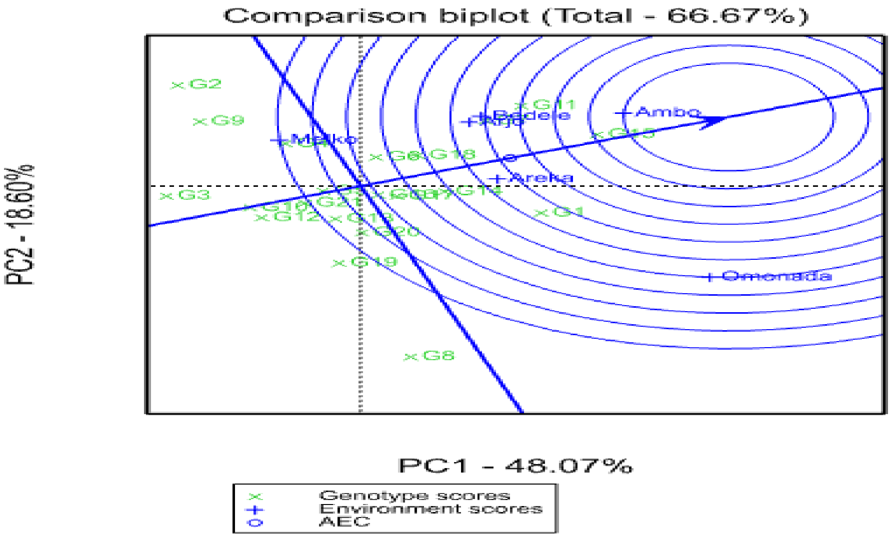

**Figure 3.Evaluation of genotypes and environments relative to ideal genotype and environments** Where,G1=Quncho,G2=Guduru,G3=Kena,G4=Etsub,G5=Kora,G6=Dagim,G7=Abola,G8=Negus,G9=Felagot,G10= Tesfa,G11=Heber1,G12=Wellenkomi,G13=,GibeG14=,Asgori,G15=Dukem,G16=Koye,G17=Holetta Key,G18=Tsedey,G19=Boset,G20=Magna and G21=Enatite

**Relationship Among Testing Environments**: The GGE biplot showed in Figure 4 explained 66.6% of the total variation and so this biplot can be used for extracting interrelationships among the environments. The environment vectors are lines that connect the biplot origin and the markers of test environments and the angle between them is related to the correlation coefficient (Kroonenberg, 1995). On the other hand, the biplot vector view is mainly used to identify test environments, which have large angle or low or negative correlations. Locations with small angles between them were highly positively correlated and they provided similar information on genotypes. According to the angles of test location vectors, the six locations are grouped into three major groups. One group includes Ambo, Bedele,Arjo and Areka was closely correlated (Figure 4), suggesting that the locations provide redundant information about genotypes while the other group involves Melko and Omonada. Location, Melko had short vector length and alone. The angle between Bedele and Omonada was greater than 90°, showing a negative correlation between them (r = -0.79***).The angle between Melko and Ambo was around 90° indicating little or no correlation (r = -0.05) between these environments. The angle between Bedele and Arjo was less than $90^0$ indicating that there was some positive correlation between them (0.25). All other locations between them had also positive correlation between themselves and with Bedele and Arjo. Obtaining reliable information on the similarity of environments and their subdivision into groups can enable breeders to use fewer test environments reducing the cost of testing and increasing breeding efficiency. With the longest vectors from the origin, environments Omonada was the most discriminating environment while, location Melko with short vector length least discriminating.

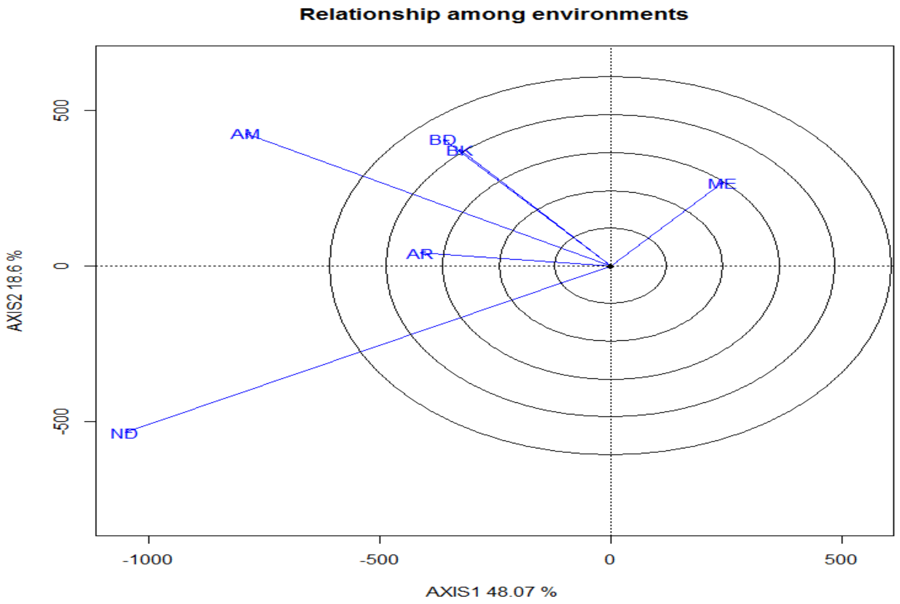

**Figure 4. Relationship among environments**

Where, AM=Ambo,ND =Omonada,ME =Melko,AR =Areka,BK=Bako/Arjo,BD =Bedele

## Conclusion

In Ethiopia, South and Southwestern part play important role in production of tef.Suitable varieties can be recommended for cultivation. Twenty one tef varieties were tested across six locations of South and Southwestern part Ethiopia. The studied varieties exhibited both crossover and non crossover type of genotype by environment interaction. In this study, the combined analysis of variance (ANOVA) indicates that the genotype (G), environments (E) and Genotype by environment interaction variance were highly significant at $P<0.001$. The GGE biplot model is an excellent tool for visual MET data analysis (Mohammadi *et al*., 2011).The varieties Heber-1 and Quncho were close to the ideal variety and can thus be used as benchmarks for the evaluation in the South and Southwestern Ethiopia.

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## Conflict of interest

The authors have not declared any conflict of interests.

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