Agronomic performance and GGE-biplot analysis of tef genotypes evaluated in multi - environment trials in western Amhara, Ethiopia

ABSTRACT

INTRODUCTION

Tef [(Zucc) Trotter] is one of the most important staple cereal crops in Amhara region where it takes the lion's share in terms of area coverage (about 1.09 million hectares), total production (about 2.1 million tons), number of farmers involved in tef production (more than 2.7 million) and higher market price as compared to the other cereal crops (CSA 2021). It grows in diverse agro ecologies of the region. As the population in the Amhara region and in the country at large is increasing and the importance of tef as healthy and supper food being recognized globally, the demand for tef is increasing both in the country as well as abroad (Yehuala et al 2022). However, the average productivity of tef remained low (about 1.9 t ha^{-1}) as compared to the productivity of some of the major cereal crops grown in the region including maize (4.3.t ha^{-1}), wheat (2.8 t ha^{-1}) and sorghum (2.6 t ha^{-1}) (CSA 2021), which created a wider gap between the ever-increasing demand and supply (Yehuala et al 2022). The most crucial bottlenecks constraining the productivity and production of tef in Ethiopia are; (a) the small size of tef seed poses several problems during sowing, weeding and threshing (b) shattering (c) lodging (d) limited attention has been paid to mechanization, processing and storage (e) low yield potential of farmers varieties under widespread cultivation (f) biotic stresses such as diseases, weeds and insect pests (g) abiotic stresses such as drought, soil acidity and low and high temperatures (h) the culture and labor intensive nature of the tef husbandry (i) inadequate research investment to the improvement of the crop and (j) weak seed and extension systems (Belete and Admasu 2021).

Improved variety is one of the major inputs required to enhance tef productivity. Assefa et al (2011), indicated that the analysis of the genetic gain in tef breeding from the release of the first varieties in 1970 until 1995 revealed genetic gain in grain yield with average annual increment of 0.8%, which amounts to about 31.6 kg ha^{-1} yr^{-1}. A number of improved tef varieties have also been released since 1995 and hence the genetic gain in grain yield is expected to be improved (Belete 2020). So far, a total of 54 improved tef varieties have been released in Ethiopia (EAA 2021). According to Ketema (1997), tef has a great potential for improvement and, with adequate research attention, it may give more than 6 t ha^{-1}. Breeders, therefore conduct multi environment variety trials using different breeding materials to develop improved varieties that outperform previously released ones in terms of yield and other agronomic traits. However, the sensitivity of crops to environmental variations frequently results significant genotype (G) by environment (E) interaction (GEI) (Teressa et al 2021). GEI refers to the differential ranking of genotypes across environments and may complicate the selection process and recommendation of a genotype for a target environment (Teressa et al 2021). It may also reduce the selection efficiency because of measured traits are less predictable and cannot be interpreted using main effects (genotype or environment) and need more analysis (Gauch et al 2008). The large GEI variation usually impairs the accuracy of yield estimation and reduces the relationship between genotypic and phenotypic values (Teressa et al 2021).

The detection of GEI has led to the development of different statistical models to describe GEI and facilitate genotype recommendations in multi environment yield trial (MEYT) (Karimizadeh

et al 2013). These models have been classified as univariate   multivariate approaches (Karimizadeh et al 2013). Unlike that of univariate statistical approaches, multivariate statistical approaches explore multi-directional aspects of GEI and attempt to extract more information from GEI components (Gauch et al 2008). Additive Main effect and Multiplicative Interaction (AMMI) and Genotype plus Genotype by Environment interaction biplot (GGE biplot) are grouped under multivariate statistical models and they are popular for graphical display of GEI pattern of MET data (Yan 2011). However, GGE biplot is superior to the AMMI in mega-environment analysis and genotype evaluation because it explains more G+GE and the discriminating power vs. representativeness view of the GGE biplot is effective in evaluating test environments, which is not possible in AMMI analysis (Yan 2011). Accordingly, it has been proposed that GGE biplot analysis is a useful method for the analysis of GEI and yield stability and had been exploited in variety evaluation of wheat (Mekonnen et al 2017) and tef (Jifar et al 2019).

The majority of the genotypes in this field trial were recombinant inbred lines (RIL) which were believed to have desirable traits. Of these, one to two genotypes with higher grain yield and stability and having moderate lodging tolerance (tolerates up to 60%) than the previously released ones were expected to be identified and recommended. Therefore, this field trial was conducted (i) to interpreate the magnitude and causes of genotype, environment and genotype by environment interaction on yield performance of 14 tef genotypes tested across nine environments (ii) to examine the possible existence of different mega environments and (iii) to identify genotypes which are high yielding, stable and having other desirable agronomic traits for possible release.

MATERIALS AND METHODS

The Study Area
The multiplication variety trial was conducted during 2016 to 2018 main cropping seasons at Adet, Motta and Bichena. Agro ecologically Adet is classified as mid land while Mota and Bichena are classified as highland. The soil type of Adet, Mota and Bichena was nitosol, cambisol and vertisol, respectively. Descriptions of the geographical coordinates and climate of the testing locations are shown in Table 1. The location-year combinations represent nine environments (E) i.e., E-1 (Adet-2016), E-2 (Mota-2016), E-3 (Bichena-2016), E-4 (Adet-2017), E-5 (Motta-2017), E-6 (Bichena-2017), E-7 (Adet-2018), E-8 (Mota-2018) and E-9 (Bichena-2018).

Table 1: Descriptions of the testing locations

Location	Latitude	Longitude	Altitude (masl)	Total rainfall (mm) during the growing season			Mean maximum temperature (°C) during the growing season			Mean minimum temperature (°C) during the growing season		
				2016	2017	2018	2016	2017	2018	2016	2017	2018
Adet	11° 17'N	37° 43'E	2240	626	625	836	25	24	25	11	11	11
Mota	11° 5'N	37° 52'E	2487	109	926	123	23	21	23	10	10	10
Bichena	10° 27'N	38° 12'E	2541	981	350	761	22	23	23	10	10	10

Source: National meteorological agency, Bahir Dar meteorology directorate

Planting Materials and Trial Management

Fourteen tef genotypes including the standard and local checks were used in the study (Table-2). Nine of the genotypes were recombinant inbred lines (RILs) obtained from Debre Zeit Agricultural Research Center (DZARC) where the crossing was done. Single Seed Descent (SSD) selection method is a fast method being used for generation advancement and selection in tef breeding program at DZARC (Solomon et al 2021). The procedure of SSD selection method is as follows: crossing parent A with parent B→F1 (a single seed is grown to generate thousands of F2 seeds → F2-F6 (single seed promoted from previous generation is sown) →- Observation Nursery (each selected line is sown in a single row) → Pre Variety Trial (selected lines are sown in 1m x 1m plots) →National Variety Trial (selected lines are sown in 2m x2m plots → Variety Verification Trial (a candidate variety for the release sown in 10m x10m plot).

The genotypes were evaluated in a randomized complete block design (RCBD) with three replications in a plot size of 2m by 2m ($4m^2$, 10 rows of 2m length and 0.2m apart). UREA (46% N) and NPS (38% P, 19% N and 7% S) were applied at a rate of 100 kg ha^{-1} each in vertisols while 100 kg ha^{-1} NPS and 50 kg ha^{-1} UREA were applied in nitosols. All NPS was applied at planting while UREA was applied half at 15 to 18 days after planting and the remaining half at 35 to 40 days after planting. Seed at a rate of 10 kg ha^{-1} was drilled in a row. Other relevant agronomic practices such as, land preparation, and weeding, were applied. Planting was done in the 1st week of July, in the 2nd week of July and in the 4th week of July at Adet, Mota and Bichena, respectively., while harvesting was done in the 2nd week of November, in the 4th week of November and in the 4th week of December at Adet, Mota and Bichena, respectively.

Data Collection

Data on days to heading (from planting to when 50% of the plants in a plot exerted panicle), days to maturity (from planting to when 85% of the plants in a plot reached physiological maturity), grain filling period (the period from days to heading to days to maturity), plant height (measured in centimeters as the distance from the base of the plant to the tip of the longest panicle), panicle length (measured in centimeters as the distance from the base of the panicle to the tip of the longest panicle), above ground dry biomass (total sundried above-ground

biomass in a plot which included both the straw and the grain and recorded in ton ha^{-1}), grain yield (dry seed measured in ton ha^{-1}) harvest index (determined by dividing the grain yield to above ground dry biomass and expressed in percent) and lodging index (estimated using 0-5 scoring scale , 0- no lodging, 1- 20% lodging, 2- 40 % lodging, 3- 60 % lodging, 4- 80% lodging and 5- 100% lodging) were collected from the eight harvestable rows (Chanyalew et al 2021). Genotypic and phenotypic correlation coefficient analysis was made among the measured traits.

Table 2: List of tef genotypes evaluated in the study

SN	Genotype name/pedigree	Gen Code	Pedigree description
1	Acc # 212927-1	G-1	Land race collection
2	Acc # 234789-2	G-2	Land race collection
3	DZ-Cr-387*DZ-01-974(RIL No.171)	G-3	DZ-Cr-387 used asfemale parent and DZ-
4	DZ-Cr-387*DZ-01-974(RIL No.181B)	G-4	01-974 as pollen donor. The cross was
5	DZ-Cr-387*DZ-01-974(RIL No.182)	G-5	made at DZARC in 2010.Selectionwas
6	DZ-Cr-387*DZ-01-974(RIL No.126B)	G-6	done at F7 after it reached homozygous. .
7	DZ-Cr-387*DZ-01-974(RIL No.164A)	G-7	If a variety is released from this cross the
8	DZ-Cr-387*DZ-01-974(RIL No.172B)	G-8	scientific name will be DZ-Cr-440
9	DZ-Cr-387*Gealmie RIL No.129)	G-9	DZ-Cr-387 was used as female parent and Gealmie as pollen donor. The cross was made at DZARC in 2010. Selection was done at F7 after it reached homozygous. If a variety is released from this cross the scientific name will be DZ-Cr-442
10	353*Key muri (RIL 205)	G-10	353 were used as female parent and key
11	353*Key muri (RIL 29)	G-11	murri as pollen donor. The cross was made at DZARC in 2003. Selection was done at F7 after it reached homozygous. If a variety is released from this cross the scientific name will be DZ-Cr-429
12	Kora (Standard check-1)	G-12	Released variety
13	Estub (Standard check-2)	G-13	Released variety
14	Local check	G-14	

Note: Genotype source (G1-G2= EBI, G3-G11= DZARC, G12-G13 AARC), EBI= Ethiopian Biodiversity Institute; AARC= Adet Agricultural Research Center,DZARC=Debre Zeit Agricultural Research Center

Statistical Analysis
The SAS software version 9.0 was used to analyze grain yield and other measured agronomic traits separately for each environment. The local checks were employed in each individual testing location, but they were excluded from combined analysis because different local cultivars were used in each respective testing location. The data were evaluated for homogeneity of error variance using Bartlett's test and followed by combined analysis of

variance (ANOVA) as suggested by (Gomez and Gomez 1984). Mean separation and significance test was performed using Duncan's multiple range test at 5% probability level. The effects of environment (E), genotype (G), and their interactions were examined using analysis of variance package in SAS software version 9.0. The multilocation grain yield data was also graphically analyzed for interpreting GEI using GGE-biplot methodology in Genstat software 18th edition. The GGE-biplot methodology combines the biplot concept and the GGE concept (Yan 2011). This methodology uses a biplot to show the factors (G and GE) that are significant in genotype evaluation as well as the sources of variation in GE interaction analysis of MET data (Yan 2011). The graphs were generated based on (i) "which-won-where" pattern, (ii) ranking of genotypes on the basis of yield and stability, and (iii) comparison of genotypes relative to an ideal genotype, (iv) relationship among testing environments and (v) comparison of environments relative to an ideal environment.

RESULTS AND DISCUSSION

Combined Analysis of Variance of Grain Yield over Years at Each Location
The combined analysis of variance over years for each location (Table 3) revealed that the effect of genotype on grain yield was highly significant ($P<0.01$) at Adet and Mota and significant ($P<0.05$) at Bichena. This could be due to changes in genotype characteristics, varying from one genotype to another. The effect of year on grain yield was significant ($P<0.05$) at Adet and highly significant ($P<0.01$) at Mota and Bichena. Genotype by year interaction had also significant effect ($P<0.05$) on grain yield at Adet, Mota and Bichena. Though, genotype, year and their interaction affected grain yield performance, genotype took the highest explained variation (50%) at Adet indicating year variation was minimal. On the other hand, year took the lion's share of the explained variation at Mota (71%) and Bichena (98.3%). In line with the result of this study, different authors such as (Fana et al 2018; Wordofa et al 2019; Seyed et al 2022) reported as the grain yield of barley, wheat and maize, respectively was affected by the environment in their MEYTs. Karimizadeh et al (2013), noted that when the effect of the unpredictable component of the environment (year) is high, plant breeder needs to develop stable genotypes that can perform reasonably well under a range of environmental conditions.

Table 3: Combined analysis of variance of grain yield (t ha^{-1}) over years at each location

Source of variation	DF	Adet			Mota			Bichena		
		Sum of squares	Mean squares	Explained Variation (%)	Sum of squares	Mean squares	Explained Variation (%)	Sum of squares	Mean squares	Explained Variation (%)
Total	125	19.3			9.41			83.3		
Gen(G)	13	6.5	0.50**	50	3.06	0.23**	22.4	1.92	0.14*	0.5
Year(Y)	2	0.7	0.35*	35	1.48	0.74**	71.8	58.0	29.0**	98.3
G*Y	26	4.1	0.15*	15	1.56	0.06*	5.8	8.85	0.34*	1.2
Error	84	7.8	0.09		3.30	0.03		14.4	0.17	

Note: ***, **** refer to significant at $p<0.05$ and $P<0.01$ probability level, respectively

Grain Yield Performance of Tef Genotypes Across Environments

The grain yield performance of the tested genotypes in each environment is indicated in Table 4. The analysis of variance for grain yield in each environment showed significant to highly significant difference among the tested genotypes. Both the highest and the lowest mean environment grain yield 3.3 t ha^{-1} and 1.8t ha^{-1}, respectively was recorded at Bichena. The lowest mean environment grain yield was believed to be resulted from the low total rain fall received during 2017 growing season at Bichena (Table 1). Different authors have emphasized the negative impact of moisture stress on tef productivity at different growth stages. Mengiste et al (2013), reported 1 t ha^{-1} grain yield reduction due to 25% soil moisture deficit at mid growth stage of the crop. Similarly, 25.5% and 51% grain yield reduction was reported to be caused by moisture stress during pre-and post-anthesis period, respectively (Shiferaw et al 2012). Among the tested genotypes, G-11 gave the highest mean grain yield (2.8 t ha^{-1}) across environments. Accordingly, it was promoted as a candidate variety into variety verification trial and verified with the standard (Abay) and local checks both on station and on farm. It gave an average grain yield of 2.6 t ha^{-1} and showed about 16 % yield advantage over the standard check.

Kaya et al (2006), noted that it is very common for MEYTs data to include a mixture of crossover and non-crossover types of GEI. Accordingly, in this study different genotypes produced the highest grain yield in different environments. Genotypes G3, G8 and G9 gave the highest grain yield in environments E6 (Bichena-2017), E5 (Mota -2017) and E7 (Adet-2018), respectively (Table 4). These differential rankings of genotypes across test environments revealed that there exists possible crossover GEI (Kaya et al 2006). However, crossover GEI is not always the case. Genotype G11 was the highest yielding in environments E1 (Adet-2016), E2 (Mota-2016), E3 (Bichena-2016), E4 (Adet-2017) and E8 (Mota-2018). These results in differential change of yield mean but not of ranking of genotype showed that GEI may also have a non-crossover nature (Liker et al 2009). The result of this study is in agreement with (Kaya et al 2006; Lker et al 2009) who reported a mixture of crossover and non-crossover types of GEI on wheat and maize MEYTs, respectively.

Table 4: Grain yield (t ha ^{1}) performance of 14 tef genotypes evaluated in each environment, during 2016 to 2018 main cropping seasons.

Code	E-1	E-2	E-3	E-4	E-5	E-6	E-7	E-8	E-9	Mean
G-1	1.7^d	2.3^{b-e}	3.4^{bc}	1.4^d	2.0^f	1.2^f	1.9^{bcd}	2.5^d	2.2^{abc}	2.1
G-2	1.8^{cd}	2.5^{a-d}	3.2^{bc}	1.4^d	2.3^{cde}	1.7^{cde}	1.8^{cd}	2.6^{bcd}	1.9^{bcd}	2.1
G-3	2.0^{bcd}	2.8^a	2.8^d	2.1^{abc}	2.5^{a-e}	2.5^a	2.1^{abc}	2.8^{ab}	1.9^{bcd}	2.4
G-4	2.6^{ab}	2.4^{a-e}	3.2^{bc}	2.3^{ab}	2.7^{a-d}	2.2^{ab}	1.8^{cd}	2.7^{a-d}	2.0^{bcd}	2.4
G-5	1.8^{cd}	2.5^{ab}	3.3^{bc}	1.9^{bc}	2.5^{a-e}	1.6^{def}	1.9^{bcd}	2.6^{bcd}	2.0^{bcd}	2.2
G-6	2.2^{a-d}	2.6^{ab}	3.7^{bc}	2.2^{abc}	2.5^{a-e}	2.0^{bc}	1.9^{bcd}	2.6^{bcd}	1.8^d	2.4
G-7	2.0^{bcd}	2.4^{a-e}	3.3^{bc}	2.2^{abc}	2.7^{ab}	1.8^{bcd}	1.8^{cd}	2.8^{abc}	1.8^d	2.3
G-8	2.2^{a-d}	2.5^{a-d}	2.9^{bc}	2.3^{abc}	2.8^a	2.2^{ab}	2.1^{ab}	2.9^{ab}	1.9^{cd}	2.4
G-9	2.2^{a-d}	2.1^e	3.2^{bc}	2.0^{abc}	2.2^{ef}	2.1^{abc}	2.3^a	2.5^{cd}	2.1^{a-d}	2.3
G-10	1.9^{bcd}	2.1^{de}	3.2^{bc}	2.0^{abc}	2.4^{b-e}	1.3^{ef}	2.2^{ab}	2.7^{a-d}	1.9^{bcd}	2.2

Gen	E-1	E-2	E-3	E-4	E-5	E-6	E-7	E-8	E-9	Mean
G-11	3.1[a]	2.9[a]	4.2[a]	2.6[a]	2.7[abc]	2.2[bcd]	2.2[bcd]	3.2[a]	2.2[bcd]	2.8
G-12	2.4[a-d]	2.4[a-e]	3.5[bc]	2.2[abc]	2.7[abc]	1.9[bcd]	1.9[bcd]	2.5[cd]	2.0[bcd]	2.4
G-13	2.4[abc]	2.6[a]	3.7[bc]	1.9[c]	2.3[de]	1.2[f]	2.1[abc]	2.9[a]	2.2[ab]	2.4
G-14	1.7[d]	2.2[cde]	3.4[bc]	1.3[d]	2.3[ef]	1.8[bcd]	1.7[d]	2.5[d]	2.4[a]	2.1
Mean	2.1	2.4	3.3	2.0	2.5	1.8	2.0	2.7	2.1	2.3
CV(%)	19.2	8.8	18.7	12.3	7.9	14.2	10.3	6.2	9.7	
Gen	*	*	*	**	**	**	*	*	*	

Note: Gen=Genotype, E-1 =Adet-2016, **E-2=** Mota-2016, **E-3**=Bichena-2016, **E-4**=Adet-2017, **E-5**=Motta- 2017, **E-6=** Bichena-2017, **E-7** =Adet-2018, **E-8=** Mota-2018, **E-9=** Bichena-2018. *, ** refers to significant at 5% and 1% level of probability, respectively

Agronomic Performances

The combined analysis of variance for the other measured agronomic parameters showed highly significant (P<0.01) difference among the tested genotypes (Table 5). Wide performance variation was observed among the tested genotypes for all measured agronomic traits including days to heading (53-61), days to maturity (103 to 116), grain filling period (46-55) plant height (91 to 115 cm), panicle length (35 to 42 cm), dry shoot biomass (7.3 to 9.7 t ha^{-1}), harvest index (27 % to 33%), grain yield (2.2 to 2.8 t ha^{-1} with the grand mean of 2.4 t ha^{-1}) and lodging index (1-5) (Table 5). The highest grain yield was obtained from G-11 which showed a grain advantage of about 18.1 % over the standard checks. The least grain yield was obtained from G-1. The variations observed among the tested genotypes for the measured traits indicating the availability of wide genetic diversity in tef germplasm which is a good opportunity for breeders to develop improved varieties with high grain yield and other desirable agronomic traits through either direct selection or intra-specific hybridization. Previous studies have identified tef genotypes with a wide range of variation for phenological, morphological, physiological, and agronomic features, as well as climate adaptation and farmer preferences (Assefa et al 2015; Bezabih et al 2020; Bezabih et al 2022).

Combined Analysis of Variance for Grain Yield (t ha $^{-1}$) Across Environments

Combined analysis of variance for grain yield of the 13 tef genotypes across nine environments revealed highly significant (P < 0.01) variations due to genotype (G), environment (E) and GEI (Table 6). The significant difference among tef genotypes and the environments suggesting the existence of considerable variation in grain yield performance due to genotype by environment interaction effect. Jifar et al (2019), also reported the existence of significant variation among tef genotypes and environments in a MEYT. Grain yield is a polygenic attribute and is highly affected by both genotypic and environmental factors (Worede et al 2020); therefore, evaluation of genotype by environmental interaction has great significance in plant breeding. The significant GEI effects for grain yield demonstrated that genotypes responded differently to the variation in environmental conditions. This also shows the difficulties in selecting new genotypes for wider production. The factors explained (%) show that grain yield was affected by genotype (8.84%), environment (74.26 %), and their interaction (16.90 %) (Table 3). The result of the present study was in agreement with the findings of (Worede et al 2020) who reported that, in multi environment yield trials (METs), E takes the lion's share of the total variation, while the share of G and GE is very minimal. However, it is G and GE that are relevant to cultivar

evaluation. The significant G*E interaction in the present study indicates unstable performance of the tef genotypes across the testing environments (Table 4).

Table 5: Combined mean performance of thirteen tef genotypes for measured parameters as evaluated at nine environments.

No.	Gen. code	Days to heading	Days to maturity	Grain filling period	Plant height (cm)	Panicle length (cm)	Dry shoot biomass (t ha^{-1})	Grain yield (t ha^{-1})	Harvest index (%)	Lodging Index (0-5)
1	G-1	54.7^g	105.5^e	50.8^{bc}	91.1^f	36.1^d	7.5^{cd}	2.07^e	31.5^{a-c}	5
2	G-2	53.6^h	108.1^d	54.5^a	93.3^{ef}	35.5^{de}	7.3^d	2.13^{de}	33.0^a	5
3	G-3	58.8^d	109.7^c	50.9^c	114.7^a	42.2^a	9.1^{ab}	2.38^{b-d}	28.6^{ef}	3
4	G-4	60.8^a	110.4^{bc}	49.6^{ef}	112.3^{ab}	41.1^{ab}	8.7^b	2.43^{bc}	30.0^{b-d}	2
5	G-5	61.0^a	111.0^{ab}	49.9^{de}	112.0^{ab}	40.6^b	8.7^b	2.23^e	28.9^{d-f}	2
6	G-6	60.7^a	110.6^{a-c}	49.8^{de}	112.7^{ab}	41.5^{ab}	9.7^a	2.38^{bc}	27.5^f	2
7	G-7	59.7^b	110.8^{ab}	51.0^c	112.9^a	41.0^{ab}	9.2^{ab}	2.31^{b-e}	27.1^f	5
8	G-8	59.9^b	109.7^c	49.8^{de}	112.6^{ab}	40.9^{ab}	9.2^{ab}	2.42^{b-d}	28.7^{ef}	5
9	G-9	56.5^f	102.7^f	46.2^g	96.2^{de}	36.2^d	7.9^c	2.30^{b-e}	32.2^{ab}	2
10	G-10	57.4^e	106.4^e	49.0^{ef}	99.0^d	34.7^e	7.8^{cd}	2.18^e	30.8^{b-d}	1
11	G-11	59.4^c	111.1^{ab}	51.6^c	109.8^{bc}	40.5^b	9.5a	2.80^a	32.2^{ab}	1
12	G-12	60.0^b	108.6^d	48.6^f	112.4^{ab}	38.8^c	8.7^b	2.38^{bc}	29.9^{b-d}	2
13	G-13	58.4^d	111.5^a	53.1^b	108.8^c	40.5^b	8.7^b	2.36^b	30.9^{bc}	2
	Mean	58.5	108.9	50.4	106.7	39.2	8.7	2.33	30.1	3
	CV(%)	1.6	1.7	3.7	5.2	6.6	13.5	13.2	11.8	
	Gen (G)	**	**	**	**	**	**	**	**	
	Env (E)	**	**	**	**	**	**	**	**	
	G*E	**	**	**	Ns	*	*	**	Ns	

Note: *, ** significant at 5% and 1% level of probability, respectively, NS= not significant

Table 6: Combined analysis of variance for grain yield (t ha^{-1}) of thirteen tef genotypes across nine environments

Source of variation	Degree of freedom	Sum of squares	Mean squares	Explained variation (%)
Total	350	117.01		
Genotype(G)	12	8.14	0.67**	8.84
Environment(E)	8	68.41	8.55**	74.26
G*E	96	15.57	0.16**	16.90
Error	234	24.89		

** Significant at P<0.01 probability level

Correlation Coefficient of Grain Yield with Other Traits

Grain yield being a complex trait, its inheritance is influenced by many genes which are linked to various traits (Assefa et al 2011). Knowledge of correlations among important traits may

facilitate selection of desired traits directly or indirectly based on the nature of the correlation. The practical utility of selecting for a given trait as a means of improving another depends on the extent to which they are correlated to the major trait under consideration (Assefa et al 2011).

The phenotypic and genotypic correlations of the different measured traits in this study are presented in Table 7. Grain yield showed highly significant (P < 0.01) and positive genotypic correlations with shoot biomass (r = 0.69), harvest index (r = 0.30) and panicle length (r= 0.55), while it was not significantly associated with the remaining traits. The highly significant and positive association between grain yield and that of shoot biomass, harvest index and panicle length indicate the possibility of improving grain yield by improving any one of these traits. The findings of the present study are in agreement with the previous study reported by (Nigus et al 2016). Grain yield also showed highly significant (P < 0.01) and positive phenotypic correlation with days to heading (r=0.13), days to maturity (r=0.26), grain filling period (r=0.29), plant height (r-0.16), panicle length (r=0.17) and shoot biomass (r-0.38). Similar results were reported by (Bogale 2019). Correlation between traits used to determine whether selection for one trait will have an effect on another. Positive and significant correlation between traits can be the result of strong coupling linkage between their genes or the characters may be the result of pleiotropic genes that control these characters in the same direction (Aklilu et al 2020).

Table 7: Phenotypic (above diagonal) and genotypic (below diagonal) correlation coefficient for 8 quantitative traits of 13 tef genotypes

Variable	DTH	DTM	GFP	PH	PL	SBM	GY	HI
DTH	1	0.82***	0.55***	-0.14***	-0.15**	-0.25***	0.13*	0.38***
DTM	0.66*	1	0.93***	-0.34***	-0.27***	-0.35***	0.26***	0.53***
GFP	-0.30ns	0.51ns	1	-0.41***	-0.29***	-0.35***	0.29***	0.53***
PH	0.92***	0.79**	-0.06ns	1	0.87***	0.73***	0.16**	-0.61***
PL	0.81***	0.81***	0.10ns	0.92***	1	0.61***	0.17**	-0.47***
SBM	0.84***	0.71**	-0.06ns	0.90***	0.89***	1	0.38***	-0.73***
GY	0.46ns	0.51ns	0.12ns	0.51ns	0.55*	0.69**	1	0.30***
HI	-0.72**	-0.51ns	0.18ns	-0.75**	-0.69**	-0.68*	0.05ns	1

Note: DTH-Days to heading, DTM- Days to maturity, GFP-Grain filling period, PH- Plant height, PL-Panicle length, SBM-Shoot biomass, GY-Grain yield, HI- Harvest index

GGE-biplot Analysis
GGE biplot is visualized on the basis of results explained for the first two principal components (Yan and Tinker 2006). In the present study, the first principal component axis (PC1) explained 58.64 % of total variation while PC2 explained 35.10%. Thus, the two axes together accounted for 93.74 % of the GGE variation for grain yield (Figure 1, 2, 3, 4, 5). In this study grain yield data of the location instead of the environment was used for GGE-biplot analysis to make meaningful recommendations. Similarly, different authors have also done GGE biplot analysis using location yield data in different crops including, bread wheat (Worku et al 2013), lentil (Karimizadeh et al 2013) and chieck pea (Farshadfar et al. 2011). The GGE biplot results are presented in five sections. The first section presents the results of "which won-where", the

second section deals with the mean performance and stability of genotypes, the third one presents ranking of genotypes relative to the ideal genotype, the fourth section shows about the relationship among the testing locations and the fifth one focus on ranking of testing locations relative to the ideal location.

Which-won-Where Pattern Analysis and Mega Environment Identification

In the "which-won-where" concept of GGE-biplot, genotype markers farthest from the biplot origin are connected with straight lines to form a polygon such that markers of all other genotypes are contained in the polygon. To each side of the polygon, a perpendicular line, starting from the origin of the biplot is drawn and extended beyond the polygon so that the biplot is divided into several sectors. The markers of test environments are separated into different sectors and the genotype at the vertex for each sector is the winner genotype at environments included in that sector (Yan 2011).

Figure 1 presents "which -won- where" GGE biplot view of tef genotypes MET data. In this biplot, three sectors are formed. G-11, G-1and G-3 were the vertex genotypes indicating that they are the best or the poorest genotypes in some or all of the environments; for they were farthest from the origin of the biplot (Yan and Kang 2003). All of the three testing locations (Adet, Mota and Bichena) fall in one sector and made one mega environment while the 13 genotypes were divided into three genotypic groups (Figure 1). G-11 was the vertex genotype in the first sector where all of the testing locations fall indicting as it was the highest yielder. G-1 and G-3 were the vertex genotypes in the second and third sectors, respectively. However, no testing location fell meaning these vertex genotypes were not the winner in any of the environments; rather, they were likely to be the poorest genotype in some or all of the environments (Figure 1).
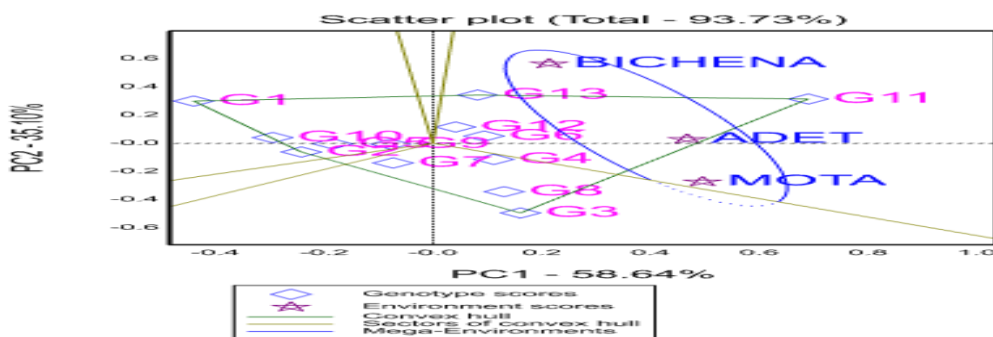

Figure 1. Polygon views of the GGE-biplot based on symmetrical scaling for which-won where pattern analysis for genotypes and environments

Mean Yield and Stability Performance of Genotypes

Ranking of thirteen tef genotypes based on mean yield performance and stability is presented in Figure 2. The single arrow line passing through the biplot origin, and the average environment indicated by the small circle is the average environments coordinate (AEC) axis, which is defined by the average PC1 and PC2 scores of all environments (Yan and Kang 2003).

This line points towards higher mean yield across environments. Hence, in the present biplot, G-11 gave the highest mean yield followed by G-4, G-8, G-3, G-6, G-13, and G-12. The mean grain yield of the remaining genotypes was below the grand mean (Figure 2).

The line which passes through the biplot origin and perpendicular to the AEC axis shows measure of stability. Either direction away from the biplot origin, on this axis, indicates greater GEI and poor stability or vice versa (Kaya et al. 2006). Thus, in terms of stability the genotypes ranked as G-5>G-9>G-10>G-6>G-2>G-12>G-7>G-4>G-11>G-13>G-1>G-8>G-3 (Figure 2). In this study most of the genotypes which showed better stability had lower mean grain yield. Fisha (2020) noted that stability has lower heritability than mean performance. Hence, it is useful only when it is considered jointly with mean performance. Yan and Tinker (2006) also noted that stability refers to the relative performance of a genotype and it is meaningful only when it is associated with mean performance.

Ranking of Genotypes Relative to an Ideal Genotype
An ideal genotype is regarded as a genotype that has the highest mean performance with absolute stability (Karimizadehi et al 2013). 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 (Karimizadehi et al 2013). Thus, using the ideal genotype as the center, concentric circles were drawn to visualize the distance between each genotype and the ideal genotype. A genotype is more favorable if it is closer to the ideal genotype. Accordingly, G-11 followed by G-13 and G-6 were closer to the ideal genotype and therefore, they are most desirable than the other tested genotypes. On the other hand, the lower yielding genotypes including G-1, G-2, G-5, G-7, G-9 and G-10 were undesirable because they are located far from the ideal genotype (Figure 3). The relative contributions of stability and grain yield to the identification of desirable genotype found in this study by the ideal genotype procedure of the GGE biplot were similar to those found in other crop stability studies (Worku et al. 2013; Karimizadeh et al 2013; Jifar et al,2019).
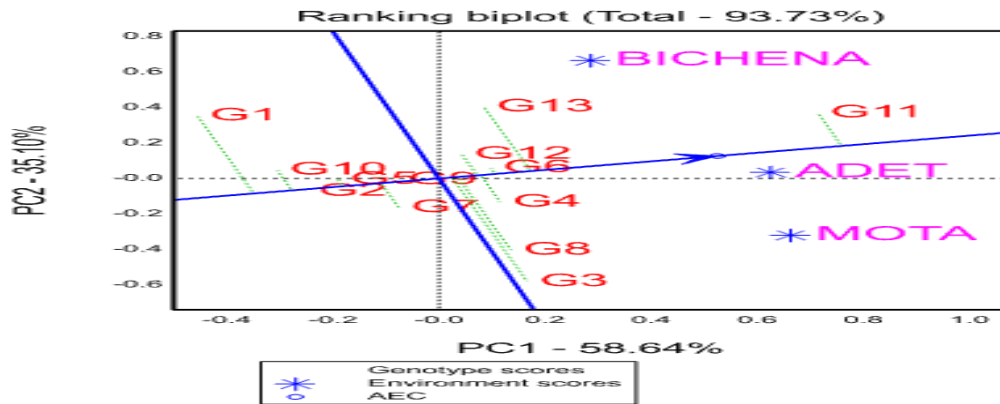
Figure 2. GGE-biplot based on environment-focused scaling for the mean performance and stability of genotypes

Relationships Among Testing Locations

Figure 4 provides a summary of interrelationships among the test locations. The location vectors are lines that connect the biplot origin and the markers of test locations and the cosine of the angle between them is related to the correlation coefficient (Yan and Kang 2003).
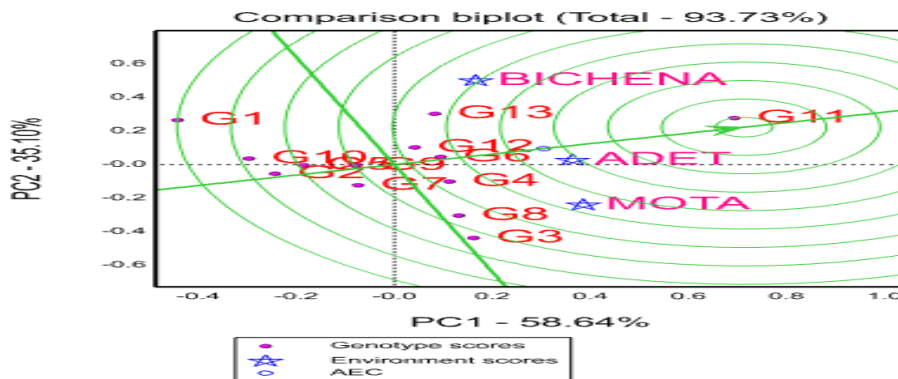

Figure 3. Ranking of genotypes relative to an ideal genotype

Based on Figure 4, the angle between Adet and Mota, Adet and Bichena and Mota and Bichena was an acute angle, indicating that all of the locations are positively correlated. Yan and Tinker (2006), noted that the presence of close associations among test environments suggests that the same information about the genotypes could be obtained from fewer test environments, and hence the potential to reduce testing cost. The purpose of test environment evaluation is to identify test environments that can be used to effectively select superior genotypes for a mega environment. An ideal test environment should be both discriminating of the genotypes (providing information about the genotypes) and representative of the target environment (Yan

and Tinker 2006). If a test environment lacks discriminating ability and not representative of the target environment, it is not only useless but also misleading since it may provide biased information about the tested cultivars. The length of the environment vectors is proportional to their standard deviation which is a measure of the discriminating ability of the environments (Yan and Tinker 2006). Therefore, the present study showed that Mota had better discriminate ability than Bichena and Adet (Figure. 4).
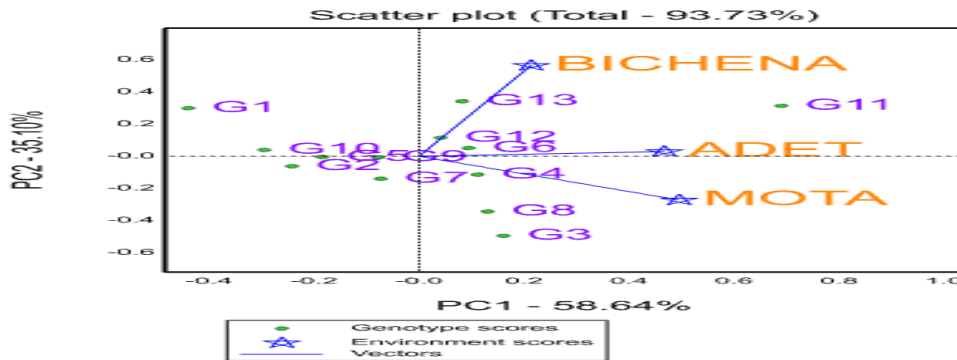

Figure 4. GGE biplot view showing the relationships among the testing locations.

Ranking Testing Locations Relative to the Ideal Location
An ideal environment is a point on the average environment axis (AEA) in the positive direction of the biplot origin and is equal to the longest vector of all environments (Yan and Tinker 2006). It is represented by an arrow pointing to it (Figure 5). Although such an ideal environment may not exist in reality, it can be used as a reference for genotype selection in the MEYTs. An environment is more desirable if it is located closer to the ideal environment. Thus, using the ideal environment as the center, concentric circles were drawn to help visualize the distance between each environment and the ideal environment (Yan and Tinker 2006). The ideal location, represented by the small circle with an arrow pointing to it, is the most discriminating of genotypes and yet representativeness of the other tests locations. Therefore, among the testing locations, Adet was very close to the ideal environment followed by Mota, whereas Bichena was plotted far away from the ideal environment and thus undesirable test location. Yan (2011), noted that there are three types of test environments based on test environment evaluation: the first one is test environments with high discriminating power and representativeness which are ideal for selecting superior genotypes; the second type is test environments with high discriminating power but not representative which cannot be used in selecting superior genotypes but useful in culling unstable genotypes; the third type is test environments with poor discriminating power and not representative of the target environment and provide little or no information about the genotypic differences and should not be used as test environments. However, the testing locations in this study were different from each other in most geographical properties such as longitude, latitude, altitude and other agro climatic factors including rainfall, temperature and soil type (Table 1), the multi environment trials shall be performed on all of them.
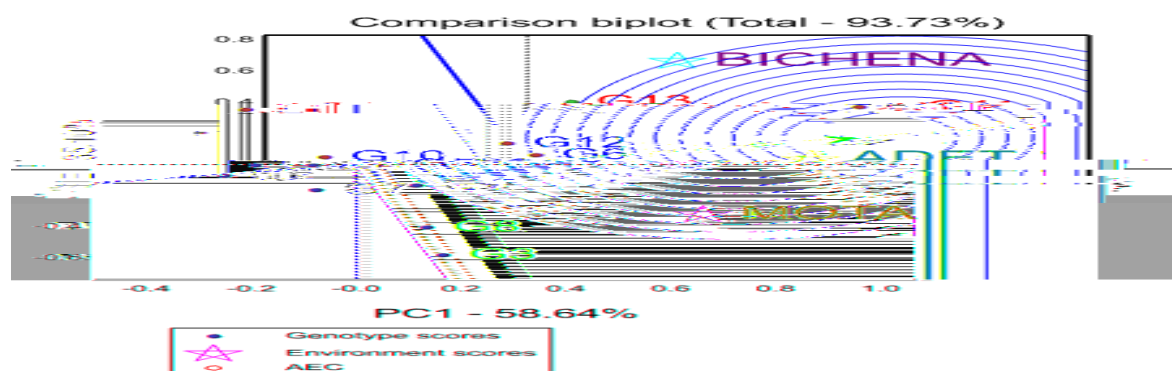
Figure 5. GGE biplot of ideal location and comparison of the locations with the ideal location

CONCLUSION AND RECOMMENDATION

Statistically significant variations were detected among the tested genotypes in grain yield and yield related traits. The grain yield performance of the tested genotypes was influenced by environment, GEI and genotype effects. The GGE biplot analysis revealed the existence of one mega environment, an ideal location, an ideal genotype and three tef genotypic groups in terms of stability (high, moderate and low). Among the testing locations, Adet was found both discriminating and representative. G-11 (353*Keymuri (RIL29) was found high yielding, stable and moderately tolerant to lodging. as compared to the other tested genotypes, and it showed about 18% yield advantage over the standard check. It is also white seeded that can fetch high market price. Considering the results of GGE-biplot analysis for grain yield, combined analysis for other measured agronomic parameters and its desirable traits, G-11 was advanced to variety verification trial. The National Variety Release Committee evaluated the performance of G11   the standard and local checks for grain yield and yield-related traits and officially approved for full release with a local name "   " for major tef producing areas of western Amhara region and similar areas in the country. This variety is believed to play a significant role in improving tef production and productivity in the region and in the country at large. Finally, to strengthen the tef breeding research program in the region, activities on tef crossing and mega environment determination are recommended to come in the front line of tef breeding strategy.

REFERENCES

Aklilu E, Degene T and Worede F (2020). Genotypic and phenotypic correlation and path coefficient analysis for yield and yield related traits in barley (Hordeum vulgare L.) landraces in north Gondar, Ethiopia. Indian Journal of applied Biosciences 8(3), 24-36.

Assefa K, Gina C,Girma D, Rizqah K, Chanyalew S and Tadele Z (2015**).** Genetic diversit in tef [(Zucc.)Trotter]. Front. Plant Sci. 6, 177. doi: 10.3389/fpls.2015.00177.

Assefa K, Yu J K, Zaid M, Belay G, Tefera H and Sorrellis E S (2011). Breeding tef [Eragrostis tef (Zucc.) trotter]: conventional and molecular approaches Plant Breeding 130, 1-9.

Belete T and Admasu S (2021). Evaluation of released tef [Eragrostis tef (Zucc.) Trotter] varieties

for the adaptability and stability using univariate stability parameters. Journal of Genetic and Environmental Resources Conservation 9(1),13-23

Belete T (.2020). Tef (Eragrostis tef (Zucc.) Trotter) breeding, achievements, challenges and opportunities in Ethiopia; incase Southwestern Ethiopia: Review. International Journal of Current Research and Academic Review 8(8), 2347-3215.

Bogale A (2019). Genetic variability, heritability and genetic advance of some varieties of tef (Eragrostis Tef (Zucc.) Trotter) in north west Ethiopia. International Journal of Research Studies in Agricultural Sciences 5(1), 27-37.

Bezabih A, Abate E, Carlo F, Mario E and Matteo D A (2022). Value of teff (Eragrostis tef) genetic resources to support breeding for conventional and smallholder farming: a review. CABI Agriculture and Bioscience,3:27 https://doi.org/10.1186/s43170-022-00076-9

Bezabih A, Caterina A, Abate E, Gebrehawaryat Y, Cado F, Mario E and Matteo D A (2020). Current and projected eco-geographic adaptation and phenotypic diversity of Ethiopian. teff ( ) across its cultivation range. Agriculture, Ecosystem and Environment, vol. 200, https://doi.org/10.1016/j.agee.2020.107020

Chanyalew S, Kebede W, Fikre T, Genet Y, Jifar H, Demssie M, Tolossa K, Tadesse M, Tadele Z And Assefa K (2021). Tef Breeding Manual. Ethiopian Institute of Agricultural Research, Debre Zeit Agricultural Research Center, National Tef Research Program, Debre Zeit, Ethiopia.

CSA, Central Statistical Agency (2021). Report on area and production of major crops of private peasant holdings in 2020/21 meher season. Statistical bulletin 590. CSA, Addis Abeba, Ethiopia.

EAA, Ethiopian Agriculture Authority (2021). Plant variety release, protection and quality control directorate. Crop variety register, issue no. 24, Addis Ababa, Ethiopia.

Fana G, Tadesse D, Sebsibe H and Verma R P S (2018). Multi environment trial analysis of food barley in Ethiopia using AMMI and GGE biplot methods. Journal of Plant Breeding and Genetics 6(3), 75-85.

Farshadfar E, Hassan Z and Reza M (2011). Evaluation of phenotypic stability in chickpea genotypes using GGE-Biplot. Annals of Biological Research 2 (6), 282-292.

Gauch H G, Piepho H P and Annicchiarico P (2008). Statistical analysis of yield trials by AMMI and GGE: Further considerations. Crop Sci 48, 866-889.

Gomez K A and Gomez A A (1984). Statistical procedures for agricultural research. 2nd edition. John Willey and Sons

Janos N (2022). Stability on maize hybrids based on GGE biplot graphical technique. Agronomy 12, 394. https://doi.org/10.3390/agronomy12020394

Jifar H, Assefa K, Tesfaye K, Dagne K and Tadele Z (2019). Genotype-by-environment interaction and stability analysis in grain yield of improved tef ( ) varieties evaluated in Ethiopia.Journal of Experimental Agriculture International 35(5), 1-13.

Karimizadehi R, Mohtasham M N, Sabaghn A A, Mahmood B and Roustami F (2013). GGE Biplot analysis of yield stability in multi environment trials of lentil genotypes under rainfed condition. Not Sci Biol 5 (2), 256-262.

Kaya, Y, Akcura M and Taner S (2006). GGE-biplot analysis of multi environment yield trials in bread wheat. Turky Journal of Agriculture 30:325-337.

Ketema S (1997). Tef ((Zucc)Trotter). Promoting the conservation and use of under

utilised and neglected crops. 12. The Institute of Plant Genetics and Crop Plant Research.Gatersleben/International Plant Genetic Resources Institute). Rome, Italy

Lker E, Fatma A, Tonk Ö and Muzaffer T (2009). Assessment of Genotype x Environment Interactions for Grain Yield in Maize Hybrids Using AMMI and GGEbiplot Analysis. Turkish Journal of Field Crop 14(2), 123 – 135.

Mekonnen A, Gebrehawaryat Y and Gashaw A (2017). Performance of bread wheat (Triticumaestivul L.) enotypes under moisture deficit conditions. In: AlemayehuAssefa, Baye Berihun, Ermias Abate and MulugetaAlemayehu (eds.). Proceedings of the 8[th]Annual Regional Conference on Completed Crop Research Activities, 13-20, February. 2014, Amhara Regional Agricultural Research Institute, Bahir Dar, Ethiopia.

Mengiste Y, Mahari A, Schultz B and Erkoss T (2013). Crop water productivity of irrigated teff in a water stressed region. Water Resource. Management 7, 3115-3125.

Nigus C, Mohammed W and Damte T (2016). Genetic Variation, Correlation and Path Coefficient Analysis in Tef [Eragrostis Tef (Zucc.) Trotter] Genotypes for Yield, Yield Related Traits at Maysiye, Northern Ethiopia. American Journal of Research Communication 4(11), 73-102.

Seyed H S , Khodadad M , Mohammad R B , Ali O , Seyed M, Nasir M, , Árpád I , Csaba B and J N (2022). Stability on maize hybrids based on GGE biplot graphical technique. Agronomy 12, 394. https://doi.org/10.3390/agronomy12020394

Shiferaw W, Balcha A and Mohammed H (2012). Genetic variation for grain yield and yield related traits in tef [(Zucc.)Trotter] under moisture stress and non-stress environments . American Journal of Plant Sciences 3, 1041-1046

Teressa T, Semahagne Z and Bejiga T (2021). Multi environments and genetic environmental interaction (GxE) in plant breeding and its challenges: a review article. International Journal of Research Studies in Agricultural Sciences 7(4), 11-18

WardOfa G, Asnake D and Mohammed H (2019). GGE biplot analysis of genotype by environment interaction and grain yield stability of bread wheat genotypes in central Ethiopia. Journal of Plant Breeding and Genetics 7(2), 75-85.

Worede F (2020). Genotype-environment interaction and stability of tef [Eragrostis tef (Zucc.) Trotter] varieties in northeast Ethiopia. Black Sea Journal od Agriculture, 3(4), 239-245.

Worku A, Henry M, Zewotir T and Taye G (2013). Additive main effects and multiplicative interactions model (AMMI) and genotype main effect and genotype by environment interaction (GGE) biplot analysis of multi-environmental wheat variety trials. African Journal of Agricultural Research 8(12) , 1023- 1040.

Yehuala K , Ndegwa H M , Mazengia W , Zeleke B and Frederick L S (2022). Yield gaps of major cereal and grain legume crops in Ethiopia: a review. Agronomy 12, 2528. https://doi.org/10.3390/agronomy12102528

Yan W (2011). GGE Biplot vs AMMI graphs for genotype-by-environment data analysis. Journal of the Indian Society of Agricultural Statistics 65(2), 181-193.

Yan W and Kang M S (2003). GGE biplot analysis: a graphical tool for breeders,   : M. S. Kang, ed. Geneticists and Agronomist. CRC Press, Boca Rato.

Yan W and Tinker N A (2006). Biplot analysis of multi –environment trial data: Principles and applications. Canadian, Journal of Plant Science 86, 623-645