1   *Original Research Article*

2

3   **Genotype-by-environment interaction and**
4   **stability analysis in grain yield of improved tef**
5   **(*Eragrostis tef*) varieties evaluated in Ethiopia**

6

7
8   .
9

10   **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.
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.

11
12   *Keywords:* AMMI, Biplot, GGE, Stability, Tef

13

14

15   **1. INTRODUCTION**

16
17   Tef is the most important staple cereal crop in Ethiopia that adapts to extreme environmental
18   conditions and present in diverse socio-economic conditions [1]. Crop performance is a
19   function of genotype, environment, and genotype by environment interactions (GEI). The
20   increase in crop production and productivity is, therefore, attained with advanced
21   understanding of the crop management and growing environments [2,3,4]. The
22   understanding of G *x* E interaction enables us to effectively allocate resources and to
23   characterize genotypic responses to diverse crop productivity levels [5]. Thus, it enables to
24   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 [5,8]. 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.

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

G25	*Quncho*	DZ-Cr-387 (RIL355)	2006	Very white	Hybridization	High potential
G26	*Guduru*	DZ-01-1880	2006	White	Selection	High potential
G27	*Gemechis*	DZ-Cr-387 (RIL127)	2007	Very white	Hybridization	Low moisture
G28	*Mechare*	Acc. 205953	2007	Pale white	Selection	High potential
G29	*Kena*	23-Tafi Adi-72	2008	White	Selection	High potential
G30	*Etsub*	DZ-01-3186	2008	White	Selection	High potential
G31	*Laketch*	DZ-Cr-387 (RIL 273)	2009	Very white	Hybridization	Low moisture
G32	*Simada*	DZ- Cr-385 (RIL295)	2009	White	Hybridization	Low moisture
G33	*Boset*	DZ-Cr-409 (RIL 50d)	2011	Very white	Hybridization	Low moisture
G34	*Kora*	DZ-Cr-438 (RIL133B)	2014	Very white	Hybridization	High potential
G35	*Werekiyu*	Acc. 214746A	2014	White	Selection	Low moisture

49

50 Nine environments from six major tef growing areas in Ethiopia, namely Adet, Alem Tena,
51 Axum, Debre Zeit, Holetta and Shambu were used in the study. Among these six locations,
52 Alem Tena, Debre Zeit and Holetta were each represented by two locations. These
53 experimental sites are situated at elevations ranging from 1580 m a. s. l. at Alem Tena to
54 2503 at Shambu. Similarly, the annual rainfall of these sites ranges from 500 mm at Alem
55 Tena to 1100 mm at Holetta. Detailed descriptions of the nine testing locations regarding
56 their geographical coordinates, climate and soil types are shown in Table 2. Randomized
57 complete block design (RCBD) with three replications was used at each location. Each plot
58 had five rows of one-meter long with the spacing of 0.2m between rows and 1m between
59 plots. All recommended agronomic and cultural practices for tef were applied. Data on grain
60 yield (GY) was recorded on plot basis which was later extrapolated to hectare basis. The
61 grain yield data were evaluated for the normality and homogeneity of variance. This was
62 followed by combined analysis of variance (ANOVA) as suggested by Gomez and Gomez
63 [12] using the generalized linear model (GLM) procedure in SAS v9 [13]. Mean separation
64 and significance test was performed using Duncan's multiple range test at 5% probability
65 level. AMMI analysis was performed following the AMMI model according to [14] using
66 GenStat software 15 edition [15]. The AMMI stability values (ASV) were calculated as
67 suggested by [16]. GGE biplot analysis, on the other hand, was performed using the
68 genotype by environment analysis in R (GEA-R) software v4.0 [17]. Thus, the first two
69 principal components (PC1 and PC2) were used to graphically represent the GEI, to identify
70 the rank of studied genotypes and environments [11].

71 **Table 2. Description of the nine study locations ***

Locations		Altitude	Latitude	Longitude	Annual rainfall (mm)	Temperature		Soil type
Code	Name					Min ^{0}C	Max ^{0}C	
E1	Adet	2240	$11^017'$ N	$37^o43'$E	921.3	7.3	31.3	Nitosol
E2	Alem Tena-1	1580	$8^020'$ N	$38^057'$E'	500	8	29.8	Light sandy
E3	Alem Tena-2	1580	$8^020'$ N	$38^057'$ E	500	8	29.8	Light sandy
E4	Axum	2100	$14^06'$N	$38^048'$E	700	12.2	26.8	Vertisol
E5	Debre Zeit-1	1900	$8^044'$ N	$38^0 58'$ E	851	8.9	28.3	PellicVertisol
E6	Debre Zeit-2	1900	$8^0 44'$ N	$38^0 58'$ E	851	8.9	28.3	PellicVertisol
E7	Holetta-1	2400	$9^044'$N	$38^0 30'$ E	1100	6	22	Nitosol
E8	Holetta-2	2400	$9^044'$ N	$38^030'$ E	1100	6	22	Nitosol
E9	Shambu	2503	$9^057'$N	$37^010'$ E				Nitosol

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

73

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 reported similar inconsistencies in yield performance which complicated the selection and recommendation of stable genotype across environments [5,7,18]. Results should be clearly described in a concise manner. Results for different parameters should be described under subheadings or in separate paragraph. Table or figure numbers should be mentioned in parentheses for better understanding.

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	-

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 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

114　G x E interaction were used to create a biplot as being employed previously in faba beans
115　[2], finger millet [20] and tef 5,7].

116

117　**Table 4. AMMI analysis of variance for grain yield (t ha^{-1}) of 35 tef genotypes grown at**
118　　　**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	*

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

121

122

123　**3.3. Mean grain yield and AMMI stability value**

124　The mean yield performance of 35 studied varieties at nine environments is shown in Table
125　5 and Fig. 1. The mean grain yield of the nine environments from 1.7 t ha-1 at E2
126　(Alem Tena) to 4.29 t ha-1 atE5 (Debre Zeit) with a mean of 2.89 t ha-1. The grain yield at
127　E5 was followed by those at E7, E6 & E8 in descending order. On the other hand, among
128　the 35 tef varieties tested across nine environments, mean grain yield ranged from 2.49 t ha-
129　1 for G29 (Kena) to 3.33 t ha-1 for G6 (Melko). The five top yielding varieties were G6 (3.33 t
130　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
131　AMMI stability values (ASV), in the present study ranged from 0.01 for G10 to 2.73 for G35
132　(Fig. 2). Thus, G10 had the lowest ASV (0.01) and moderately higher grain yield (3.0 t ha-1)
133　whereas G6 had the highest yield (3.33 t ha-1) with relatively lower ASV (0.71) followed by
134　G34 which had the next highest yield (3.27 t ha-1) with ASV (1.16) (Table 5). Hence, when
135　considering higher grain yield, varieties such as G6, G34 and G25 with high grain yield and
136　relatively more stable could be selected instead of varieties such as G10 and G20 which
137　were more stable but with moderately low yield.

138
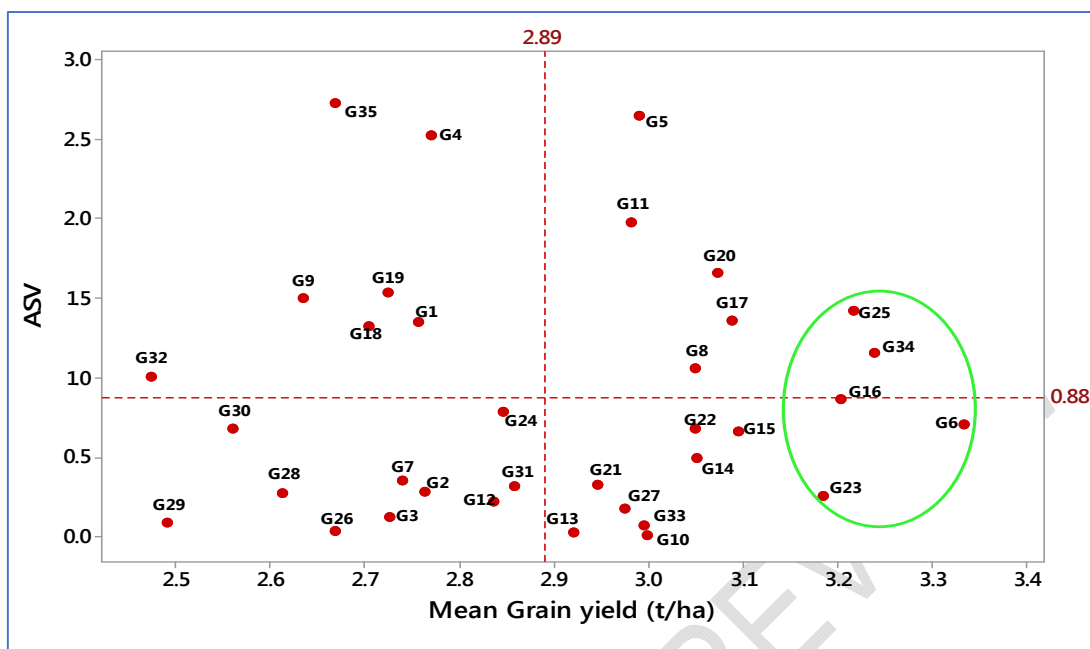
139
Figure 1. Plot showing mean grain yield (t ha^{-1}) versus AMMI stability value (ASV). The
141 reference line on the x-axis is the average grain yield (2. 89 **t ha^{-1}**) whereas that on the y-axis is
142 (ASV=0.88) indicating stability of genotype).

143

144

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

Code	Environments									Mean	ASV	ICPA1	ICPA2
	E1	E2	E3	E4	E5	E6	E7	E8	E9				
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**

147 **Key:** G1 to G35 name of genotypes; E1= Adet, E2=Alem Tena (2015), E3= Alem Tena (2016), E4=
148 Axum, E5= Debre Zeit (2015), E6= Debre Zeit (2016), E7=Holetta (2015), E8= Holetta (2016), E9=
149 Shambu. IPCA = Interaction Principal Component Axis, ASV = AMMI Stability Value.
150
151

3.4. Analysis of GGE biplot

153 GGE biplot is visualized on the basis of results explained for the first two principal
154 components [23]. In the present study, the first two principal components of GGE biplot
155 explained 72.8 % (PC1=49.8 and PC2=23.0%) of the total variations (Fig. 2). In the polygon
156 view, genotypes found furthest away from the origin are the vertex genotypes having the
157 highest yield in their respective sector [24,25]. In the present study, these genotypes include
158 G19, G25, G6, G13, G9 and G29 and they all have the highest yield in their respective
159 sector. In GGE biplot graph, various lines emanating from the origin and become
160 perpendicular to the line connecting the vertex genotypes are useful to divide the testing
161 environments and genotypes into different sectors. Therefore, the nine testing environments
162 were divided into four mega environments while the 35 genotypes were divided into seven
163 genotypic groups (Fig. 3). The four mega environments consisted of Group-I (E1, E4 and
164 E6), Group-II (E2, E3, E7 and E8), Group-III (E9), and group-IV (E5). Varieties G6 and G25
165 were the vertex and highest yielding genotypes at three environments namely E1, E4 and
166 E6. Similarly, G13 was the vertex and highest yielding genotype in the sector where E2, E3,
167 E7 and E8 exist while, G19 was the highest yielding at E9. The other vertex genotypes (G9
168 and G29), however, had no corresponding environment and hence are the poorest yielding
169 in all the testing environments. Sector four (E5) which consisted of G17, G33 and G27 had
170 no vertex genotype, though their mean yields were substantially higher than the grand mean
171 and they were also among the top yielding genotypes in their neighboring environments.
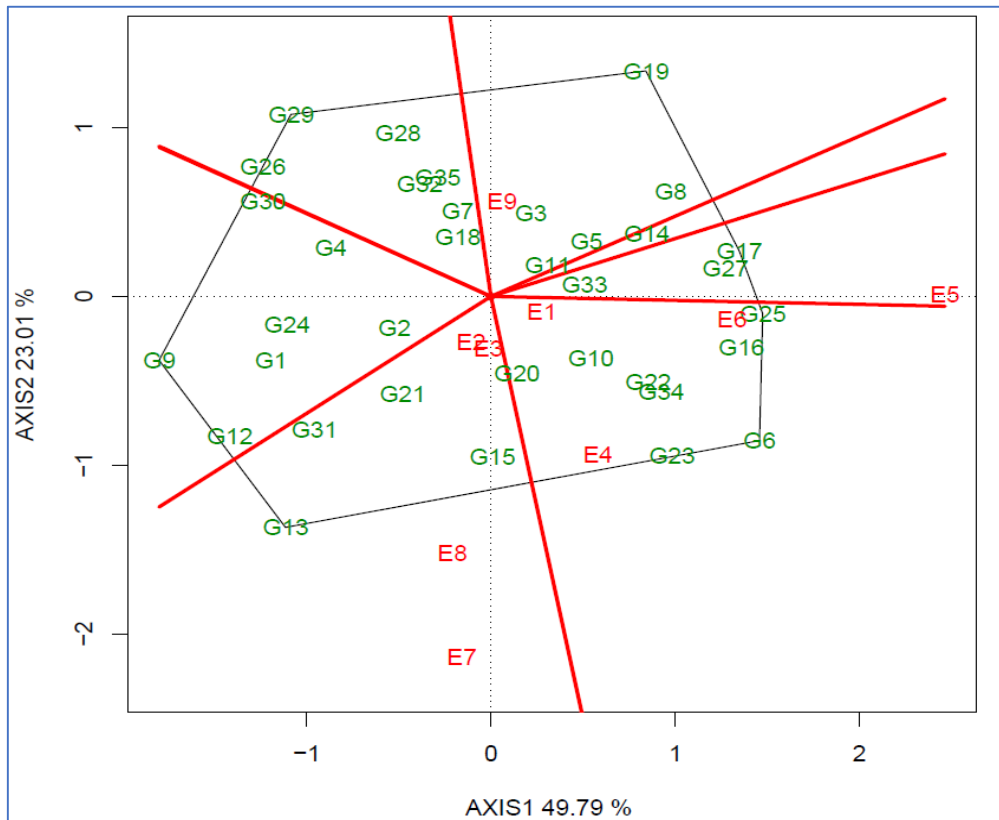
173
174 **Fig 2. Which performed where view of the GGE biplot showing the grouping**
175 **ofgenotypes and environments into various sectors.**
176
177

178 ## 3.5. Relationship among environments and discriminative vs
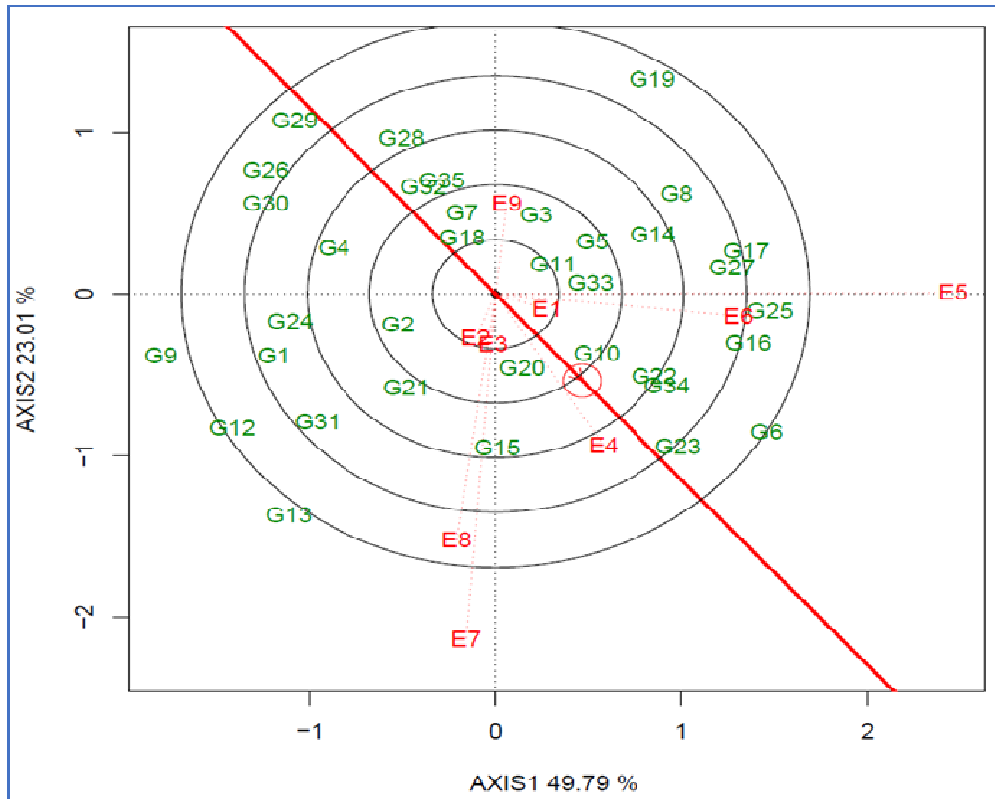179 ## representativeness
180

181 The angle between the vectors of two environments has a meaningful relation with the
182 correlation coefficient between them [3,25,26] and are used to group the test environments.
183 The relationships among the nine test environments in the present study are presented in
184 Fig. 3a. Based on this graph, the angle between E5, E6, E1 and E4 was less than 900
185 indicating the existence of positive correlation between them. Similarly, E7, E8, E2 and E3
186 had acute angle (<90^{0}) indicating that these environments were positively correlated. On the
187 other hand, the angle between E9 & E5, E6 & E7 is nearly 900 showing that these
188 environments are not correlated. Furthermore, E9 had obtuse angle (>90^{0}) with E6, E1, E4,
189 E3, E7, E8 and E2 showing that it has negative correlation with these environments. Thus, if
190 environments are negatively correlated, genotypes performing best in one environment
191 would perform less in the other environment and vice versa. However, if environments are
192 positively correlated genotypes performing best in one environment will have the same
193 performance in the other environment too [3,25].
194

195 The GGE biplot is useful to assess how much a test environment is capable of generating
196 unique information about the differences among genotypes as well as how representative
197 the mega-environment is. A vector length, for instance, is the absolute distance between the
198 marker of an environment and the plot origin [23,26,27] 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 are presented in Fig. 3b. Based on this, E5, E7
and E6 which had the longest vector were identified as the most discriminating environments
whereas E1, E2 and E3 were the least discriminating of all test environments. According to
[27], 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).
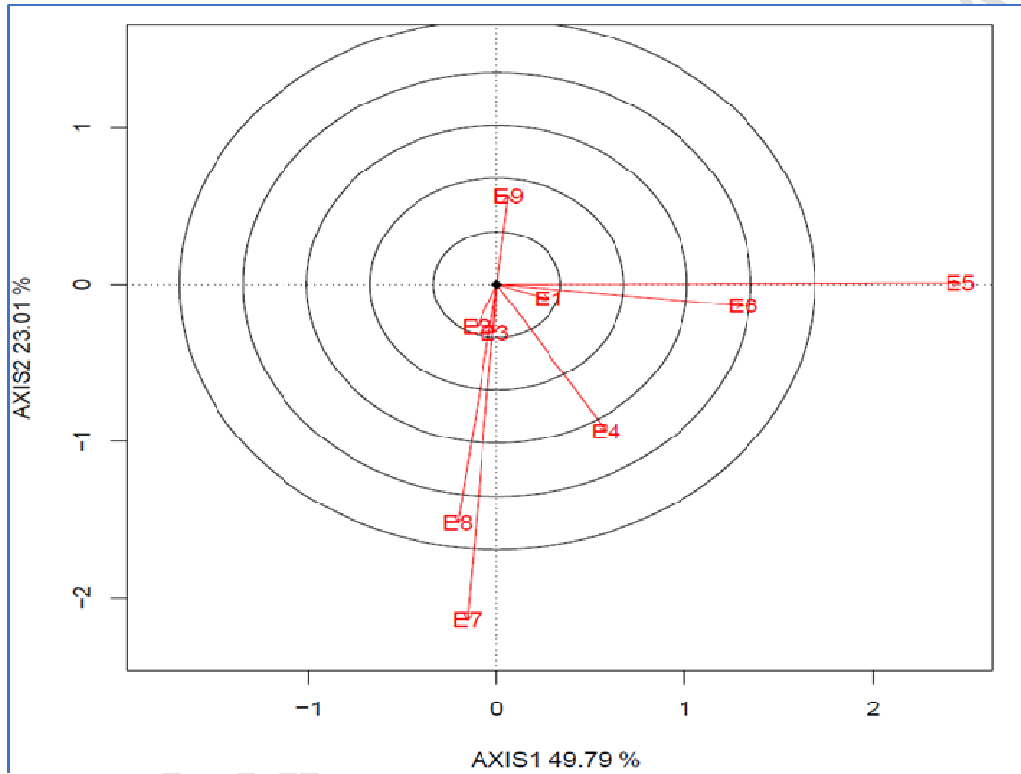
3a)

3b)

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

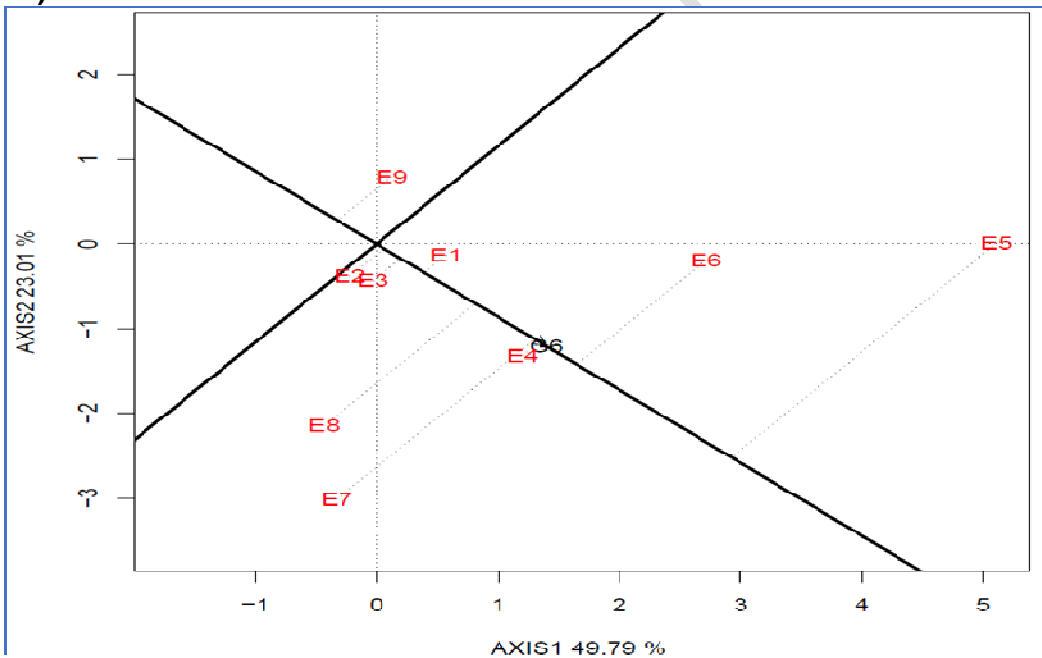## 3.6. Ranking testing environments relative to the ideal environment and genotype

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 [27]. 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 [23,26].

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.

238
239 **4a)**
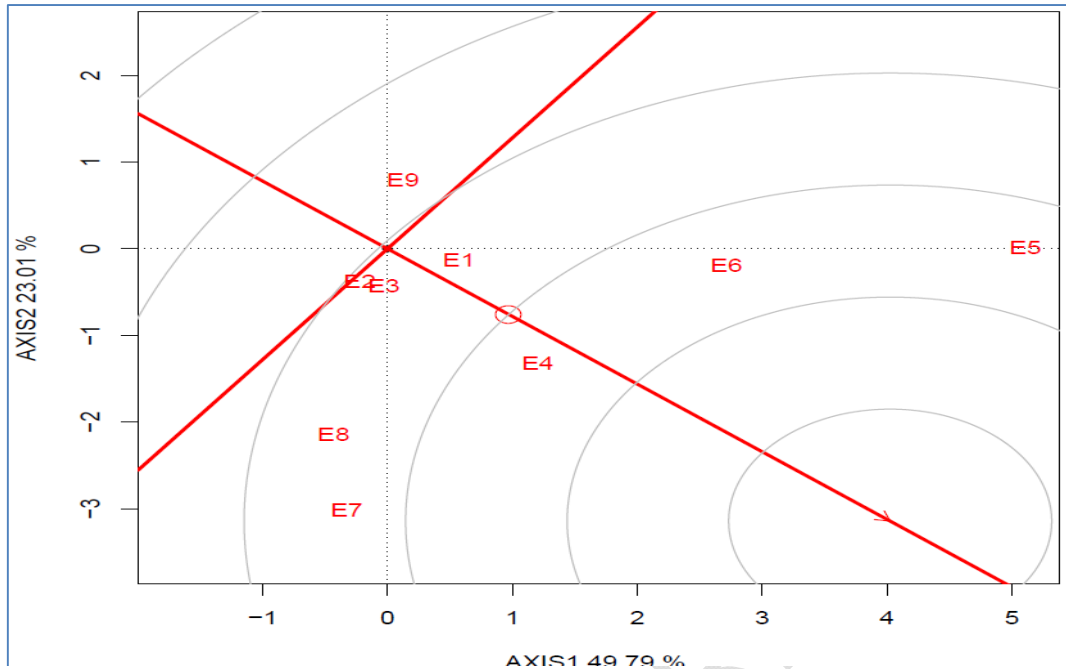
240
241 **b)**
242 **Figure 4. GGE biplot showing ranking of test environments relative to an ideal test**
243 **environment (a) and relative to the best genotypes (b)**
244
245
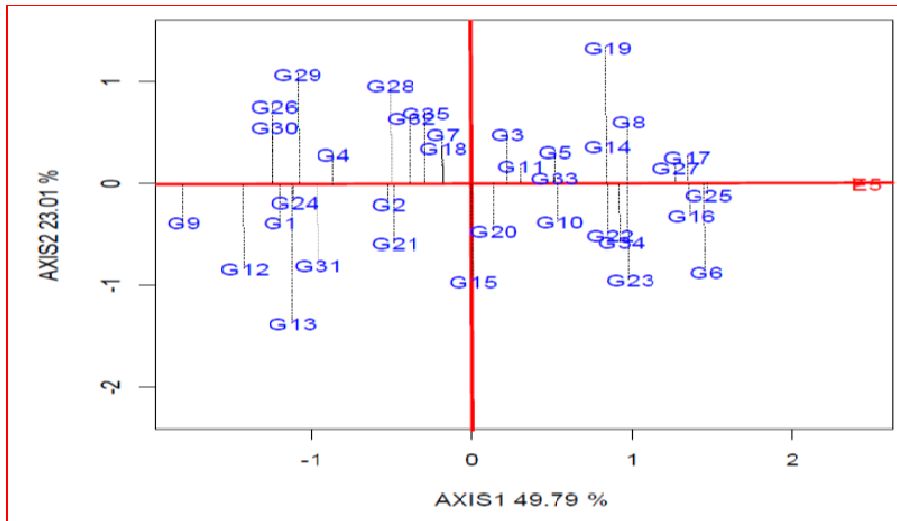246 **Ranking genotypes relative to the ideal genotype and environment**
247
248 The average environment coordination view of the GGE biplot shows the ranking of
249 genotypes based on the performance of an ideal genotypes (Fig. 5a). The relative

250 adaptation of the ideal genotype is evaluated by drawing a line passing through the biplot
251 origin and the best genotype marker. This line is called a genotype axis and is connected to
252 the best genotype [11]. Such ranking of genotypes based on performance of ideal genotype
253 revealed that G6 followed by G23, G34, G22, G16 and G25, respectively were among the
254 top yielding genotypes. Thus, G6 with the highest average yield was identified to be the ideal
255 genotype to evaluate the performance of test genotypes relative to it.
256
257 In ranking genotypes relative to the best environment, E5 was identified to be the best
258 environment to evaluate the performance of genotypes (Fig. 5b). Thus, the best environment
259 axis was drawn towards E5 and then, a perpendicular line to this axis that passes through
260 the biplot origin was also drawn to separate genotypes yielding above and below the mean
261 in the ideal environment. G6, G34, G25, G27, G16, G17, G23 and G22 which appeared on
262 the same direction with E5 were, therefore, found to perform above average in the
263 environment of E5.
264
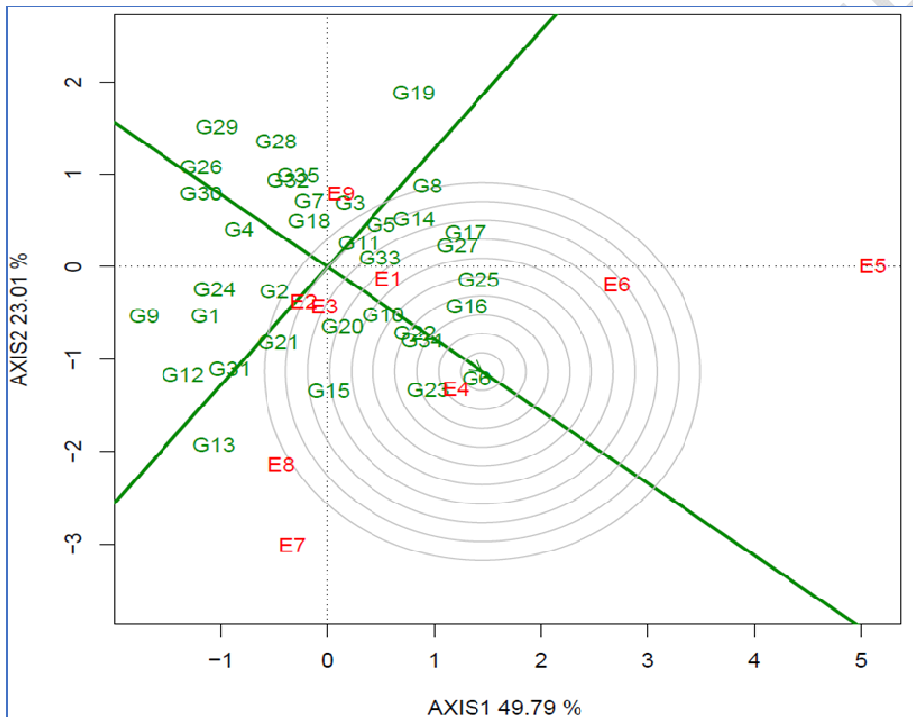
265
266 5a)
267

268
269   5b)
270   **Figure 5. Ranking genotypes relative to the ideal genotype (a) and the best**
271   **environment (b)**
272
273   **3.7. Genotypes mean yield and stability**
274

275   The average environment coordination (AEC) is a line that passes through the origin and
276   points to the higher mean yield across environments and it shows the increase in rank of
277   genotypes towards the positive end [11]. This line was reported to be useful to evaluate
278   mean grain yield and stability of genotypes [25,29,30]. According to such reports, genotypes
279   considered to be stable are those appeared closer to the origin with the shortest vector from
280   the AEC. Thus, Fig. 6 in the present study shows the mean performance and stability of the
281   genotypes. Based on this, G6, G34, G22 and G10 with the shortest vector from the AEC axis
282   were identified as the most stable genotypes while G13, G19, G12 and G9 with the longest
283   vector from AEC were the most unstable genotypes. On the other hand, G6 followed by
284   G23, G34, G16 and G25 scored higher grain yield whereas G29, G26, G30 and G28
285   attained inferior grain yield in all environments. An ideal genotype for a specific environment
286   has the highest mean yield and responds best at that particular environment while it is less
287   stable in the other environments and need to be recommended for a specific environment
288   [23,26]. According to the same authors, ideal cultivars have large PC1 scores (high mean
289   yield) and small PC2 scores (high stability) [21,26]. Thus, in the present study, G6, G25,
290   G16, G23 and G34 which had larger PC1 and smaller PC2 scores were identified to be high
291   yielding and stable.
292
293
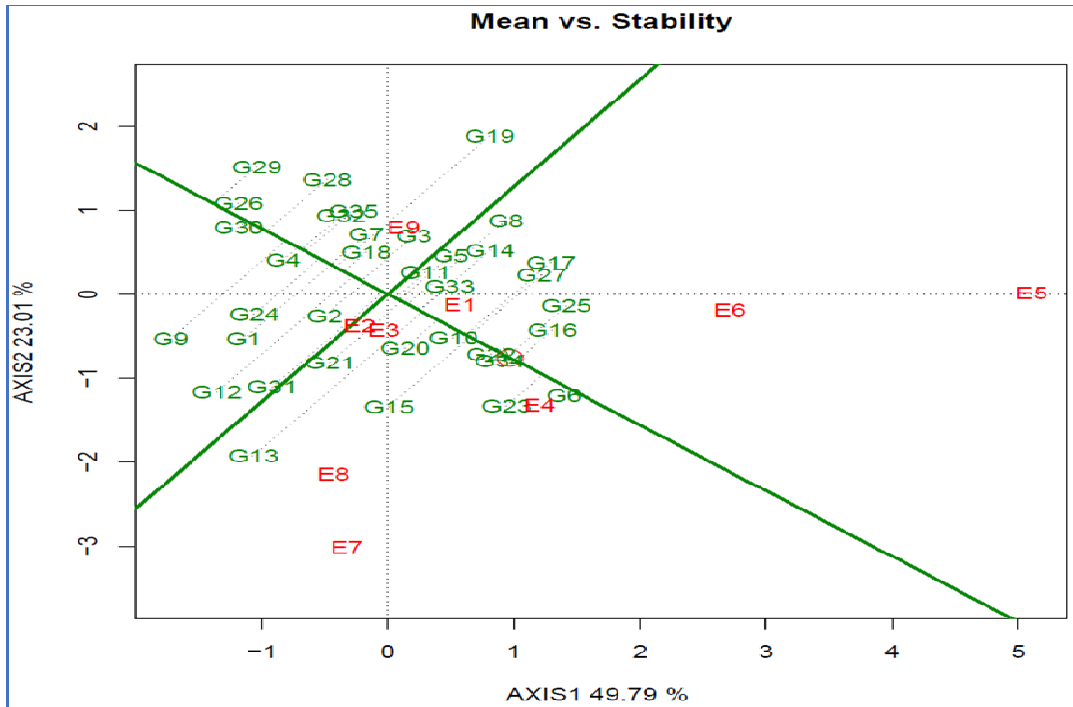
294
Figure6. Ranking based on mean performance and stability of 35 improved varieties
across nine environments (E1-E9).

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.

313
314
CONSENT (WHEREEVER APPLICABLE)
315
316
317 Not applicable.
318
319
ETHICAL APPROVAL (WHEREEVER APPLICABLE)
320
321
322 Not applicable
323
324
325
REFERENCES
326
327

328 1. Assefa K, Chanyalew S, Tadele Z. Tef, *Eragrostis tef* (Zucc.) Trotter. In: Patil JV,
329   Editor. *Millets and Sorghum: Biology and Genetic Improvement*, 1st Ed. New York:
330   Wiley & Sons; 2017.
331 2. Tolossa T, Keneni G, Sefera T, Jarso M, Bekele Y. Genotypes X Environment
332   Interaction and performance Stability for grain Yield in Field Pea (*Pisum sativum* L.)
333   Genotypes. *International J. Plant Breeding* 2013; 7(2): 116-123.
334 3. Yan W, Kang MS. GGE Biplot Analysis: A Graphical Tool for Breeders, Geneticists
335   and Agronomists. 1st Ed., Florida: CRC Press LLC; 2003.
336 4. Basford KE & Cooper M. Genotype x environment interactions and some
337   considerations for their amplifications for wheat breeding in Australia. *Australian J.
338   Agric. Res.*1998; 49: 154-174.
339 5. Kefyalew T, Tefera H, and Assefa K. Phenotypic diversity for qualitative and
340   phenologic characters in germplasms collections of tef (*Eragrostis tef*). *Genet. Resour.
341   Crop Evol.* 2000; 47: 73–80.
342 6. GrunebergWJ, ManiiqueK, Zhang D, Hermann M. Genotypexenvironment interactions
343   for a diverse of sweet potato clones evaluated across varying eco-geographic
344   conditions in Peru. *Crop Sci.* 2005; 45: 2160-2171.
345 7. Kefyalew T. Genotype x environment interaction in tef. In: Tefera H, Belay G, Sorrells
346   M (eds). *Narrowing the Rift*: Tef Research and Development. Proceedings of the
347   International Workshop on Tef Genetics and Improvement, Debre Zeit: EARO; 2001.
348 8. Ashamo A, Belay G. Genotype x Environment Interaction Analysis of Tef Grown in
349   Southern Ethiopia Using Additive Main Effects and Multiplicative Interaction Model.
350   *Journal of Biology, Agriculture and Healthcare. 2012;* 2 (1):66-73.
351 9. Oliveira RLD, Von Pinho RG, Balestre M, Ferreira DV. Evaluation of maize hybrids
352   and environmental stratification by the methods AMMI and GGE biplot. *Crop Breed
353   Appl Biot.*2010; 10:247-253.
354 10. Munawar M, Hammad G, Shahbaz. Evaluation of maize (*Zea mays* L.) hybrids under
355   different environments by GGE biplot analysis. *Am-Eurasian J Agric Environ Sci.*2013
356   ; 13 :1252-1257.
357 11. Yan W, Hunt LA, Sheng Q, Szlavnics Z. Cultivar evaluation and Mega environment
358   investigation based on the GGE biplot. *Crop Science.* 2000; 40:597-605
359 12. Gomez K A, Gomez A. *Statistical Procedures for Agricultural Research.* New York:
360   John Wiley & Sons; 1984.
361 13. SAS (2002) System Analysis Software. Version 9.0. Cary, North Carolina: SAS
362   Institute Inc; 2002.
363 14. Gauch HG. A simple protocol for AMMI analysis of yield trials. *Crop Sci.* 2013; 53:
364   1860-1869.

365   15. Payne R. A Guide to ANOVA and Design in GenStat. Hertfordshire, VSN International;
366   2015

367   16. Lule D, Fetene M, de Villiers S, Tesfaye K. Additive Main Effects and Multiplicative
368   Interactions (AMMI) and genotype by environment interaction (GGE) biplot analyses
369   aid selection of high yielding and adapted finger millet varieties. *J Appl Biosci.*2014;
370   76:6291–6303.

371   17. Pacheco A, Vargas M, Alvarado G, Rodríguez F, López M, Crossa, J et al. GEA-R
372   (Genotype x Environment Analysis with R for Windows.) Version 4.0; 2016.

373   18. Hundera F, Tefera H, Assefa K, Tefera T, Kefyalew T, Girma, T. Grain yield and
374   stability analysis in late maturing genotypes of tef [Eragrostis tef (Zucc.) Trotter]. J.
375   Genet. Breed. 2000; 54: 13-18.

376   19. Kefyalew T. Assessment of genotype environment interaction for grain yield and Yield
377   related traits in tef [*Eragrostis tef* (Zucc.) Trotter]. MSc thesis, School of Graduate
378   Studies, Alemaya University; 1999.

379   20. Lule D. Assessment of genetic diversity, genotype by environment interaction, blast
380   (M*agnaporthe oryzae*) disease resistance, and marker development for finger millet
381   germplasm from Ethiopia and introduced**. P**hD Thesis, Addis Ababa: Addis Ababa
382   University; 2015.

383   21. Crossa J. Statistical analysis of multi-location trials. *Advances in Agron.*1990; 44: 55-
384   85

385   22. Gauch HG, Zobel RW. Identifying mega-environments and targeting genotypes. *Crop
386   Sci* 1997; 37: 311-32

387   23. Yan W, Cornelius PL, Cross J, Hunt L.A. Biplot Analysis of Multi-environment Trial
388   Data. *Crop Sci.* 2001; 41:656-663.

389   24. Farshadfar E, Hassan Z, Mohammadi R. GGE Biplot analysis of genotypes x
390   environment interaction in chick pea genotypes. E*uropean J. Experimental
391   Biology*2011; 3 (1): 417-423

392   25. Yan W. Singular-value partitioning in biplot analysis of multi-environment trial data.
393   *Agron. J.* 2002; 94:990-996.

394   26. Kroonenberg PM. Introduction to Biplots for GXE Tables, Brisbane: University of
395   Queensland; 1995.

396   27. Yan W and Rajcan I. Biplot analysis of test sites and trait relations of soybean in
397   Ontario. *CropSci*2002 ; 42 :11-20.

398   28. Yan W, Tinker NA. Biplot analysis of multi- environment trial data: Principles and
399   applications. *Can J Plant Sci.* 2006; 86: 623-645

400   29. Yan W. GGE biplot: A Windows Application for Graphical Analysis of Multi
401   environment Trial Data and Other Types of Two-Way Data. Agron. J. 2001; 93:1111-
402   1118

403   30. Yan W, Hunt LA. Biplot analysis of diallel data. *Crop Sci.* 2000; 42:21–30