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Genetic Variability of Tef [*Eragrostis Tef* (Zucc.) Trotter] Genotypes for Acid Soil Tolerance

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Abstract

Genetic variability studies provide basic information for breeders to develop different stress-tolerant varieties. In the present study, forty-nine Tef genotypes were evaluated under strong acid soil (pH 4.97) and lime treated (pH 5.90) soils in the lathouse at Assosa Agricultural Research Center in 2017 to estimate the genetic variability, heritability and genetic advance of various traits of tef genotypes in relation to soil acidity stress. The result indicated that there was high significant ($p<0.01$) differences among genotypes for all traits under both environments; except for shoot biomass in the combined data analysis. The two environments differed significantly in their effect on all traits except on plant height, panicle length, culm length, total and fertile tillers and number of primary branches, although environment contribution to total TSS was less than 10% in 13 of the 17 traits studied; its high contribution was to harvest index (42.6%) and grain yield pot^{-1} (32.5%). Big reduction due to soil acidity was recorded for yield of primary panicle (27.78%), grain yield pot^{-1} (33.85%) and harvest index (35.6%). A contribution of G was from 44.5% in harvest index to 90.5% in panicle length. The GxE interaction was also significant for all traits and it contributed more than 15% in 11 of the traits, indicating inconsistency of performance of genotypes under acidic and lime treated soils. PCV, GCV, and GAM were high (>20%) for fertile tillers per plant, panicle weight, yield of primary panicle, grain yield, and harvest index under both acidity levels and in the combined analysis. Heritability was high (>60%) for all traits except for shoot biomass in the combined analysis and lime treated soil. In general, there was wide genetic variability in the traits studied pointing to the possibility of improving the desired traits, including grain yield under both environments and over environments through the selection of elite genotypes.

Keywords: Acid tolerance; Genetic advance; Genetic variability; Heritability.

1. Introduction

Tef, Eragrostis tef (Zucc.) Trotter is one of the crops that originated and were diversified in Ethiopia [1]. It has been distributed to various parts of the world via different organization and individuals. For instance, in 1866 the Royal Botanic Gardens imported the seed of tef from Ethiopia and distributed to India, Australia, USA, and South Africa [2].

In Ethiopia, tef serves as a staple food, and the majority of Ethiopian people prefer the grain of tef for food by making injera, porridge, unraised non-fermented bread (kitta) and local beverage [2]. It is highly nutritious, and excellent in amino acid and mineral content like iron, calcium, and phosphorus when compared to other cereal crops [2, 3]. The other importance of tef is, it's free of gluten which found in the other cereal crops and can cause a celiac disease by the response of T-cells in the small intestine [4]. On the other hand, straw tef is used for feeding of livestock because tef straw is very palatable and nutritious when compared to other cereal crops [2].

Tef is grown on over three million hectares of land in Ethiopia [5]. It is majorly grown in Oromia, Amhara, Tigray, South nation nationalities of people region and Benishangul Gumuz regions of Ethiopia. Benishangul Gumuz region has a large area of land for the production of crops. In 2017 cropping season, the average productivity of tef was estimated at 1.75 and 1.34 tons hectare-1 for Ethiopia at the country level and Benishangul Gumuz Region, respectively [5]. Still, the productivity is low in Ethiopia; and this is mainly due to its susceptibility to lodging, attributed to poor crop husbandry, and moisture stress [2].

On the other hand, soil acidity is also one of the limiting factors of crop production in Ethiopia. According to Angaw and Desta [6], soil acidity severely reduces the yields of many crops in the high rainfall areas of western, southern and south-western Ethiopia. This also true for Benshangul Gumuz Region where the dominant soil is the Nitosols with the average pH value of 5.5 [7].

One of the options to combat the impact of soil acidity on crop yield is the development of tolerant cultivars through selection, hybridization, and other breeding methods. Genetic variability is the pre-requisite for obtaining suitable segregants with desirable traits. Genetic variability is also useful for proper choice of parents for realizing higher heterosis and obtaining useful recombinants. It is also indispensable for the improvement of wider adaptation

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to stress environments like drought, salinity, acidity and heat tolerance, desirable quality and pest resistance [8]. Several studies have to date been made on the magnitude, extent, and utilization of genetic diversity of tef [9-16]. However, there is little available information on the magnitude of tef genetic variability in respect to soil acidity. Therefore, this study was conducted to assess the extent of genetic variability of tef genotypes for acid soil tolerance based on agronomic traits.

2. Materials and Methods

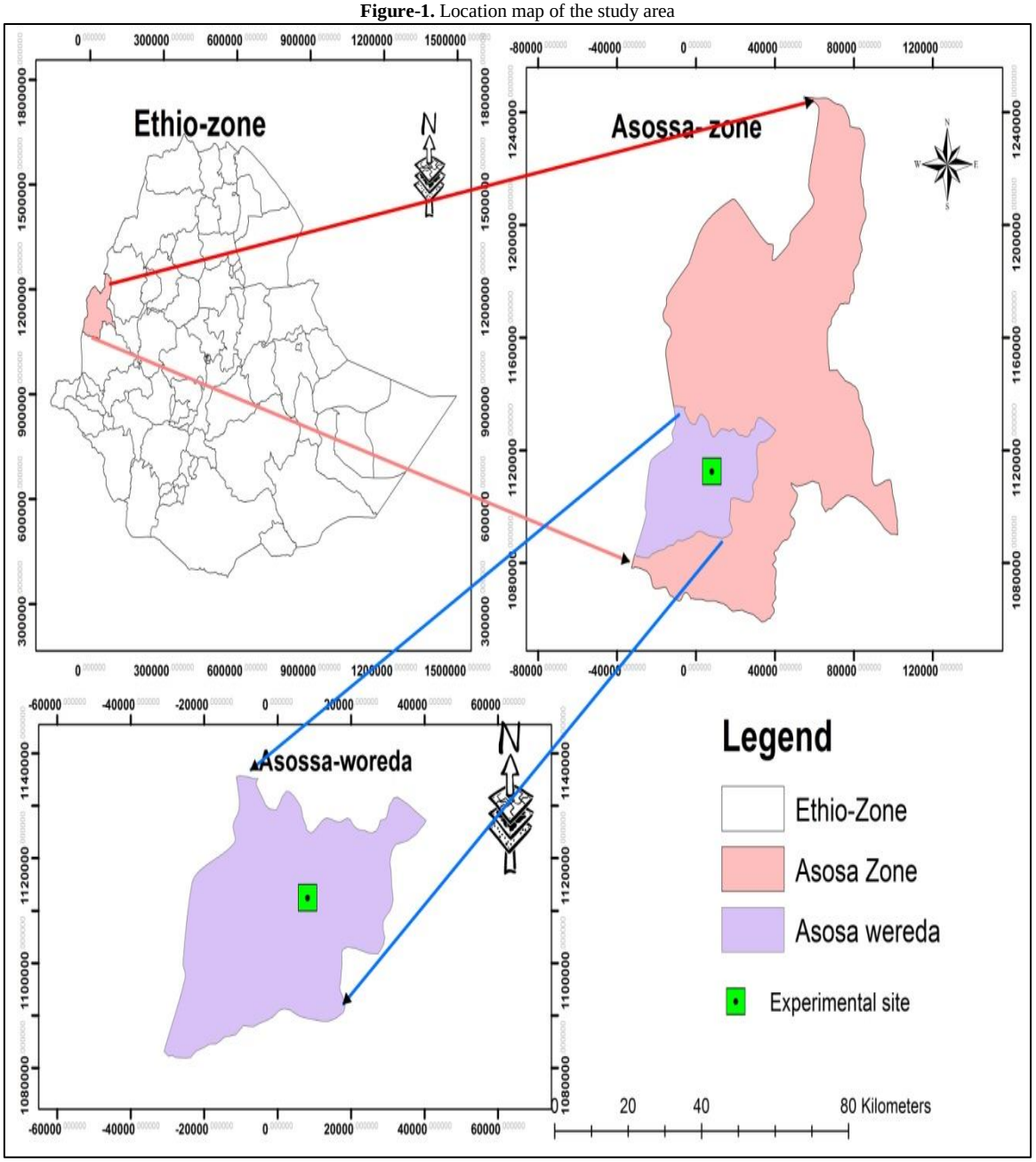
2.1. Description of the Experimental Site

The experiment was conducted in the lathouse of Assosa Agricultural Research Center (AsARC) found in the Benishangul Gumuz Region, Ethiopia. The region is geographically located at a latitude of 9^0 30' to 11^0 39" N and longitude of 34^0 20' to 36^0 30" E covering a total land area of 50,000 square kilometers. Assosa is one of the districts of the Benishangul Gumuz region, located at 10^0 02' 05" N latitude and 34^0 34' 09" E longitudes. Its altitude is 1547 meters above sea level (m.a.s.l.). The rainfall pattern of Assosa is unimodal, which starts from the end of April and extends up to mid-November. The total annual average rainfall of Assosa is 1275 mm. The minimum and maximum temperatures are 17 ^{0}C and 28 ^{0}C, respectively. The dominant soil type is Nitosols.

2.2. Experimental Plant Materials

Forty-nine tef genotypes, including 44 germplasms collected from different areas of Ethiopia, 4 improved varieties (Ambo Toke, Etsuib, Kora and Quncho), and one local check were used for this study. These materials were obtained from Debre Zeit Agricultural Research Center (DZARC).

Figure-1. Location map of the study area



Source: AsARC Metrology station, 2017

Table-1. List of tef germplasms and released varieties used in the experiment

No.	Genotype	Area of collection	No.	Genotypes	Area of collection
1	DZ- 01-1531	-	26	DZ-01-1512	-
2	DZ-01-1821	West Showa	27	DZ-01-2086	Awi
3	DZ-01-1908	West Wollega	28	DZ-01-3492	Jimma
4	DZ-01-2111A	West Wollega	29	DZ-01-3733	South West Showa
5	DZ-01-280	Debre Zeit	30	DZ-01-3738	South West Showa
6	DZ-01-16	Debre Zeit	31	DZ-01-3753	South West Showa
7	DZ-01-1676A	West Wollega	32	DZ-01-3724	Minjar
8	DZ-01-272	East Showa	33	DZ-01-3394	Jimma
9	DZ-01-305	East Showa	34	DZ-01-3405	Jimma
10	DZ-01-306	East Showa	35	DZ-01-3486	Jimma
11	DZ-01-1551	-	36	DZ-01-3497	Jimma
12	DZ-01-1482	East Gojjam	37	DZ-01-3535	Jimma
13	DZ-01-1809	West Showa	38	DZ-01-3533	Jimma
14	DZ-01-1573A	-	39	DZ-01-3507	Jimma
15	DZ-01-999	West Showa	40	Dabo Banja	Awi
16	DZ-01-728	Ambo	41	DZ-01-3704	Minjar
17	DZ-01-1722	Jimma	42	DZ-01-3688	South West Showa
18	DZ-01-1311	Arsi Negele	43	DZ-01-3692	South West Showa
19	DZ-01-855	East Showa	44	DZ-01-3747	South West Showa
20	DZ-01-1978	West Wollega	45	Ambo toke	Released in 1999
21	DZ-01-1769A	-	46	Estuib	Released in 2008
22	DZ-01-1234	Central Tigray	47	Quncho	Released in 2006
23	DZ-01-229	Debre Zeit	48	Kora	Released in 2014
24	DZ-01-383	Debre Zeit	49	Local check	Assosa
25	DZ-01-1841A	East Wollega			

2.3. Soil Sampling and Analysis

Soil samples were taken from the field of AsARC randomly at 0-20 cm depth using Auger sampler in a zigzag form. The soil samples taken were bulked into one composite sample. The was air-dried, ground using mortar and pestle, sieved through 2 mm mesh and packed in a polyethylene bag. The soil sample was analyzed at Assosa Agricultural Research center for the major soil physical and chemical properties. Its pH was identified by using glass electrode pH meter in 1:2.5 soils to water ratio [17]. Bulk density was determined using the core sampling method [18]. The total nitrogen analysis was done using the Kjeldahl method described by Jackson [19]. Exchangeable acidity was determined using the method described by McLean [20]. Cation exchange capacity (CEC) was determined by the ammonium-acetate saturation method [21]. Available soil P was analyzed according to the standard procedure of Olsen [22] extraction method. Exchangeable bases (Ca, Mg, Na, and K) and microelements (Fe, Zn, Cu, and Mn) were determined using Mehlich-3 Extraction procedures [23]. Organic carbon content was determined using Walkey-Black wet oxidation method described by Walkley and Black [24]. Electrical conductivity (EC) was measured in 1: 2.5 sample to water ratio using a conductive meter [25].

2.4. Soil Preparation and Lime Application

Collected acid soil was grouped into two: - one used as it is (acidic soil) without application of lime and the other was used for lime treatment. The lime requirement in tons hectare-1 was obtained based on the results of bulk density (1.4 mg m-3) and exchangeable acidity (3.86 Cmol. kg-1) of the soil by using the formula used in Bruce [26]. Accordingly, to raise the pH value near to 6.0, 2 kg of acid soil was limed with 4.71 g of fine particles of quicklime (CaO) which is equivalent to 4 t ha-1 lime. It was thoroughly mixed on the clean tray and then filled into the pot which has a 14 cm top and a 10.2 cm bottom diameter, with 17.4 cm height. Pots were incubated for two weeks in the lathouse before beginning the experiments.

2.5. Experimental Design and Management

Two sets of experiments, lime treated and lime un-treated (acid soil); each was conducted by using Completed Randomized Design with three replications and both sets of experiments were arranged side by side in the lathouse of Assosa Agricultural Research center. Tef seed was sown on the pots at 20 September 2017 and then thinning was done to get five plants per pot after the three weeks. Fertilizer rate of 46 kg ha^{-1} P_2O_5 and 23 kg ha^{-1} N_2 was applied. Frequently hand weeding was practiced to control the weeds.

2.6. Data Collection

The collected data was done on the pot basis and individual plant basis. Accordingly, days to heading (DTH), days to maturity (DTM), grain filling period (GFP), grain yield/pot (GY), shoot biomass (SBM) and harvest index (HI) data were collected on the basis of the pot. While plant height (PH), panicle length (PL), culm length (CL), peduncle length (PDUL), number of total tillers per plant (TT), number of productive (Fertile) tillers per plant (FT),

number of primary panicle branches (PPB), first basal culm internodes diameter (FBID), second basal culm internode diameter (SBID), panicle weight (PW) and grain yield of primary panicle (YPP) were collected from the five plants per pot and the average was used for the analyses.

2.7. Statistical Analyses

Analysis of variance was done for each respective soil environment (lime treated and acid soil) and combined data over the two soil conditions based on the method described by Gomez and Gomez [27] using SAS software version 9.0 [28]. Mean separation done using least significance difference at 5% level of probability. Prior to doing a combined analysis, variance homogeneity was tested using the F-max test method of Hartley [29]. The variance components for the individual environment were estimated using the method suggested by Dewey and Lu [30]. The phenotypic, genotypic and environmental coefficients of variation at were estimated using the formula adopted by Johanson, *et al.* [31] and classified as low (0-10%), moderate (10-20%) and high (>20) values. Broad-sense heritability (H2) and genetic advance for selection intensity (k) at 5% were estimated based on the formula described by Allard [32].

3. Results and Discussions

3.1. Major Physical and Chemical Properties of the Soil Used in the Experiments

The soil chemical analysis results for major physical and chemical properties are presented in Table 2. The Soil acidity changed from strongly acidic to slightly acidic classes [33] and the deficiencies of certain plant nutrients were observed. The application of lime raised the soil pH from 4.97 to 5.90 and dropped exchangeable acidity from 3.86 to 0.42 Cmol (+) kg-1 and most of the nutrients were relatively increased (Table 2). The Organic Carbon (OC) content was changed from 2.26 to 2.29 %, which is low according to Landon [34] who classified the OC content as very low (< 2%), low (2-4%), medium (4-10%) and high (10-20%). This has an impact on the organic matter content availability in the soil. He also categorized the total nitrogen content as very low (<0.1%), low (0.1-0.2%), medium (0.2-0.5%), high (0.5-1%) and very high (>1%); accordingly, the availability of the total nitrogen content of this soil was low. Electrical conductivity (EC) was very low, implying the soil is free of the salt problem.

A deficiency of the most essential plant elements including potassium and phosphorus was observed (Table 2). In similar, the study conducted at two sites of Assosa district indicated the low availability of OC, potassium, phosphorus, and nitrogen [35]. The deficiencies of such nutrients are mainly due to soil acidity. Soil acidity characterized by a deficiency of essential plant nutrients such as P, K, N, Ca, Mg, and Mo [36], therefore, acid soil improvement practices are imperative in the study area to reduce the constraints of soil acidity.

Table-2. Major physio-chemical properties under lime treated and non-treated soil

Sample	Acid soil	Decision	Limed	Decision
pH (H_2O)	4.97	Strongly acidic	5.90	Slightly acidic
Ex. Acidity (Cmol $_{(+)}$ kg^{-1})	3.86	Very high	0.42	Very low
CEC (Cmol $_{(+)}$ kg^{-1})	19.30	Optimum	25.50	Optimum
EC (ds/m)	0.082	Very low	0.062	Very low
Organic Carbon (%)	2.26	Low	2.29	Low
Total Nitrogen (%)	0.16	Low	0.17	Low
Ca^+ (Cmol $_{(+)}$ kg^{-1})	4.75	Low	17.54	Optimum
P (Cmol $_{(+)}$ kg^{-1})	0.91	Very low	1.47	Very low
K^+ (Cmol $_{(+)}$ kg^{-1})	0.10	Very low	0.12	Very low
Mg^{2+} (Cmol $_{(+)}$ kg^{-1})	2.86	Optimum	2.90	Optimum
Na^+ (Cmol $_{(+)}$ kg^{-1})	0.24	Low	0.28	Low
S (Cmol $_{(+)}$ kg^{-1})	3.57	Optimum	4.36	Optimum
Fe (Cmol $_{(+)}$ kg^{-1})	8.02	Optimum	7.64	Optimum
Mn (Cmol $_{(+)}$ kg^{-1})	4.64	High	4.61	High
Zn (Cmol $_{(+)}$ kg^{-1})	0.01	Low	0.01	Low
Cu (Cmol $_{(+)}$ kg^{-1})	0.12	Optimum	0.13	Optimum

3.2. Analysis of Variance

The analysis of variance for the individual environment and for data combined across two soil conditions were done for 17 characters studied, and results are presented in Tables 3 and 4. There was a highly significant difference ($p<0.01$) between the tested tef genotypes for all characters studied at individual soil conditions (un-limed and limed) indicating that considerable genetic variability exists between the 49 tef genotypes for phenology, growth, yield, and yield-related traits studied. This result is agreed with the reports of Kebebew, *et al.* [37]; Solomon, *et al.* [16]; Habte, *et al.* [38]; Chekole, *et al.* [9] and Mizan, *et al.* [39].

As the analysis of variance for combined data indicated, the mean square of genotypes were highly significant ($p<0.01$) for all characters except shoot biomass tested across two soil acidity conditions. Besides, significant environmental effects were observed for all characters, except for plant height, cum and panicle length, number of total and fertile tillers, and number of primary panicle branches indicating the effect of soil acidity on the majority indicators of phenology, growth and yield traits of the tef genotypes (Table 3). The absence of significant

environmental effects for the insignificant variables cited above was also agreed with the reports of Kebebew, *et al.* [40]. Solomon, *et al.* [16], also found no significant environmental effect on plant height.

Similarly, the interaction of genotypes with soil acidity environments was highly significant ($p \leq 0.01$) for days to heading, grain filling period, culm and panicle length, plant height, shoot biomass, yield of primary panicle, number of total tillers per plant, harvest index, primary panicle branch, first and second basal culm internode diameter. This implies that the genotypes were responding differentially under these two soil acidity conditions with respect to these characters studied (Table 4). The performance of the genotypes was inconsistent over the two acidity levels. Similar to our results, [39] reported that the test of genotype by environment interaction showed highly ($p \leq 0.01$) significant difference for all traits except the lodging index studied under moisture stress and irrigated environments. Wondewosen, *et al.* [41], also reported that grain yield and all yield-related traits were affected significantly by environment and interaction of genotype by environment.

The environment did contribute near to zero to the variability in plant height, panicle and culm length, and primary panicle branches, and it contributed less than 10% to total treatment (G+E+GEI) in eight other traits (Table 5). The maximum environment contribution was 32.5% to grain yield pot^{-1} and 42.6 % to harvest index. The GxE interaction made a contribution of more than 15% to 11 traits, its highest contribution being to the variability of shoot biomass (41.5%), second basal culm internode diameter (26.7%), total tillers per plant (23.5%) and fertile tillers per plant (20.4%). There was an inconsistency of performance among the genotypes over the two soil acidity environments in these traits. The major portion of the total variability of traits in the combined analysis came from the genotypes (from 44.5% for the harvest index to 90.5% for the variability of panicle length). Genotype contributed more than 70% to the variability of 13 of the 17 traits. The higher reduction due to environmental effect was found for harvest index (37.7%), grain yield (34%) and yield of primary panicle (28%) (Table 3). The remaining traits had relatively low percent reduction.

Generally, the present results indicate the existence of considerable genetic variation among the 49 tef genotypes tested under the two soil environments. Several reports confirmed the existence of substantial genetic variability among tef genotypes for their tolerance to various stress [13, 41-43].

Table-3. The significance of mean squares of 17 traits for individual (acid and limed) soil environments

Traits	Acid soil (Un-limed)				Limed				PCRD
	Genotype [1]df=48	Error [1]df=98	Mean	CV%	Genotype [1]df=48	Error [1]df=98	Mean	CV%	
DTH	88.25**	6.84	40.33	6.49	73.74**	10.57	43.1	7.54	6.43
DTM	39.13**	4.95	79.4	2.8	36.08**	5.88	80.35	3.02	1.18
GFP	65.47**	9.29	39.06	7.8	50.81**	10.95	37.26	8.88	-4.83
PH	111.74**	12.69	62.16	5.73	214.87**	12.67	62.15	5.73	-0.02
PL	26.22**	2.24	24.55	6.09	36.03**	3.47	24.4	7.63	-0.62
CL	48.01**	8.89	37.61	7.93	103.6**	8.92	37.74	7.91	0.34
PDUL	11.98**	2.68	11.4	14.35	18.73**	2.77	12.95	12.86	11.97
TT	32.24**	10.10	14.4	22.07	29.69**	10.98	14.13	23.45	-1.91
FT	20.26**	5.70	11.41	20.92	23.69**	6.62	10.77	23.89	-5.94
PW	0.023**	0.006	0.37	20.07	0.03**	0.007	0.43	19.69	13.95
YPP	0.007**	0.002	0.13	36.82	0.01**	0.003	0.18	32.92	27.78
SBM	6.49**	2.16	13.39	10.99	5.13**	2.57	12.56	12.77	-6.61
GY	0.72**	0.22	1.61	29.22	1.45**	0.43	2.44	26.84	33.85
HI	33.19**	13.09	12.1	29.91	77.08**	15.96	19.41	20.59	37.66
FBID	0.09**	0.02	1.1	11.38	0.1**	0.01	1.13	8.62	2.65
SBID	0.13**	0.04	1.02	20.04	0.12**	0.04	1.09	17.37	6.42
PPB	24.19**	3.53	23.07	8.17	31.53**	3.99	22.99	8.67	0.35

**: significant difference at 0.01 probability level, [1] Degree of freedom, DTH: days to heading, DTM: days to maturity, GFP: grain filling period, PH: plant height, PL: panicle length, CL: culm length, PDUL: peduncle length, TT: number of total tillers $plant^{-1}$, FT: number of fertile tillers $plant^{-1}$, PW: panicle weight, YPP: grain of primary panicle, SBM: shoot biomass, GY: grain yield pot^{-1}, HI: harvest index, FBID: first basal culm internode diameter, SBID: second basal culm internode diameter, PPB: primary panicle branches, PCRD: percent reduction.

Table-4. The significance of mean squares of 17 traits for data combined over two soil environments

Traits	Environment [1]df=1	Genotype [1]df=48	G*E [1]df=48	Error [1]df=196	CV %	Mean
DTH	560.7**	142.2**	19.8**	8.704	7.07	41.71
DTM	67.62**	66.48**	8.73*	5.41	2.91	79.87
GFP	238.9**	93.53**	22.8**	10.12	8.34	38.16
PH	0.023ns	292.9**	33.7**	12.69	5.73	62.15
PL	0.82ns	55.04**	5.75**	2.81	6.85	24.47
CL	0.57ns	129.8**	22.7**	8.2	7.92	37.68
PDUL	177.4**	26.72**	3.99*	2.723	13.55	12.18
TT	51.04ns	50.56**	15.87**	9.24	22.76	14.27
FT	30.7ns	34.88**	9.07*	6.16	22.38	11.09
PW	0.25**	0.043**	0.01*	0.006	19.9	0.40
YPP	0.18**	0.016**	0.005**	0.003	34.75	0.15
SBM	50.88**	6.35ns	5.26**	2.37	11.86	12.97
GY	50.01**	1.69**	0.47*	0.32	28.15	2.03
HI	3926**	85.49**	24.78**	14.53	24.19	15.75
FBID	0.321*	0.155**	0.03**	0.012	10.02	1.10
SBID	0.3**	0.18**	0.07**	0.04	18.68	1.05
PPB	0.52ns	44.89**	10.8**	3.762	8.42	23.03

ns: no significant difference, * and **: significant difference at 0.05 and 0.01 probability level respectively, [1] Degree of freedom, G*E: genotype by environment interaction, DTH: days to heading, DTM: days to maturity, GFP: grain filling period, PH: plant height, PL: panicle length, CL: culm length, PDUL: peduncle length, TT: number of total tillers plant^{-1}, FT: number of fertile tillers plant^{-1}, PW: panicle weight, YPP: grain of primary panicle, SBM: shoot biomass, GY: grain yield pot^{-1}, HI: harvest index, FBID: first basal culm internode diameter, SBID: second basal culm internode diameter, PPB: primary panicle branches, CV: coefficients of variation.

Table-5. The proportion of Total Treatment SS contributed by Genotype, Environment and GxE

Variables	Genotype	Environment	G x E
Days to heading	81.878	6.726	11.396
Days to maturity	86.763	1.839	11.399
Grain filling period	77.134	4.104	18.762
Plant height	89.691	0.001	10.308
Panicle length	90.515	0.028	9.457
Culm length	85.111	0.008	14.882
Peduncle length	77.744	10.695	11.561
Number of total tillers per plant	74.912	1.575	23.513
Number of fertile per plant	78.148	1.458	20.395
Panicle weight	73.394	8.963	17.643
Yield of primary panicle	65.756	15.457	18.787
Shoot biomass	50.101	8.365	41.534
Grain yield pot^{-1}	52.771	32.476	14.753
Harvest index	44.512	42.582	12.906
1st basal culm internode diameter	80.890	3.474	15.635
2nd basal culm internode diameter	70.685	2.560	26.755
Primary panicle branches	80.538	0.019	19.442

3.4. Variability in Tef Traits

3.4.1. Genotypic and Phenotypic Coefficients of Variation

The estimates of variance components and coefficients of variations for the lime treated and acidic soils and the combined data are given in Tables 6 and 7. The phenotypic coefficient of variation was ranged from 4.55% and 4.32% for days to maturity to 37.42% and 38.68% for the yield of primary panicle under acid and lime treated soil conditions, respectively (Table 6). Estimates of phenotypic coefficients of variation (PCV) under acid and lime treated conditions respectively were relatively high for yield of primary panicle (37.42% and 38.68%) followed by grain yield pot^{-1} (30.30% and 28.49%), harvest index (27.49% and 26.12%), number of total tillers per plant (22.77% and 22.26%) and number of fertile tillers per plant (22.76% and 26.09%). PCV values under acidic and lime treated soils were low for days to maturity (4.55% and 4.32) and plant height (9.8 only under acidic soil). While they were low for days to maturity (4.55% and 4.32%) and plant height (9.8% only under acid soil). Intermediate (10-20%) PCV values in both soil environments were obtained for days to heading, grain filling period, panicle, peduncle, and culm length, shoot biomass, first basal culm internode diameter, and primary panicle branches (Table 6).

Coefficient of variation at genotypic level was ranged from 4.25% and 3.95% for days to maturity to 30.79 % and 33.70 % for the yield of primary panicle under acidic and lime treated soil conditions, respectively (Table 6). The yield of primary panicle, panicle weight, grain yield pot^{-1}, harvest index and fertile tillers per plant had index had high (>20%) GCV values under both soil conditions. Low (<10%) GCV values were recorded for days to

maturity and shoot biomass under both soil conditions and plant height and culm length under only acidic soil. Days to heading, panicle and peduncle length, total and fertile tillers per plant, first and second basal culm internode diameter and primary panicle branches were categorized under intermediate (10-20%) GCV values in both soil conditions.

In the combined data yield of primary panicle, grain yield pot^{-1} and harvest index scored high (>20%) GCV, while low (<10%) GCV were observed for days to maturity, grain filling period and shoot biomass. The rest of the traits had an intermediate (10-20%) GCV estimates. In a similar way, high PCV values were observed from combined data for yield of primary panicle (34.22%), grain yield pot^{-1} (26.21%), harvest index (23.96), number of fertile tillers per plant (21.74%) and panicle weight (21.17%), whereas low PCV estimates were found for days to maturity (4.17%) and shoot biomass (7.93%). For all other traits intermediate (10-20%) PCV values were obtained in the combined analysis (Table 7).

The range of GCV and PCV values in our study agreed with previous studies by Habte and Gugssa [44], Tsion [45], and Chekole, *et al.* [9]; although the values are relatively less than those reported by Solomon [46] who observed 4.2 to 54.2% and 10.5 to 51.0% range for GCV and PCV values, respectively. Similarly, [41], reported that low values of genotypic and phenotypic coefficients of variation for days to maturity, grain filling period, plant height, and high values for total biomass, panicle weight, and grain yield pot-1 under stress environment. They also reported high GCV estimates of 22.4% and 25.9% for main shoot panicle weight under drought stress and irrigated conditions respectively. In addition, Habtamu, *et al.* [10] also reported low GCV for days to maturity and high GCV for harvest index. The low GCV for days to maturity, grain filling period and shoot biomass implies that selection for improvement of such traits may be misleading.

Generally, in the present study, the difference between the two PCV and GCV values were very small in magnitude and indicating that environment and genetics have a comparative effect on the expression of traits. The presence of high GCV values among genotypes evaluated under the two soil environments indicated that selection can be successful in most important traits. Particularly, the higher GCV estimates for grain yield pot^{-1} under acidic soil than under lime treated soil suggests the relative better scope of improvement through selection under acid stress conditions.

3.4.2. Broad-Sense Heritability

Broad sense heritability was ranged from 61% to 92% under acid soil and from 50% to 94% under limed soil (Table 6). High heritability estimates under un-limed and limed soil conditions, respectively, in that order were found for days to heading (92% and 86%), days to maturity (87% and 84%), grain filling period (86% and 78%), plant height (89% and 94%), panicle length (92% and 90%), and culm length (82% and 91%). On the other hand, relatively low heritability was found for harvest index (61%) from acid soil and shoot biomass (50%) from lime treated soil environment.

The ranges of heritability are agreed with the reports of Wondewosen, *et al.* [41] who found 59% to 96% and 73% to 94% under drought stress and non-stress environments, respectively. In line with our results various researchers observed high heritability for days to heading [40, 44, 47], panicle length [40, 48], grain yield [49], and harvest index [9]. The high heritability indicates that the influence of environment on the expression of the trait is minimum [32]. Hence, heritability is a value of a character only for the population and the environment to which the genetic materials are subjected and it depends on the magnitude of all the components of variance, and a change in any of these will affect it. According to the present results, selection in tef traits, which had high heritability value (such as days to heading and maturity, plant height, panicle and culm length, panicle weight, and primary panicle branches), might be effective under both acidic and limed soils.

However, the heritability of shoot biomass was relatively low (67% and 50%) under acid and lime treated soils, respectively, when compared to other characters; which implies that improvement of this trait under both soil types through selection might be unworthy. Kebebew, *et al.* [50] found similar low heritability for shoot biomass/plant (17%) and higher heritability for panicle length (75%). Moreover, Mizan, *et al.* [13] in a similar way reported low heritability of 8.6% for shoot biomass under drought stress.

3.4.3. Genetic Advance

Genetic advance (GA) ranged from 8% and 7% for days to maturity to 52% and 60% for a yield of primary panicle under acid and limed soil, respectively (Table 6). High genetic advance values as a percent of the mean (>20%) were found for days to heading, panicle weight and length, peduncle length, total and fertile tillers per plant, yield of primary panicle, grain yield pot^{-1}, first and second basal culm internode diameter, harvest index, and primary panicle branches. A low (<10%) GA estimate was found only for days to maturity under both soil conditions. The GA values for all traits were generally high under both soil conditions.

From the analysis of the combined data for shoot biomass and days to maturity, the results scored low (<10%) for GA as % of the mean, while all other traits scored high (>20%) GA as % of the mean, except grain filling period (16.1%) and number of primary panicle branches (18.5%), which had intermediate GA as % of the mean (Table 7).

The range (7% to 60%) of GA is high for most of the characters as compared to previous studies of Solomon, *et al.* [16]; Habte and Gugssa [44] and Chekole, *et al.* [9]. Inline to the present results, Mizan, *et al.* [13] reported high GA for grain yield (31.5%) and yield of primary panicle (40%) from 144 tef genotypes evaluated under moisture stress and irrigated environments. The low GA observed in the present result was in agreement with the report of Habte and Gugssa [44] and Chekole, *et al.* [9].

According to Johanson, *et al.* [31], high heritability coupled with high genetic advance is usually more useful than heritability alone in predicting the resultant effect of selecting the best individuals, and this implies the role of the additive gene for the expression of the characters and thus could be effective in improving upon selection. In this study, relatively high heritability coupled with high GA as % mean was observed for days to heading, plant height, panicle length, culm length, peduncle length, panicle weight, a yield of primary panicle and grain yield pot-1. Thus, selection upon these traits is important for effective yield improvement.

Table-6. Estimate of coefficients of variations, heritability (H^2) and genetic advance for 17 traits of 49 tef genotypes tested under acid and limed soil environments

Traits	PCV		GCV		H^2%		GA		GA(% mean)	
	Acid	Limed	Acid	Limed	Acid	Limed	Acid	Limed	Acid	Limed
DTH	13.45	11.50	12.92	10.65	92.25	85.67	10.26	8.71	25.43	20.20
DTM	4.55	4.32	4.25	3.95	87.36	83.71	6.47	5.95	8.15	7.41
GFP	11.96	11.05	11.08	9.78	85.82	78.44	8.22	6.62	21.04	17.76
PH	9.82	13.62	9.24	13.21	88.64	94.10	11.09	16.33	17.84	26.27
PL	12.04	14.20	11.52	13.50	91.48	90.37	5.54	6.42	22.58	26.31
CL	10.64	15.57	9.60	14.89	81.48	91.39	6.68	11.01	17.77	29.17
PDUL	17.53	19.29	15.45	17.80	77.68	85.19	3.18	4.36	27.92	33.69
TT	22.77	22.26	18.86	17.67	68.66	63.02	4.61	4.06	32.05	28.76
FT	22.76	26.09	19.30	22.15	71.85	72.05	3.83	4.15	33.53	38.54
PW	23.48	23.54	20.43	20.61	75.67	76.67	0.14	0.16	36.42	36.99
YPP	37.42	38.68	30.79	33.70	67.72	75.89	0.07	0.11	51.95	60.18
SBM	10.98	10.41	8.97	7.35	66.64	49.88	2.01	1.34	15.00	10.65
GY	30.30	28.49	25.17	23.91	69.01	70.39	0.69	1.00	42.86	41.12
HI	27.49	26.12	21.39	23.26	60.56	79.29	4.13	8.24	34.13	42.46
FBID	16.10	15.88	14.70	15.08	83.32	90.18	0.29	0.33	27.50	29.36
SBID	20.25	18.16	16.62	15.14	67.34	69.49	0.29	0.28	27.96	25.87
PPB	12.35	14.05	11.42	13.13	85.43	87.32	4.97	5.80	21.63	25.15

PCV: phenotypic correlation coefficient, GCV: genotypic correlation coefficient, H^2: broad sense heritability, GA: genetic advance, GA (%): genetic advance as percent mean, DTH: days to heading, DTM: days to maturity, GFP: grain filling period, PH: plant height, PL: panicle length, CL: culm length, PDUL: peduncle length, TT: number of total tillers/plant, FT: number of fertile tillers/plant, PW: panicle weight, YPP: grain of primary panicle, SBM: shoot biomass, GY: grain yield/pot, HI: harvest index, FBID: first basal culm internode diameter, SBID: second basal culm internode diameter, PPB: primary panicle branches.

Table-7. Estimate of coefficients of variations, heritability (H^2) and genetic advance for 17 traits of 49 tef genotypes based on combined analyses over two soil environments

Characters	Mean	σ^2_g	σ^2_{ge}	σ^2_p	PCV	GCV	H^2%	GA	GA (%)
DTH	41.71	20.4	3.7	23.7	11.67	10.83	86.08	8.59	20.59
DTM	79.87	9.62	1.11	11.08	4.17	3.88	86.86	5.93	7.42
GFP	38.16	11.8	4.21	15.59	10.35	9	75.68	6.13	16.05
PH	62.15	43.21	6.99	48.82	11.24	10.58	88.51	12.68	20.4
PL	24.48	8.47	0.96	9.42	12.54	11.89	89.87	5.65	23.1
CL	37.68	17.55	4.76	21.41	12.28	11.12	81.96	7.77	20.63
PDUL	12.18	3.79	0.42	4.45	17.33	15.98	85.06	3.68	30.22
TT	14.27	4.79	2.01	7.56	19.27	15.35	63.44	3.58	25.06
FT	11.09	4.3	0.97	5.81	21.74	18.7	74	3.66	32.98
PW	0.4	0.005	0.001	0.007	21.17	18.46	76.01	0.13	32.99
YPP	0.15	0.002	0.001	0.003	34.22	28.95	71.6	0.08	50.22
SBM	12.97	0.18	0.97	1.06	7.93	3.28	17.1	0.36	2.78
GY	2.03	0.2	0.05	0.28	26.21	22.25	72.05	0.78	38.72
HI	15.75	10.12	3.42	14.25	23.96	20.19	71.02	5.5	34.88
FBID	1.1	0.02	0.01	0.03	14.63	13.13	80.54	0.27	24.16
SBID	1.05	0.02	0.01	0.03	16.34	12.89	62.2	0.22	20.83
PPB	23.03	5.67	2.36	7.48	11.88	10.34	75.86	4.25	18.47

σ^2_g: genotypic variance, σ^2_{ge}: genotype by environment interaction variance, σ^2_p: phenotypic variance, PCV: phenotypic correlation coefficient, GCV: genotypic correlation coefficient, H^2: broad sense heritability, GA: genetic advance, GA (%): genetic advance as percent mean, DTH: days to heading, DTM: days to maturity, GFP: grain filling period, PH: plant height, PL: panicle length, CL: culm length, PDUL: peduncle length, TT: number of total tillers/plant, FT: number of fertile tillers/plant, PW: panicle weight, YPP: grain of primary panicle, SBM: shoot biomass, GY: grain yield/pot, HI: harvest index, FBID: first basal culm internode diameter, SBID: second basal culm internode diameter, PPB: primary panicle branches.

4. Summary and Conclusion

Analysis of variance for the data from individual environments and the combined indicated the considerable variation among 49 tef genotypes for almost all studied traits, although the environment made a minimum contribution to total treatment sum of squares (TSS). The interaction of genotype by environment was also

significant in most of the traits revealing differential performances of the genotypes under the two soil conditions. Most of the variability was due mainly to the contribution of genotypes.

High (>20%) phenotypic and genotypic coefficients of variations were found for a grain yield pot^{-1}, panicle weight, yield of primary panicle, harvest index and fertile tillers per plant under both environments (acidic and limed soil). The PCV was also high for total tiller per plant. Intermediate PCV and GCV values were observed from both soils for all remaining traits, except for days to maturity where it was low (<10%) under both soil acidity levels and plant height only under acid soil. Heritabilities were higher than 60% for all traits under both soil environments except for shoot biomass under lime treated soil, indicating that genetics had a comparative effect on the expression of such traits. The genetic advance was high (>20%) for all traits except for shoot biomass where it was intermediate and for days to maturity, where it was low (<10%). The high heritability, along with high genetic advance as percent of mean observed for most of the traits evaluated under these soil conditions, indicated that there is a predominance of additive gene action; and it suggests the improvement of tef through the selection of these traits is a more efficient approach. The overall partitioning of the components of variation confirmed the existence of adequate variation that can be exploited and utilized for improvement through selection.

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