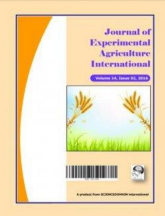

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Genotype-by-Environment Interaction and Stability Analysis in Grain Yield of Improved Tef (*Eragrostis tef*) Varieties Evaluated in Ethiopia

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Authors' contributions

This work was carried out in collaboration among all authors. Author HJ designed the study, executed the experiment, performed the statistical analysis and wrote the first draft of the manuscript. Authors KA, KT, KD and ZT supervised the study. All authors read and approved the final manuscript.

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ABSTRACT

Aims: To assess the magnitude of genotype by environment interaction; possible existence of different mega-environments; and discriminating ability and representativeness of the testing environments.
Study Design: Randomized complete Block Design with three replications.

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Place and Duration of Study: The study was conducted at Debre Zeit, Holetta and Alem Tena for two years (2015 and 2016) and at Adet, Axum and Bako for one year (2015).
Methodology: Thirty-five improved tef varieties were evaluated at nine environments. The G × E interaction were quantified using additive main effects and multiplicative interaction (AMMI) and the genotype and genotype by environment (GGE) biplot models.
Results: Combined analysis of variance revealed highly significant (P = 0.01) variations due to genotype, environment and genotype by environment interaction effects. AMMI analysis revealed 4.3%, 79.7% and 16% variation in grain yield due to genotypes, environments and G x E effects, respectively. G_6 gave the highest mean grain yield (3.33 t/ha) over environments whereas G_{29} gave the lowest mean yield (2.49 t/ha). The GGE biplot grouped the nine testing environments and the 35 genotypes into four mega environments and seven genotypic groups. The four mega environments include: G-I (E_1, E_4 and E_6); G-II (E_2, E_3, E_7 and E_8); G-III (E_9), and G-IV (E_5). E_5, E_6, E_7 and E_8 which had the longest vector were the most discriminating of all environments while, E_1 and E_4 which had the smallest angle with the average environmental axis were the most representative of all environments. Regarding genotypes, G_6, G_{25}, G_{34} and G_{16} were identified as the best yielding and relatively stable genotypes to increase tef productivity.
Conclusion: AMMI and GGE were found to be efficient in grouping the tef growing environments and genotypes.

Keywords: AMMI; biplot; GGE; stability; Tef.

1. INTRODUCTION

Tef is the most important staple cereal crop in Ethiopia that adapts to extreme environmental conditions and present in diverse socio-economic conditions [1]. Crop performance is a function of genotype, environment, and genotype by environment interactions (GEI). The increase in crop production and productivity is, therefore, attained with advanced understanding of the crop management and growing environments [2,3,4]. The understanding of G *x* E interaction enables us to effectively allocate resources and to characterize genotypic responses to diverse crop productivity levels [5]. Thus, it enables to eliminate unnecessary spatial and temporal replication of yield trials as well as to establish additional testing environment when the existing ones are under-represented [4]. In general, such information enables breeders to determine optimum breeding strategy to make informed choices of the locations and input systems to be used in the breeding efforts [6] and to develop and release crop varieties suitable for various agro-ecologies. As there are very limited studies on G x E in tef crop, the importance of conducting more studies across major tef growing environments have been suggested [5,7,8]. By so doing, breeders will be able to identify adaptable, stable and high yielding genotypes. Additive main effects and multiplicative interaction (AMMI) and the genotype and genotype by environment (GGE) are some of the most widely used stability models to estimate the magnitude of *GXE* interactions [9,10]. Both analyses enable to delineate and explain mega-environments, to identify high yielding and better adapted genotypes [9]. GGE biplot, especially, is useful, to graphically represent the GE interaction, and to rank the studied genotypes and environments [11]. The objectives of this study, therefore, were: (i) to assess the magnitude of GE interaction and stability; (ii) to examine the possible existence of different mega-environments; and (ii) to determine the discriminating ability and representativeness of the environments.

2. MATERIALS AND METHODS

Thirty-five improved tef varieties released by the National Agricultural Research Systems in Ethiopia from the inception of the tef breeding program to the year 2014 were used. These varieties differ in their seed color, suitable environment and other parameters. Detailed descriptions of the varieties are shown in Table 1.

Nine environments from six major tef growing areas in Ethiopia, namely Adet, Alem Tena, Axum, Debre Zeit, Holetta and Shambu were used in the study. Among these six locations, Alem Tena, Debre Zeit and Holetta were each represented by two locations. These experimental sites are situated at elevations ranging from 1580 m a. s. l. at Alem Tena to 2503 at Shambu. Similarly, the annual rainfall of these sites ranges from 500 mm at Alem Tena to 1100 mm at Holetta. Detailed descriptions of the

Table 1. Description of the 35 Tef genotypes used in this study

Genotype			Year of release	Seed color	Breeding method	Suitable environment
Code	Common name	Variety name				
G_1	*Enatit*	DZ-01-354	1970	Pale white	Selection	High potential
G_2	*Asgori*	DZ-01-99	1970	Brown	Selection	High potential
G_3	*Magna*	DZ-01-196	1978	Very white	Selection	High potential
G_4	*Wolenkomi*	DZ-01-787	1978	Pale white	Selection	High potential
G_5	*Menagesha*	DZ-Cr-44	1982	White	Hybridization	High potential
G_6	*Melko*	DZ-Cr-82	1982	White	Hybridization	High potential
G_7	*Tseday*	DZ-Cr-37	1984	White	Hybridization	Low moisture
G_8	*Gibe*	DZ-Cr-255	1993	White	Hybridization	High potential
G_9	*Ziquala*	DZ-Cr-358	1995	White	Hybridization	High potential
G_{10}	*Dukem*	DZ-01-974	1995	White	Selection	High potential
G_{11}	*Holeta Key*	DZ-01-2053	1999	Brown	Selection	High potential
G_{12}	*Ambo-Toke*	DZ-01-1278	2000	White	Selection	High potential
G_{13}	*Gerado*	DZ-01-1281	2002	White	Selection	Low moisture
G_{14}	*Koye*	DZ-01-1285	2002	White	Selection	High potential
G_{15}	*Key Tena*	DZ-01-1681	2002	Brown	Selection	Low moisture
G_{16}	*Gola*	DZ-01-2054	2003	Pale white	Selection	High potential
G_{17}	*Ajora*	PGRC/E 205396	2004	Pale white	Selection	High potential
G_{18}	*Genet*	DZ-01-146	2005	Pale white	Selection	High potential
G_{19}	*Zobel*	DZ-01-1821	2005	Pale white	Selection	High potential
G_{20}	*Dima*	DZ-01-2423	2005	Brown	Selection	High potential
G_{21}	*Yilmana*	DZ-01-1868	2005	Pale white	Selection	High potential
G_{22}	*Dega Tef*	DZ-01-2675	2005	Pale white	Selection	Waterlogged soil
G_{23}	*imbichu*	DZ-01-899	2005	Pale white	Selection	Waterlogged soil
G_{24}	*Amarach*	Ho -Cr-136	2006	Pale white	Hybridization	Low moisture
G_{25}	*Quncho*	DZ-Cr-387 (RIL355)	2006	Very white	Hybridization	High potential
G_{26}	*Guduru*	DZ-01-1880	2006	White	Selection	High potential
G_{27}	*Gemechis*	DZ-Cr-387 (RIL127)	2007	Very white	Hybridization	Low moisture
G_{28}	*Mechare*	Acc. 205953	2007	Pale white	Selection	High potential
G_{29}	*Kena*	23-Tafi Adi-72	2008	White	Selection	High potential
G_{30}	*Etsub*	DZ-01-3186	2008	White	Selection	High potential
G_{31}	*Laketch*	DZ-Cr-387 (RIL 273)	2009	Very white	Hybridization	Low moisture
G_{32}	*Simada*	DZ- Cr-385 (RIL295)	2009	White	Hybridization	Low moisture
G_{33}	*Boset*	DZ-Cr-409 (RIL 50d)	2011	Very white	Hybridization	Low moisture
G_{34}	*Kora*	DZ-Cr-438 (RIL133B)	2014	Very white	Hybridization	High potential
G_{35}	*Werekiyu*	Acc. 214746A	2014	White	Selection	Low moisture

nine testing locations regarding their geographical coordinates, climate and soil types are shown in Table 2. Randomized complete block design (RCBD) with three replications was used at each location. Each plot had five rows of one-meter long with the spacing of 0.2m between rows and 1m between plots. All recommended agronomic and cultural practices for tef were applied. Data on grain yield (GY) was recorded on plot basis which was later extrapolated to hectare basis. The grain yield data were evaluated for the normality and homogeneity of variance. This was followed by combined analysis of variance (ANOVA) as suggested by Gomez and Gomez [12] using the generalized linear model (GLM) procedure in SAS v9 [13]. Mean separation and significance test was performed using Duncan's multiple range test at

Table 2. Description of the nine study locations *

Locations		Altitude	Latitude	Longitude	Annual rainfall (mm)	Temperature		Soil type
Code	Name					Min °C	Max °C	
E_1	Adet	2240	11°17' N	37°43'E	921.3	7.3	31.3	Nitosol
E_2	Alem Tena-1	1580	8°20' N	38°57'E'	500	8	29.8	Light sandy
E_3	Alem Tena-2	1580	8°20' N	38°57' E	500	8	29.8	Light sandy
E_4	Axum	2100	14°6′N	38°48′E	700	12.2	26.8	Vertisol
E_5	Debre Zeit-1	1900	8°44' N	38°58' E	851	8.9	28.3	PellicVertisol
E_6	Debre Zeit-2	1900	8°44' N	38°58' E	851	8.9	28.3	PellicVertisol
E_7	Holetta-1	2400	9°44'N	38°30' E	1100	6	22	Nitosol
E_8	Holetta-2	2400	9°44' N	38°30' E	1100	6	22	Nitosol
E_9	Shambu	2503	9°57'N	37°10' E				Nitosol

**Climatic and edaphic information was obtained from their respective research and sub centers*

5% probability level. AMMI analysis was performed following the AMMI model according to [14] using GenStat software 15 edition [15]. The AMMI stability values (ASV) were calculated as suggested by [16]. GGE biplot analysis, on the other hand, was performed using the genotype by environment analysis in R (GEA-R) software v4.0 [17]. Thus, the first two principal components (PC1 and PC2) were used to graphically represent the GEI, to identify the rank of studied genotypes and environments [11].

3. RESULTS AND DISCUSSION

3.1 Analysis of Variance

Combined analysis of variance for grain yield of the 35 improved tef varieties across nine testing environments revealed highly significant ($P < 0.01$) variations due to genotype, environment and genotype by environment interactions (Table 3). The significant variability among the tef varieties in the present study is in line with the previous reports in tef [7]. The significant GXE interaction in the present study indicates unstable performance of the tef varieties across the testing environments (Fig. 1). While, Debre Zeit and Holetta were high yielding environments Alem Tena, Adet, Axum and Shambu were low yielding environments. Although not at all locations, variety G6 (Melko) performed better than others at least at three low yielding environments (Adet, Alem Tena and Axum) and one high yielding environment (Debre Zeit). Apart from this, tef varieties with higher productivity at specific testing sites were at Holetta (Gerado, Key Tena and Gimbichu), at Debre Zeit (Melko, Gola, Ajora, Quncho and Gemechis), at Shambu (Guduru and Gibe), at Axum (Kora, Dukem, Quncho, Laketch and Melko), and at Alem Tena (Melko, Amarach and Quncho). Interestingly, the three top yielding varieties at Adet (Quncho, Laketch and Kora) have very close kinship. While Quncho and Laketch are sister lines obtained from the same crossing group, Kora was obtained from the cross where Quncho was used as one parental line. The huge variability in the grain yield among the 35 tef varieties at the nine environments might be due to wide variability in climatic and soil conditions. Earlier works also

Table 3. Analysis of variance for grain yield (t/ha) of tef varieties evaluated at nine environments

Source of variation	Degree of freedom	Mean squares
Genotype (G)	34	1.35***
Environment (E)	8	104.93***
Replication (E)	18	0.011ns
G x E	272	0.62***
Error	612	0.014
Total	944	-

reported similar inconsistencies in yield performance which complicated the selection and recommendation of stable genotype across environments [5,7,18].

3.2 AMMI Analysis of Variance for Grain Yield

AMMI analysis revealed highly significant (P = 0.01) differences for grain yield (t ha-1) of 35 tef varieties due to genotypes, environments and their interaction. This is in line with the previous works [5,7,19]. The AMMI analysis partitioned the G x E variance into principal component (PC) axes where the results are presented in Table 4. Based on this, the first and second interaction principal components explained for 72.5% (IPCA1=53.04% and IPCA2=19.49%) of the total variation. Previously, however, PC1 value of 52.1% [5], 66.1% [20], 93.1% [21] were reported. In the present study, the variation explained by the environment which was about four times higher than that of genotype and GE interaction is in line with the earlier findings [2,22]. The first two IPCAs that contributed for over 70% of the G x E interaction were used to create a biplot as being employed previously in faba beans [2], finger millet [20] and tef [5,7].

3.3 Mean Grain Yield and AMMI Stability Value

The mean yield performance of the 35 tef varieties at nine environments is shown in Table 5 and Fig. 1. The mean grain yield of the nine environments ranged from 1.7 t ha-1 at E2 (Alem Tena) to 4.29 t ha-1 atE5 (Debre Zeit) with a mean of 2.89 t ha-1. The grain yield at E5 was followed by those at E7, E6 and E8 in descending order. On the other hand, among the 35 tef varieties tested across nine environments, mean grain yield ranged from 2.49 t ha-1 for G29 (Kena) to 3.33 t ha-1 for G6 (Melko). The five top yielding varieties were G6 (3.33 t ha-1), G34 (3.27 t ha-1), G25 (3.22 t ha-1), G16 (3.2 t ha-1) and G23 (3.18 t ha-1). The AMMI stability values (ASV), in the present study ranged from 0.01 for G10 to 2.73 for G35 (Fig. 2). Thus, G10 had the lowest ASV (0.01) and moderately higher grain yield (3.0 t ha-1) whereas G6 had the highest yield (3.33 t ha-1) with relatively lower ASV (0.71) followed by G34 which had the next highest yield (3.27 t ha-1) with ASV (1.16) (Table 5). Hence, when considering higher grain yield, varieties such as G6, G34 and G25 with high grain yield and relatively more stable could be selected instead of varieties such as G10 and G20 which were more stable but with moderately low yield.

3.4 Analysis of GGE Biplot

GGE biplot is visualized on the basis of results explained for the first two principal components [23]. In the present study, the first two principal components of GGE biplot explained 72.8% (PC1=49.8 and PC2=23.0%) of the total variations (Fig. 2). In the polygon view, genotypes found farthest away from the origin are the vertex genotypes having the highest yield in their respective sector [24,25]. In the present study, these genotypes include G19, G25, G6, G13, G9 and G29 and they all have the highest yield in their respective sector. In GGE biplot graph, various lines emanating from the origin and become perpendicular to the line connecting the vertex genotypes are useful to divide the testing environments and genotypes into different sectors. Therefore, the nine testing environments were divided into four mega environments while the 35 genotypes were divided into seven genotypic groups (Fig. 3). The four mega environments consisted of Group-I (E1, E4 and E6), Group-II (E2, E3, E7 and E8), Group-III (E9), and Group-IV (E5). Varieties G6 and G25 were the vertex and highest yielding genotypes at three environments namely E1, E4 and E6. Similarly, G13 was the vertex and highest yielding genotype in the sector where E2, E3, E7 and E8 exist while, G19 was the highest yielding at E9. The other vertex genotypes (G9 and G29), however, had no corresponding environment and hence are the poorest yielding in all the testing environments. Sector four (E5) which consisted of G17, G33 and G27 had no vertex genotype, though their mean yields were substantially higher than the grand mean and they were also among the top yielding genotypes in their neighboring environments.

3.5 Relationship among Environments and Discriminative vs Representativeness

The angle between the vectors of two environments has a meaningful relation with the correlation coefficient between them [3,25,26] and are used to group the test environments. The relationships among the nine test environments in the present study are presented in Fig. 3a. Based on this graph, the angle between E5, E6, E1 and E4 was less than 900 indicating the existence of positive correlation between them. Similarly, E7, E8, E2 and E3 had

acute angle (<90°) indicating that these environments were positively correlated. On the other hand, the angle between E9 and E5, and between E6 and E7 is nearly 90° showing that these environments are not correlated. Furthermore, E9 had obtuse angle (>90°) with E6, E1, E4, E3, E7, E8 and E2 showing that it has negative correlation with

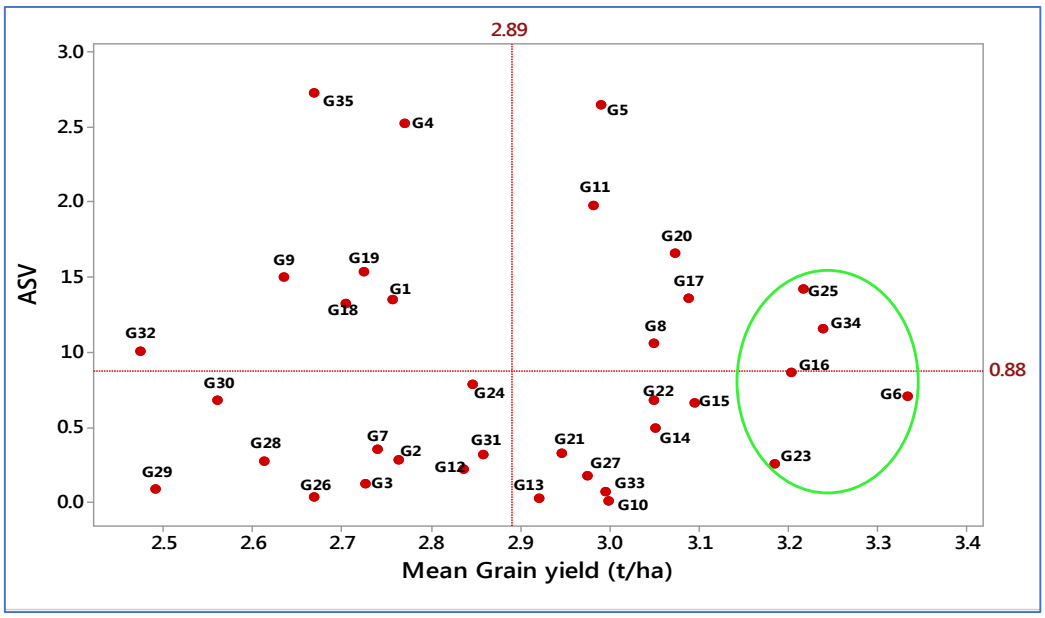


Fig. 1. Plot showing mean grain yield (t ha^{-1}) versus AMMI stability value (ASV)

The reference line on the x-axis is the average grain yield (2. 89 t ha^{-1}) whereas that on the y-axis is (ASV=0.88) indicating stability of genotype)

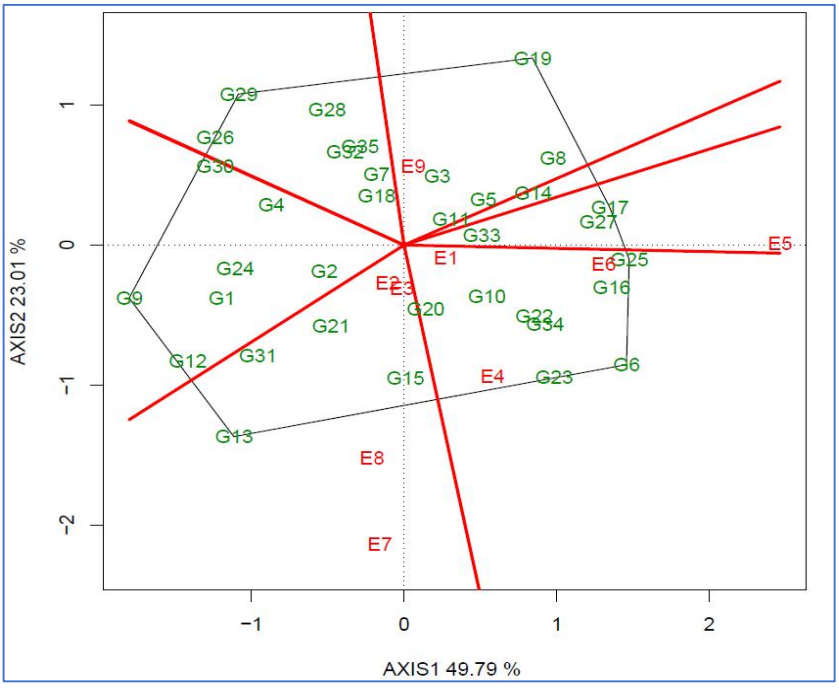


Fig. 2. Which performed where view of the GGE biplot showing the grouping of genotypes and environments into various sectors

Table 4. AMMI analysis of variance for grain yield (t ha^{-1}) of 35 tef genotypes grown at nine environments

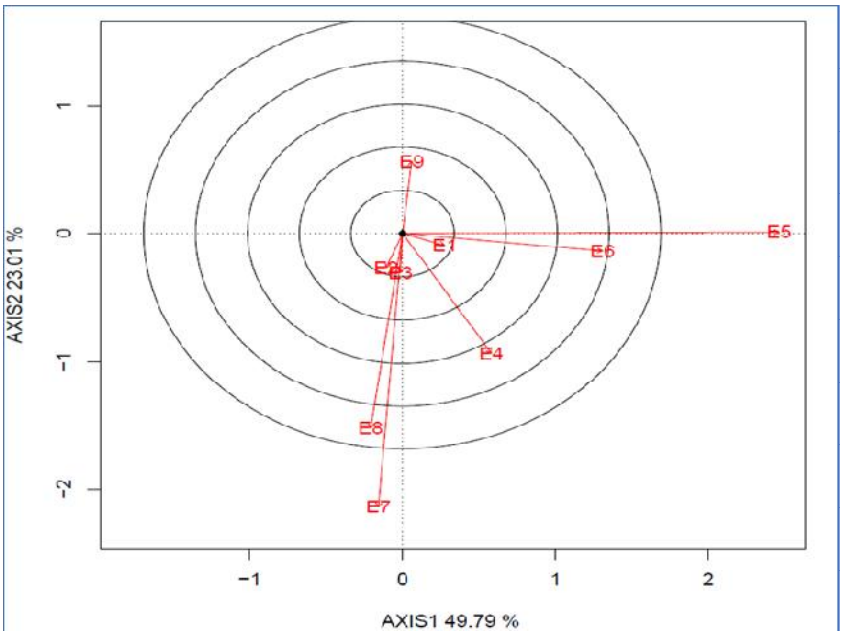
Source of variation	DF	SS	MS	F value	Explained % of SS
Environment	8	839.5	104.9	9292.9***	79.66
Genotype	34	45.90	1.35	97.1***	4.34
GEI	272	168.4	0.62	44.5***	15.98
PC1	41	89.3	2.18	156.6***	53.04
PC2	39	32.7	0.84	60.2***	19.41
Residuals	192	46.4	0.24	17.4	*

GEI= Genotype by Environment interaction; DF= Degrees of freedom; SS= Sums of square; MS= Means square

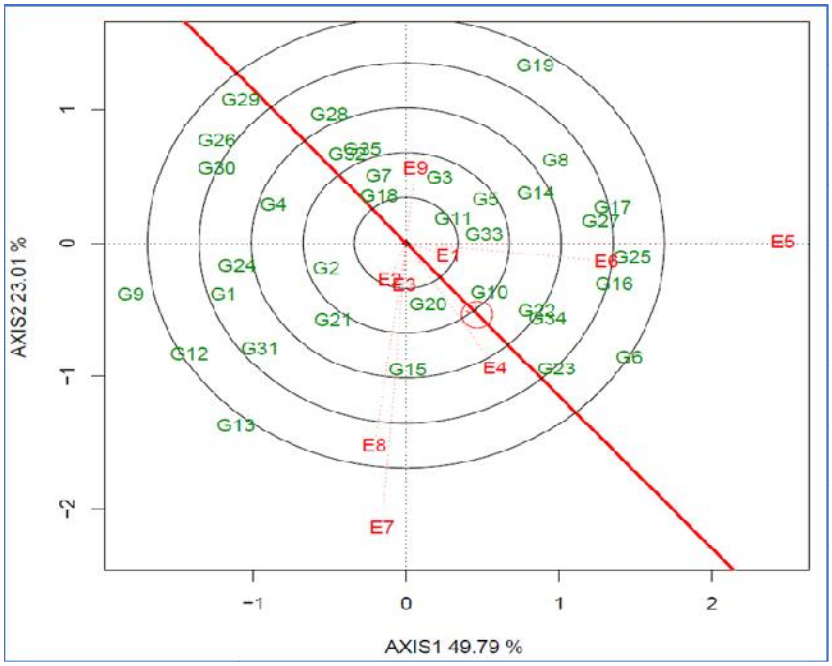
Table 5. Mean grain yield (t ha-1) of Tef varieties evaluated at nine environments in Ethiopia

Code	Environments												
	E1	E2	E3	E4	E5	E6	E7	E8	E9	Mean	ASV	ICPA1	ICPA2
G1	2.21	1.80	1.85	2.93	3.07	2.84	4.12	4.01	1.99	2.76	1.35	-0.70	-0.11
G2	2.14	1.50	1.61	2.33	3.86	3.15	4.35	3.81	2.13	2.76	0.29	0.22	-0.39
G3	2.33	1.56	1.43	2.37	4.47	3.54	3.49	3.51	1.84	2.73	0.13	0.15	0.26
G4	2.46	2.15	1.87	1.88	3.63	2.89	3.89	3.73	2.44	2.77	2.53	-0.95	-0.25
G5	2.68	1.91	1.77	2.15	4.74	3.82	3.73	3.68	2.43	2.99	2.65	-0.88	-0.73
G6	2.13	1.75	2.49	3.09	5.71	4.07	4.54	4.12	2.11	3.33	0.71	0.46	0.36
G7	2.30	1.33	1.57	1.74	4.29	3.24	4.06	3.43	2.71	2.74	0.36	-0.25	-0.43
G8	2.77	1.78	1.75	2.16	5.08	4.14	3.63	3.35	2.80	3.05	1.06	0.60	-0.25
G9	1.98	1.63	1.85	1.52	2.63	2.98	4.82	4.03	2.27	2.63	1.50	0.74	0.10
G10	2.22	1.76	1.50	3.05	4.84	3.49	4.10	4.00	2.05	3.00	0.01	0.06	-0.03
G11	2.18	1.96	1.94	2.30	4.66	3.53	4.02	3.58	2.68	2.98	1.98	0.80	0.47
G12	2.16	2.24	1.98	2.63	2.87	2.97	4.64	4.21	1.84	2.84	0.23	-0.27	-0.20
G13	2.07	1.82	1.84	2.47	3.31	3.06	5.17	4.72	1.82	2.92	0.03	-0.09	-0.10
G14	1.93	2.14	1.98	2.36	5.00	4.13	3.90	3.28	2.74	3.05	0.50	-0.41	-0.22
G15	1.92	1.79	1.83	2.68	4.39	3.44	4.95	4.32	2.52	3.10	0.67	0.36	-0.55
G16	2.59	1.76	1.86	2.12	5.60	4.31	4.44	3.88	2.27	3.20	0.87	0.31	-0.78
G17	1.88	1.94	1.84	2.47	5.54	4.24	4.00	3.29	2.61	3.09	1.36	-0.68	0.30
G18	2.17	1.60	1.39	2.31	4.20	3.26	3.41	4.03	1.99	2.70	1.33	0.69	-0.14
G19	2.63	1.36	1.53	2.22	5.03	3.76	2.63	3.22	2.15	2.73	1.54	-0.53	0.88
G20	2.30	1.75	1.69	2.50	4.49	3.50	4.34	4.38	2.72	3.07	1.66	0.76	-0.29
G21	2.49	1.82	1.74	2.32	3.82	3.38	4.57	4.19	2.19	2.95	0.33	-0.01	0.57
G22	2.59	1.55	1.46	2.51	5.06	3.98	4.66	3.75	1.90	3.05	0.68	-0.28	0.68
G23	2.54	1.80	1.66	2.36	5.36	3.95	4.56	4.71	1.71	3.18	0.26	0.31	-0.03
G24	2.19	2.15	2.03	1.83	3.37	3.01	4.35	4.07	2.63	2.85	0.79	-0.48	0.40
G25	2.89	2.17	1.78	3.06	5.49	4.23	3.82	3.58	1.94	3.22	1.42	-0.67	-0.44
G26	2.19	1.91	1.77	1.91	3.15	2.86	3.60	3.50	3.14	2.67	0.04	0.12	-0.06
G27	2.15	1.36	1.38	2.71	5.39	4.20	3.71	3.76	2.13	2.98	0.18	0.26	0.06
G28	1.71	1.71	1.70	2.66	3.74	3.12	3.02	3.30	2.57	2.61	0.28	0.28	-0.26
G29	2.40	1.92	1.51	1.37	3.42	2.86	3.35	3.28	2.31	2.49	0.09	0.06	0.28
G30	2.23	1.78	1.81	2.03	3.10	2.92	3.56	3.52	2.11	2.56	0.68	-0.43	0.43
G31	2.80	2.10	1.57	2.98	3.30	2.92	4.39	4.20	1.48	2.86	0.32	0.30	0.27
G32	1.60	1.28	1.44	1.38	4.19	3.25	3.84	3.41	1.88	2.47	1.01	0.51	-0.55
G33	2.53	1.60	1.65	2.92	4.74	3.45	4.07	3.43	2.27	2.96	0.08	0.05	0.28
G34	2.92	1.93	1.64	3.42	4.88	3.99	4.35	3.76	2.57	3.27	1.16	0.58	0.49
G35	2.57	1.84	1.71	2.67	3.88	3.22	3.24	3.13	1.77	2.67	2.73	-1.00	-0.03
Mean	**2.31**	**1.78**	**1.70**	**2.38**	**4.29**	**3.48**	**4.04**	**3.78**	**2.25**	**2.89**	**0.88**	**0.00**	**0.00**

Key: G1 to G35 name of genotypes; E1= Adet, E2=Alem Tena (2015), E3= Alem Tena (2016), E4= Axum, E5= Debre Zeit (2015), E6= Debre Zeit (2016), E7=Holetta (2015), E8= Holetta (2016), E9= Shambu. IPCA = Interaction Principal Component Axis, ASV = AMMI Stability Value



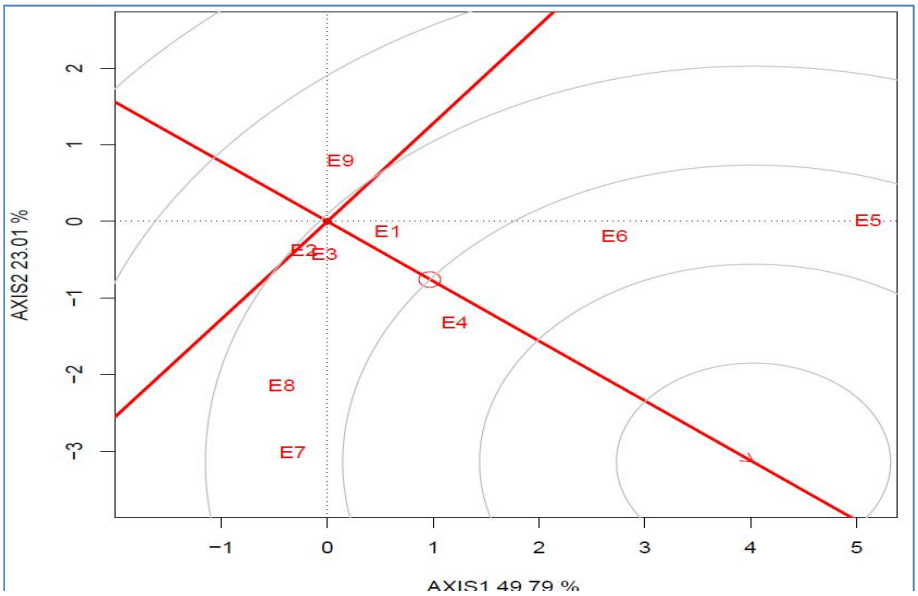
3a)



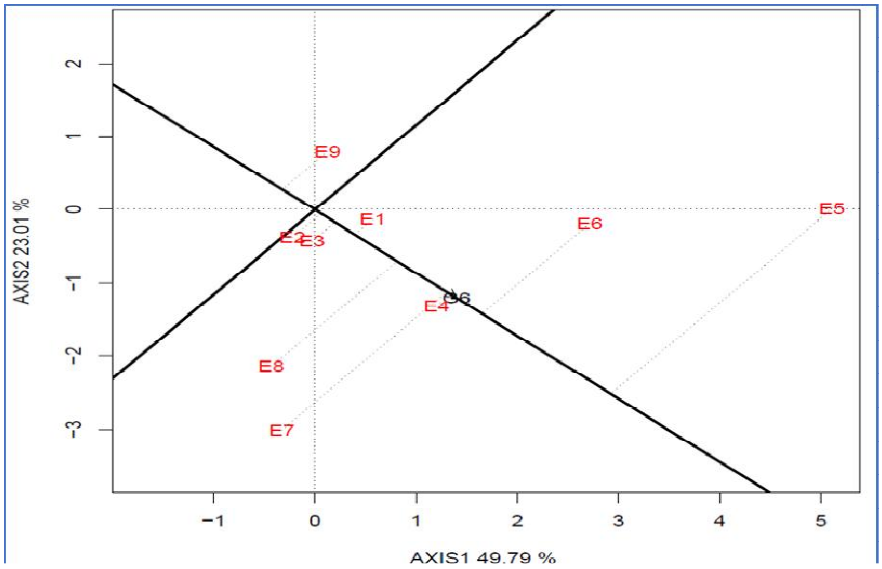
3b)

Fig. 3. GGE biplot view showing the relationship among the testing environments (a) and discriminativeness vs representativeness (b)

these environments. Thus, if environments are negatively correlated, genotypes performing best in one environment would perform less in the other environment and vice versa. However, if environments are positively correlated genotypes performing best in one environment will have the same performance in the other environment too [3,25].



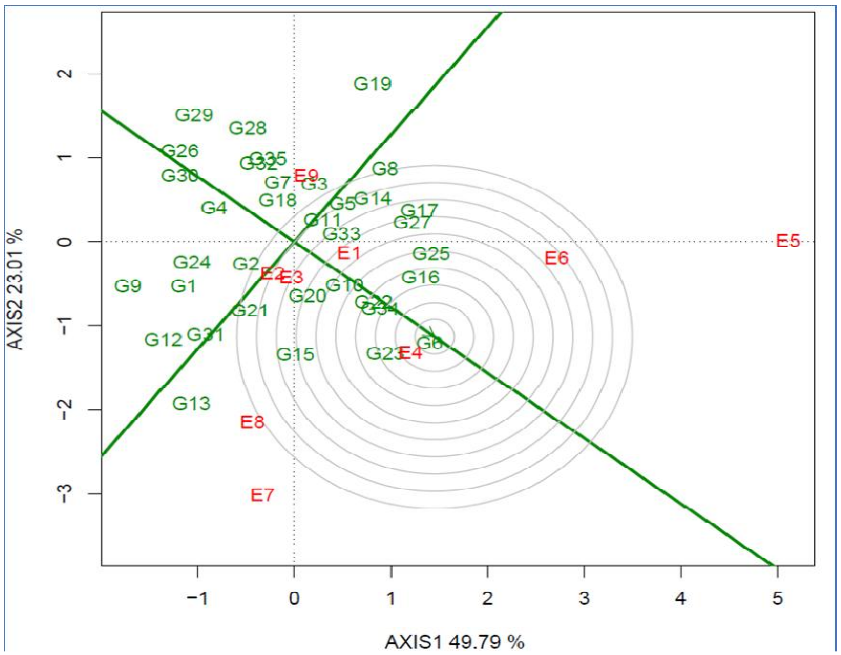
4a)



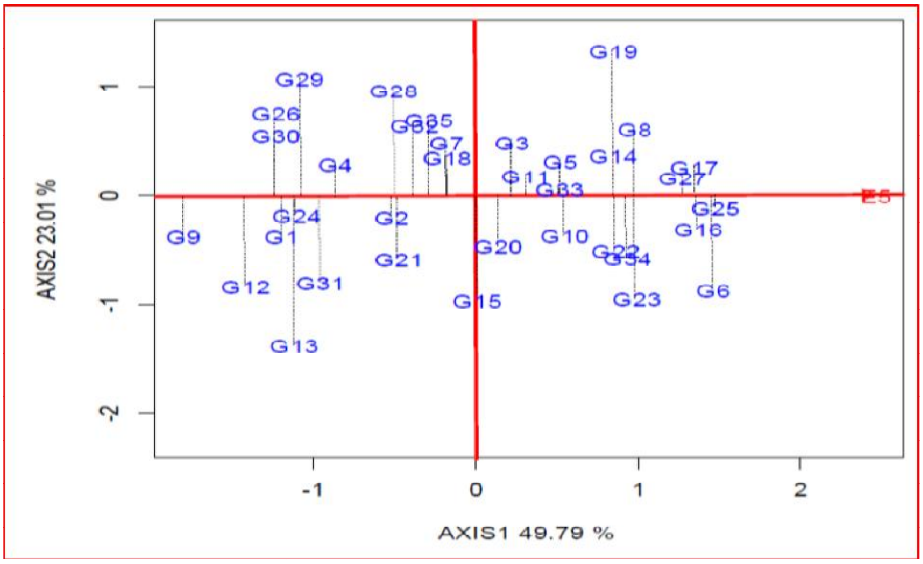
b)

Fig. 4. GGE biplot showing ranking of test environments relative to an ideal test environment (a) and relative to the best genotypes (b)

The GGE biplot is useful to assess how much a test environment is capable of generating unique information about the differences among genotypes as well as how representative the mega-environment is. A vector length, for instance, is the absolute distance between the marker of an environment and the plot origin [23,27,28] and it is used to measure the discriminating ability of an environment. Thus, the longer the vector, the better the discriminating power of an environment. The variation in vector length among the different testing environments in the present study is presented in Fig. 3b. Based on this, E5, E7 and E6 which had the longest vector were identified as the most discriminating environments



5a)



5b)

Fig. 5. Ranking genotypes relative to the ideal genotype (a) and the best environment (b)

whereas E1, E2 and E3 were the least discriminating of all test environments. According to [28], testing environment with smaller angle and average environmental axis is said to be more representative of the other testing environments. Hence, E4 and E1 which had the smallest angle with the average environmental axis were identified to be the most representative environments. E9, however, was the least representative of all studied environments and was the poorest for selecting cultivar adapted to the whole region (Fig. 3b).

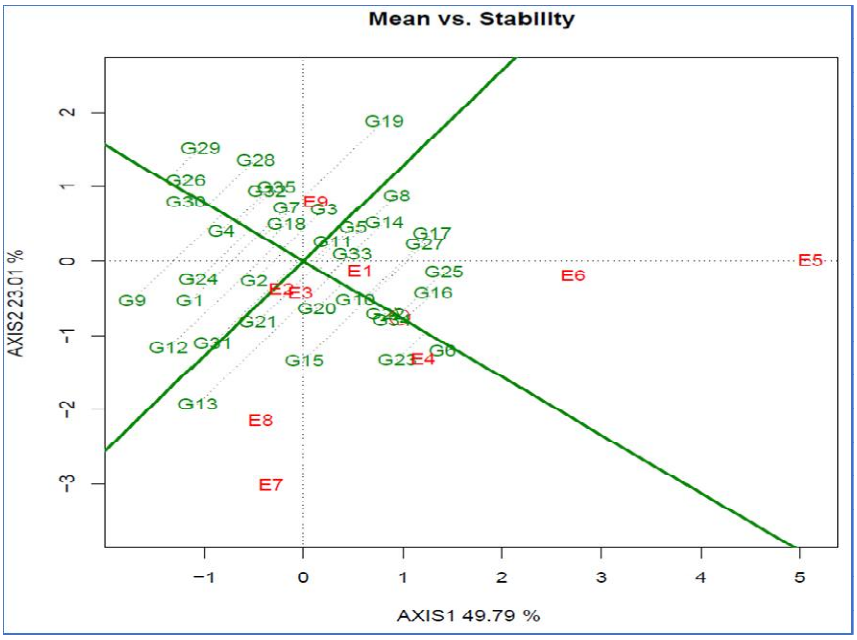


Fig. 6. Ranking based on mean performance and stability of 35 improved varieties across nine environments (E1-E9)

3.6 Ranking testing Environments Relative to the Ideal Environment and Genotype

Average environmental axis (AEA) is a line passing through the origin and pointing to the positive direction with its distance equal to the longest vector. Besides, an ideal environment is a point on the AEA in the positive direction of the biplot origin and is equal to the longest vector of all environments [28]. Thus, the ranking of environments has identified E5 as the most ideal environment followed by E6 and E4 whereas, E9 followed by E2, E3 and E1 were the least ideal environments (Fig. 4a). All study environments other than E9 were found to have above average performance for genotype evaluation. Ideal environments are generally, expected to have more power of discriminating genotypes and more representative of the overall environments [23,27].

On the other hand, the length of environmental projections appeared onto a genotype axis shows the performance of the best genotype at different environments relative to the other environments. Thus, E5 followed by E7, E6 and E8 had the longest projection from the axis where G6 ranked first (Fig. 4b). Hence, all environments other than E9 were found to be best for the performance of G6.

3.7 Ranking Genotypes Relative to the Ideal Genotype and Environment

The average environment coordination view of the GGE biplot shows the ranking of genotypes based on the performance of an ideal genotypes (Fig. 5a). The relative adaptation of the ideal genotype is evaluated by drawing a line passing through the biplot origin and the best genotype marker. This line is called a genotype axis and is connected to the best genotype [11]. Such ranking of genotypes based on performance of ideal genotype revealed that G6 followed by G23, G34, G22, G16 and G25, respectively were among the top yielding genotypes. Thus, G6 with the highest average yield was identified to be the ideal genotype to evaluate the performance of test genotypes relative to it.

In ranking genotypes relative to the best environment, E5 was identified to be the best environment to evaluate the performance of genotypes (Fig. 5b). Thus, the best environment axis was drawn towards E5 and then, a perpendicular line to this axis that passes through the biplot origin was also drawn to separate genotypes yielding above and below the mean in the ideal environment. G6, G34, G25, G27, G16, G17, G23 and G22 which appeared on the same direction with E5 were, therefore, found to perform above average in the environment of E5.

3.8 Genotypes Mean Yield and Stability

The average environment coordination (AEC) is a line that passes through the origin and points to the higher mean yield across environments and it shows the increase in rank of genotypes towards the positive end [11]. This line was reported to be useful to evaluate mean grain yield and stability of genotypes [25,29,30]. According to such reports, genotypes considered to be stable are those appeared closer to the origin with the shortest vector from the AEC. Thus, Fig. 6 in the present study shows the mean performance and stability of the genotypes. Based on this, G6, G34, G22 and G10 with the shortest vector from the AEC axis were identified as the most stable genotypes while G13, G19, G12 and G9 with the longest vector from AEC were the most unstable genotypes. On the other hand, G6 followed by G23, G34, G16 and G25 scored higher grain yield whereas G29, G26, G30 and G28 attained inferior grain yield in all environments. An ideal genotype for a specific environment has the highest mean yield and responds best at that particular environment while it is less stable in the other environments and need to be recommended for a specific environment [23,26]. According to the same authors, ideal cultivars have large PC1 scores (high mean yield) and small PC2 scores (high stability). Thus, in the present study, G6, G25, G16, G23 and G34 which had larger PC1 and smaller PC2 scores were identified to be high yielding and stable.

4. CONCLUSION

Overall, the studied tef varieties had sufficient variability for identifying stable and high yielding genotypes. The results of this study revealed the existence of four mega environments and seven tef genotypic groups. Based this study, E5 (Debre Zeit-1) is the most ideal environment for tef cultivation while E9 (Shambu) was the poor yielding and least representative environment. On the other hand, G6 (Melko) with the highest mean grain yield and moderate stability across wide range of environments was an ideal location to boost the productivity of tef in Ethiopia.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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