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Multivariate analysis of phenotypic variability in Tef [*Eragrostis tef* (Zucc.) Trotter] genotypes from Ethiopia

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Tef [*Eragrostis tef* (Zucc.) Trotter] is an important food crop in Ethiopia. The present research was conducted to characterize the phenotypic variability of 68 tef genotypes collected from Ethiopia. Where a Bi-replicated 7×10 alpha lattice design was used to evaluate the 70 tef genotypes at Holetta and Debre Zeit Research Centers during 2015. Based on the results of cluster analysis (CA), genotypes were grouped into twelve clusters and twenty nine genotypes formed a single cluster; whereas, nine clusters comprised of five or few genotypes. The first five principal components (PC) with eigenvalue greater than one accounted for 80% of the total genetic variation, height related traits, the diameters of the two basal culm internodes, and number of spikletes and primary branches per main panicle were traits that chiefly contribute for the total variance accounted for by the first PC. The second PC gross variation originated due mainly to variations in yield and yield related traits like grain yield, total biomass, straw yield and harvest index. In addition, genetic distances (D^2) which ranged from 326.22 to 25.07 were measured among the 12 clusters. Thus, indicates their chance of giving better genetic recombination and segregation of progenies.

Key words: Cluster analysis, genetic distance, multivariate, principal component, Tef.

INTRODUCTION

Tef (*Eragrostis tef* (Zucc.) Trotter) is traditionally grown as a staple cereal crop in Ethiopia and it is produced by more than 6.5 million small scale farmers (CSA, 2015). The grain is ground into flour, which is used to make a pancake-like local bread called "*injera*" (Ketema, 1997).

The grain is also used to make a local drink. In addition, tef has been used as a forage or pasture crop for cattle in some parts of the world (Assefa et al., 2009). The straw also serves as bedding material, mulch and domestic fuel source (Assefa et al., 2001b). Tef is better adapted to excessive or low soil moisture conditions than other cereals and often sown as a rescue crop (Tefera and Ketema, 2001).

Therefore, tef is considered an important food security crop. In Ethiopia, tef shows low productivity, because of the lack of lodging resistant varieties, low yielding varieties under a wide range of cultivation, pest problem, drought and labor intensive nature of cultivation (Assefa

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et al., 2013). The development of improved tef varieties had been successful (Assefa et al., 2013; MoARD, 2016). The existence of genetic variability is an important factor in the development and selection of improved varieties. Therefore, estimating the genetic variation among landraces will enhance breeding activities (Assefa et al., 2015; Kefyalew et al., 2000). Tef is an ancient crop in Ethiopia and cultivated across a wide range of environments, which can contribute to greater genetic variation. The Ethiopian Biodiversity Institute (EBI) currently holds 6000 tef landraces mostly from altitudes ranging from 800 to 3200 m.a.s.l. (Tesema, 2013). Hence, multivariate analysis is a useful tool for characterization and classification of plant genetic resources evaluated for several pheno-morphic and agronomic traits (Assefa et al., 2003). The present study was conducted to study variability of newly collected local tef genotypes.

MATERIALS AND METHODS

The experiment was planted during 2015 growing season at Holetta (9°03'N and 38°30'E) and Debre Zeit (8°44'N and 38°58' E). Sixty-eight locally collected genotypes along with two checks genotypes were evaluated in a 7×10 alpha lattice designs with two replications (Table 1). Tef accessions were initially (each contain 50-100 panicles selected from individual plants) collected from farmers' field within 15 km interval and also sown in separate rows for purification at Debre Zite Agricultural Research Center during the 2013 and 2014 main-cropping seasons and the 2015 off-season.

Genotypes were planted in a plot area of 1 m^2 (1 m × 1 m). A spacing of 0.2, 0.5 and 1.5 m were used between rows, plots and replications, respectively. For the seven month (from June to December) growing season, average rainfall, minimum and maximum temperatures of Holetta and Debre Zeit were: 710 mm, 5.6°C, 19.5°C and 73 mm, 18.8°C, 24.9°C, respectively.

Data collections were made on eighteen traits. Days to heading, days to maturity, days to grain filling period, lodging index, total biomass (g), grain yield (g), straw yield (g), thousand seed weight (g), and harvest index (HI) where taken on plot base. In contrast, plant height (cm), panicle length (cm), culm length (cm), number of total tillers per plant, number of fertile tillers per plant, number of spikelets per panicle, number of primary branches per main panicle, first basal culm internode diameter (mm), and second basal culm internode diameter (mm) were recorded on five random sample individual plants.

For multivariate analysis, the mean data of the 70 test genotypes for each of the traits were the first pre-standardized to mean zero and variance unity to avoid bias due to differences in measurement scales.

Multivariate statistical analysis methods included cluster analysis (CA) and principal component analysis (PCA) using the MINITAB statistical computer package, version 14.00 (MINITAB, 2003). Points where local peaks of the pseudo F statistic join with small values of the pseudo t^2 statistic followed by a larger pseudo t^2 for the next cluster fusion were observed to decide the number of clusters (SAS Institute, 2002).

Genetic distance between clusters was computed using the generalized Mahalanobis's D^2 statistics formula as suggested in Singh and Chaudhary (1996) and distance analysis was computed using the SAS computer software (SAS Institute, 2002). It was also made based on the mean values for the 18 quantitative traits and 70 tef genotypes over the two locations.

$$D^2_p = (Xi\text{-}Xj)' \, S^{-1} \, (Xi\text{-}Xj).$$

where D^2_p= total generalized distance based on p characters, Xi and Xj are the p mean vectors of 70 test genotypes I and j, respectively, S^{-1}=pooled error variance and co-variance matrix.

The D^2 value obtained for pairs of clusters was considered as the calculated value of Chi-square and was tested for significance at 5 and 1% levels of probability against the tabulated values of X^2 at 'q' degrees of freedom, where q represents the number of traits studied (Fikreselassie, 2012).

RESULTS AND DISCUSSION

Cluster analysis

Using a 73% similarity level, the genotypes formed 12 clusters (C). The number of genotypes in each cluster ranged from 1 to 29 (Figure 1 and Table 2). The largest cluster (C-3) contains different tef germplasm collected from all zones, while C-6 was the second largest cluster and it comprised 14 germplasm accessions of which 13 were from Jimma and Horo Gudru Zones of Oromya, while the remaining tef germplasm lines were from North Wello Zone of Amhara Region. The third big cluster (C-5) constituted the improved variety Quncho (DZ-Cr-387) and other 8 local germplasm accessions of which two (Oro-ACC#8-L13 and Oro-ACC#9-L45) were from Jimma zone and the remaining 6 were equally distributed between North Wello and West Shewa zones of Amhara and Oromya, respectively. Beside those major clusters, each of clusters 7 and 2 comprised 5 and 3 tef germplasm lines, respectively. Regarding their origin, cluster 7 comprised of tef germplasm entirely collected from North Wello and North Shewa Zones of Amhara Region, while those in cluster 2 originated from North Wello Zone of Amhara. In addition, clusters 1, 4 and 9 each comprised two germpalsm accessions, with the former two containing types from North Wello of Amhara and West Shewa of Oromya Region, while the latter one contained accessions collected from Jimma Zone of Oromya. Four of the twelve clusters comprising single genotype including the germplasm accessions Oro-ACC#8-L30 (C-8), Oro-ACC#4-L18(C-10), Oro-ACC#4-L25) (C-11), and the released variety "*Tseday*" (C-12). Those unclear patterns of genotypes grouping in respect to their origin could be a result of free exchange of genotypes and the expansion of improved tef varieties.

In line with the present results, Assefa et al. (1999) categorized 320 tef lines into 14 major complexes consisting of 1 to 183 tef lines. Previous cluster analyses with different sets of tef materials have also demonstrated variable groupings of tef genotypes based on similarity (Assefa et al., 2000, 2001a, 2003).

The cluster mean comparison for the 18 traits evaluated depicted that the first cluster consisted of tef germplasm lines with early panicle emergence and maturity, short grain filling period, thin first and second basal culm internodes. In contrast, this cluster is

Table 1. Tef genotypes used in the study and area of collection.

S/N	Name	Collection zones	No.	Name	Collection zones
1	Amh-ACC#1-L50	North Wello	36	Oro-ACC#16-L38	Jima
2	Amh-ACC#1-L51	North Wello	37	Oro-ACC#16-L48	Jima
3	Amh-ACC#1-L56	North Wello	38	Oro-ACC#16-L51	Jima
4	Amh-ACC#1-L59	North Wello	39	Oro-ACC#16-L52	Jima
5	Amh-ACC#5-L4	North Wello	40	Oro-ACC#7-L1	Horo Gudru
6	Amh-ACC#5-L63	North Wello	41	Oro-ACC#7-L15	Horo Gudru
7	Amh-ACC#6-L5	North Wello	42	Oro-ACC#7-L19	Horo Gudru
8	Amh-ACC#6-L11	North Wello	43	Oro-ACC#9-L2	Horo Gudru
9	Amh-ACC#6-L41	North Wello	44	Oro-ACC#9L5	Horo Gudru
10	Amh-ACC#8-L13	North Wello	45	Oro-ACC#9-L26	Horo Gudru
11	Amh-ACC#8-L20	North Wello	46	Oro-ACC#9-L28	Horo Gudru
12	Amh-ACC#8-L51	North Wello	47	Oro-ACC#9-L38	Horo Gudru
13	Amh-ACC#8-L61	North Wello	48	Oro-ACC#1-L1	South WestShewa
14	Amh-ACC#9-L4	North Wello	49	Oro-ACC#1-L21	South WestShewa
15	Amh-ACC#9-L45	North Wello	50	Oro-ACC#1-L37	SouthWestShewa
16	Amh-ACC#11-L13	North Wello	51	Oro-ACC#4-L18	South WestShewa
17	Amh-ACC#11-L44	North Wello	52	Oro-ACC#4-L25	South WestShewa
18	Amh-ACC#11-L22	North Shewa	53	Oro-ACC#4-L47	South WestShewa
19	Amh-ACC#11-L36	North Shewa	54	Oro-ACC#8-L10	South WestShewa
20	Amh-ACC#12-L2	North Shewa	55	Oro-ACC#8-L17	South WestShewa
21	Amh-ACC#12-L4	North Shewa	56	Oro-ACC#8-L25	South WestShewa
22	Amh-ACC#12-L29	North Shewa	57	Oro-ACC#15-L8	South WestShewa
23	Amh-ACC#14-L21	North Shewa	58	Oro-ACC#15-L12	South WestShewa
24	Amh-ACC#14-L23	North Shewa	59	Oro-ACC#15-L30	South WestShewa
25	Amh-ACC#14-L24	North Shewa	60	Oro-ACC#16-L42	WestShewa
26	Oro-ACC#8-L13	Jima	61	Oro-ACC#16-L49	West Shewa
27	Oro-ACC#8-L30	Jima	62	Oro-ACC#19-L32	West Shewa
28	Oro-ACC#8-L32	Jima	63	Oro-ACC#19-L36	West Shewa
29	Oro-ACC#8-L5	Jima	64	Oro-ACC#27-L3	West Shewa
30	Oro-ACC#9-L34	Jima	65	Oro-ACC#27-L17	West Shewa
31	Oro-ACC#9-L37	Jima	66	Oro-ACC#30-L7	West Shewa
32	Oro-ACC#9-L45	Jima	67	Oro-ACC#30-L14	West Shewa
33	Oro-ACC#11-L15	Jima	68	Oro-ACC#30-L29	West Shewa
34	Oro-ACC#11-L26	Jima	69	Quncho (DZ-Cr-387)	Released variety (2006*)
35	Oro-ACC#11-L36	Jima	70	Tsedey (DZ-Cr-37)	Released variety (1984*)

*Year of release.

characterized by tef materials having high harvest index, lodging index and grain yield. On the other hand, except relatively high values of tiller number (total and fertile) and harvest index, the remaining characters of the genotypes included in the second cluster scored small values (Tables 3 and 4).

However, most quantitative traits of tef germplasm lines measured within C-3, 5, 6 and 10 showed relatively high values. Unlike their common characters, C-3, 5 and 6 contained the largest number tef germplasm lines, while C-10 contained a locally collected single tef germplasm line (Oro-ACC#4-L18). In addition, both C-5 and C-6 showed lower tiller numbers (total and fertile) and lodging index values. On top of this, relatively lower values of harvest index were exhibited by cluster 10. Days to maturity and grain filling period showed the highest mean value in C-7, but the lowest cluster mean values of total biomass and grain yield, lower value of straw yield, lodging index, number of fertile and total tillers were noted for this cluster. Cluster 4 is characterized by tef germplasm lines which have relatively small number of primary panicle branches, high total tiller number, longer grain filling period, late maturity, and high values of total biomass, grain yield and straw yield. The lowest cluster mean values of most traits were noted for C-8, which contained the single tef germplasm line (Oro-ACC#8-L30)

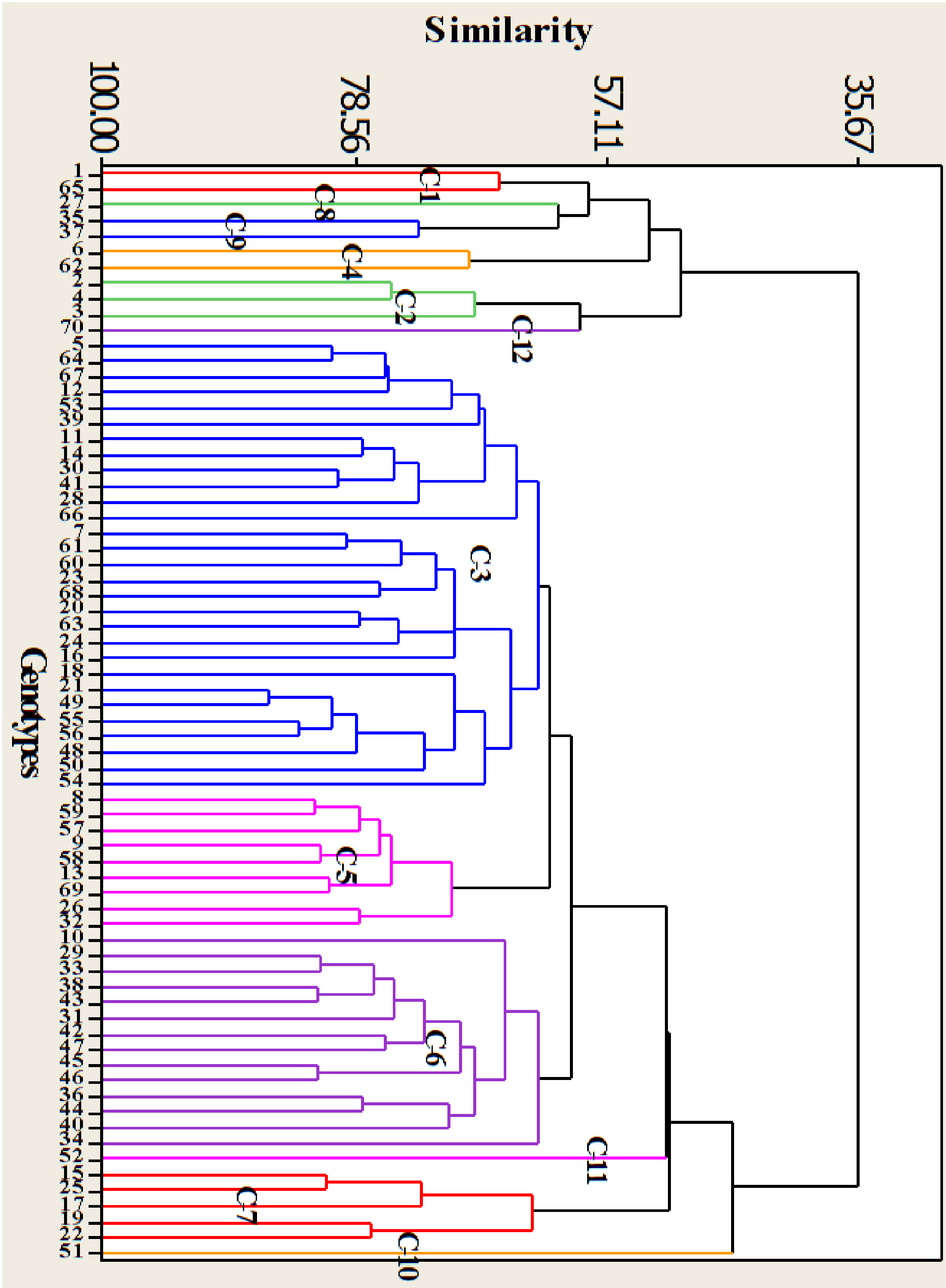

Figure 1. Dendrogram of seventy genotypes based on average linkage and Euclidean distance of 18 traits evaluated at two locations.

exhibiting the lowest value of height related traits (plant height, panicle length and culm length), basal culm diameters, number of total tillers, and lower number spikletes per main panicle and number of fertile tillers. On the other hand, these traits scored similarly low values in C-9. Contrary to this, the highest mean grain yield and

Table 2. List of tef genotypes grouped in 12 clusters (average linkage Euclidean distance cluster analyses) using 18 traits evaluated at two locations.

Cluster	No. of genotypes	Tef genotypes
1	2	Amh-ACC#1-L50 and Oro-ACC#27-L17
2	3	Amh-ACC#1-L51, Amh-ACC#1-L56 and Amh-ACC#1-L59
3	29	Amh-ACC#5-L4, Amh-ACC#6-L5, Amh-ACC#8-L20, Amh-ACC#8-L51, Amh-ACC#9-L4, Amh-ACC#11-L13, Amh-ACC#11-L22, Amh-ACC#12-L2, Amh-ACC#12-L4, Amh-ACC#14-L21, Amh-ACC#14-L23, Oro-ACC#8-L32, Oro-ACC#9-L34, Oro-ACC#16-L52, Oro-ACC#7-L15, Oro-ACC#1-L1, Oro-ACC#1-L21, Oro-ACC#1-L37,Oro-ACC#4-L47, Oro-ACC#8-L10, Oro-ACC#8-L17, Oro-ACC#8-L25, Oro-ACC#16-L42, Oro-ACC#16-L49, Oro-ACC#19-L36, Oro-ACC#27-L3, Oro-ACC#30-L7, Oro-ACC#30-L14 and Oro-ACC#30-L29
4	2	Amh-ACC#5-L63 and Oro-ACC#19-L32
5	9	Amh-ACC#6-L11, Amh-ACC#6-L41, Amh-ACC#8-L61, Oro-ACC#8-L13, Oro-ACC#9-L45, Oro-ACC#15-L8,Oro-ACC#15-L12, Oro-ACC#15-L30 and Quncho (DZ-Cr-387)
6	14	Amh-ACC#8-L13, Oro-ACC#8-L5, Oro-ACC#9-L37, Oro-ACC#11-L15, Oro-ACC#11-L26, Oro-ACC#16-L38,Oro-ACC#16-L51, Oro-ACC#7-L1, Oro-ACC#7-L19, Oro-ACC#9-L2, Oro-ACC#9L-5, Oro-ACC#9-L26,Oro-ACC#9-L28 and Oro-ACC#9-L38)
7	5	Amh-ACC#9-L45, Amh-ACC#11-L44, Amh-ACC#11-L36, Amh-ACC#12-L29 and Amh-ACC#14-L24
8	1	Oro-ACC#8-L30
9	2	Oro-ACC#11-L36and Oro-ACC#16-L48
10	1	Oro-ACC#4-L18
11	1	Oro-ACC#4-L25
12	1	Tsedey (DZ-Cr-37)

higher total biomass and straw yield means were noted for C-8. Similarly, C-9 holds tef materials which passed higher lodging index but lower total biomass and straw yield mean values.

Cluster 11 which comprised the solitary tef germplasm line Oro-ACC#4-L25, scored the lowest number of primary branches per main panicle and harvest index (Tables 3 and 4). Additionally, this cluster is characterized by tef genotype which had high mean value for height related traits, longer grain filling period and low grain yield. The last cluster (C-12) which contained only the single released variety "*Tseday*", scored the lowest values in phenological traits (days to maturity and grain filling period) and the highest value in total and fertile tiller numbers. Similarly, higher harvest index value, earliness in panicle emergence, lower total biomass, and straw yield were the characteristics features of this cluster. In addition, this specific character of the tef variety "*Tseday*" is in agreement with the inherent nature of the variety, because this variety is manly released for use in low moisture stress areas, and it possesses characteristics of earliness in phenological traits to escape terminal drought. Finally, most of tef germplasm lines which included in the two big clusters (3 and 5) had best performance with respect to most important traits under consideration. Those genotypes, therefore, can be recommended for further evaluation.

Inter cluster distances (D^2)

Most inter cluster distances showed highly significant ($P<0.01$) differences, while there were no significant inter-cluster distances between C-3 and C-5 and C-3 and C-6 (Table 5). In addition, the shortest ($D^{2=}$25.07) inter-cluster D^2 values were estimated between C-3 and C-5, while the largest ($D^{2=}$326.22) was estimated between C-8 and C-10, each of which contain one local tef germplasm line Oro-ACC#8-L3 and Oro-ACC#4-L18, respectively. Similarly, C-8 and C-11 comprised the second most divergent ($D^{2=}$275.22) groups and in this case Oro-ACC#8-L30 formed far inter-cluster distance with Oro-ACC#4-L25. In addition, the other clusters (C 8 and C 12) which in that order contain the solitary local tef germplam

Table 3. Means for the 12 clustered for the 18 quantitative traits of 70 Tef genotypes clustered into 12 groups.

Cluster	DH	DM	GFP	PH	PL	CL	NSPP	NPB	FBCD
C-1	40.38^{e}	93.50^{c}	53.13^{cd}	88.02^{de}	33.09^{def}	54.93^{de}	322.25^{bcd}	21.35^{cdef}	1.67^{def}
C-2	44.42^{cd}	97.17^{c}	52.75^{cd}	79.40^{f}	28.33^{fg}	51.07^{ef}	242.66^{d}	19.63^{ef}	1.59^{efg}
C-3	48.79^{b}	112.04^{ab}	63.25^{ab}	99.68^{bc}	37.12^{abcd}	62.56^{abc}	397.97^{abc}	25.76^{abc}	2.12^{abc}
C-4	47.75^{bc}	110.88^{ab}	63.13^{ab}	88.24^{de}	32.73^{def}	55.51^{de}	295.61^{cd}	20.33^{def}	1.93^{bcde}
C-5	49.44^{ab}	106.00^{b}	56.56^{bcd}	108.63^{a}	41.30^{a}	67.34^{a}	479.97^{a}	26.96^{ab}	2.28^{ab}
C-6	48.80^{b}	112.96^{ab}	64.16^{ab}	105.55^{ab}	38.74^{abc}	66.81^{a}	431.57^{ab}	28.60^{a}	2.37^{a}
C-7	47.30^{bc}	113.90^{a}	66.60^{a}	90.63^{d}	34.89^{cde}	55.75^{cde}	341.21^{bcd}	25.09^{abcd}	2.26^{abc}
C-8	44.25^{cd}	105.75^{b}	61.50^{ab}	74.99^{f}	27.13^{g}	47.85^{f}	247.35^{d}	21.80^{cdef}	1.25^{g}
C-9	47.13^{bc}	105.75^{b}	58.63^{bc}	81.49^{ef}	30.50^{efg}	50.99^{ef}	298.99^{cd}	21.16^{cdef}	1.54^{fg}
C-10	52.75^{a}	112.25^{ab}	59.50^{abc}	104.45^{ab}	37.70^{abcd}	66.75^{a}	486.97^{a}	23.54^{bcde}	1.90^{cdef}
C-11	44.75^{cd}	108.25^{ab}	63.50^{ab}	104.49^{ab}	40.50^{ab}	63.99^{ab}	383.71^{abc}	17.44^{f}	1.99^{bcd}
C-12	41.25^{de}	91.25^{c}	50.00^{d}	95.54^{cd}	35.80^{bcde}	$59.74a^{bcd}$	384.70^{abc}	23.70^{bcde}	1.67^{def}
LSD at 0.05	3.73	7.83	7.74	8.45	5.36	6.95	116.87	4.82	0.37

Entry	SBCD	LI	NTT	NFT	TSW	TBM	GY	SY	HI
C-1	1.71^{def}	75.35^{abc}	4.25^{c}	3.78^{cd}	0.28	11750^{cde}	4115^{a}	7635^{de}	34.50^{a}
C-2	1.73^{def}	66.00^{bcd}	5.92^{ab}	5.46^{b}	0.29	9458^{ef}	3288^{bcd}	6171^{e}	34.87^{a}
C-3	2.28^{ab}	69.45^{abcd}	4.07^{c}	3.57^{cd}	0.30	13519^{abc}	3994^{ab}	9525^{bc}	29.64^{bc}
C-4	1.86^{def}	68.38^{bcd}	5.46^{b}	4.42^{c}	0.30	14125^{abc}	4187^{a}	9939^{abc}	29.49^{bc}
C-5	2.40^{a}	65.86^{bcd}	3.48^{c}	3.07^{d}	0.30	14861^{a}	4310^{a}	10551^{ab}	29.02^{bc}
C-6	2.46^{a}	59.09^{d}	3.58^{c}	3.24^{d}	0.31	11813^{cde}	3145^{cd}	8668^{cd}	26.60^{cd}
C-7	2.26^{abc}	63.75^{cd}	3.58^{c}	3.16^{d}	0.30	8800^{f}	2569^{d}	6231^{e}	28.61^{bc}
C-8	1.55^{f}	73.75^{abc}	3.25^{c}	3.10^{d}	0.31	14375^{ab}	4484^{a}	9892^{abc}	31.62^{ab}
C-9	1.61^{ef}	77.25^{ab}	3.88^{c}	3.66^{cd}	0.27	9875^{def}	3157^{cd}	6719^{e}	31.90^{ab}
C-10	2.02^{bcd}	81.50^{a}	6.15^{ab}	5.70^{ab}	0.30	15250^{a}	3671^{abc}	11579^{a}	23.99^{d}
C-11	1.93^{cde}	72.00^{abc}	4.21^{c}	3.34^{d}	0.36	12125^{bcd}	2789^{d}	9336^{bcd}	22.88^{d}
C-12	2.02^{bcd}	73.50^{abc}	6.75^{a}	6.50^{a}	0.30	9250^{f}	3114^{cd}	6136^{e}	34.63^{a}
LSD at 0.05	0.34	12.54	1.20	1.03	NS	2400.4	815.38	1830	4.02

Genotypes followed by the same letter are not significantly different at $P < 0.05$.

Table 4. The Generalized Squared inter cluster distance of 18 quantitative traits of 70 tef genotypes evaluated over two locations

Cluster	1	2	3	4	5	6	7	8	9	10	11
1	0										
2	54.06^{**}	0									
3	94.01^{**}	140.73^{**}	0								
4	70.74^{**}	87.85^{**}	52.40^{**}	0							
5	133.33^{**}	219.18^{**}	25.07ns	117.65^{**}	0						
6	180.63^{**}	232.30^{**}	26.76ns	131.45^{**}	32.29^{*}	0					
7	125.67^{**}	144.76^{**}	36.70^{**}	76.78^{**}	97.44^{**}	46.22^{**}	0				
8	100.46^{**}	124.82^{**}	127.34^{**}	103.99^{**}	216.47^{**}	233.95^{**}	155.42^{**}	0			
9	48.40^{**}	45.35^{**}	80.04^{**}	55.41^{**}	158.72^{**}	159.90^{**}	73.87^{**}	66.81^{**}	0		
10	190.02^{**}	228.77^{**}	112.33^{**}	161.78^{**}	95.21^{**}	132.37^{**}	202.01^{**}	326.22^{**}	200.02^{**}	0	
11	145.08^{**}	210.71^{**}	86.13^{**}	138.72^{**}	89.65^{**}	84.52^{**}	110.17^{**}	275.22^{**}	166.59^{**}	86.23^{**}	0
12	106.84^{**}	62.87^{**}	190.60^{**}	188.98^{**}	226.55^{**}	250.08^{**}	214.67^{**}	273.28^{**}	131.61^{**}	184.92^{**}	199.21^{**}

lines Oro-ACC#8-L30 and the released tef variety "*Tseday*" constituted the third most divergent (D^2=273.28) group, while the fourth most divergent (D^2 = 250.08) groups were cluster C-6 which constituted local tef

Table 5. Eigenvectors and eigenvalues of the first five principal components for 18 traits of 70 tef genotypes evaluated at Debre Zeit and Holetta during the 2015 main cropping season

Traits	PC1	PC2	PC3	PC4	PC5
Days to heading	-0.223	-0.001	-0.159	-0.074	-0.401
Days to maturity	-0.229	0.157	-0.539	-0.117	-0.042
Grain filling period	-0.163	0.19	-0.57	-0.103	0.153
Plant height	-0.328	-0.077	0.196	-0.002	0.09
Panicle length	-0.295	-0.109	0.157	0.054	0.129
Culm length	-0.298	-0.043	0.192	-0.039	0.049
Number of spikletes per panicle	-0.286	-0.114	0.193	-0.13	-0.076
Number of primary panicle branches	-0.259	0.087	0.232	-0.146	0.062
First basal culm diameter	-0.305	0.182	0.109	-0.099	0.169
Second basal culm diameter	-0.311	0.127	0.122	-0.186	0.12
Lodging index	0.099	-0.33	-0.245	0.019	0.318
Number of total tillers	0.193	-0.184	0.029	-0.634	-0.046
Number of fertile tillers	0.200	-0.169	0.063	-0.632	-0.059
Thousand seed weight	-0.123	-0.023	-0.136	-0.179	0.639
Total biomass	-0.202	-0.456	-0.132	0.052	-0.152
Grain yield	-0.084	-0.523	-0.077	0.162	0.078
Straw yield	-0.233	-0.389	-0.144	0.002	-0.235
Harvest index	0.214	-0.213	0.117	0.142	0.368
Eigenvalue	7.1661	2.8857	1.6609	1.4726	1.1191
Percent of total variation explained	39.8	16	9.2	8.2	6.2
Cumulative percent of total variance explained	39.8	55.8	65.1	73.3	79.5

germplasm lines mostly collected from Jimma and Horo Gudru Zones of Oromya region and C-12 containing the released variety "*Tseday*".

Overall, the released variety "*Tseday*" and the locally collected tef germplasm line (Oro-ACC#8-L30) had large genetic distance with most of the other clusters in this experiment. On top of this, the high inter-cluster distances noted among different clusters may result from locations in which those tef germplasms were collected and different genetic background of those tef materials (released vs. local tef germplasm lines). Generally, a wide generalized squared distance (D^2) serves as a better indicator for selecting crossing materials. Consequently, most divergent clusters noted in this study are expected to give maximum genetic recombination and genetic variation in the subsequent segregating generations.

Principal components analysis

The first five principal components (PCs) having a minimum eigenvalue of one accounting for 80% of the total variability observed among the 70 tef test genotypes (Table 6). Of these, the first PC alone explained about 40% of the total variance mainly due to the variations in height related traits (that is, plant height, panicle length, and culm length), first and second basal culm internode diameters, and number of spiklets and primary branches per main panicle. On the other hand, even if relatively lower percent variation was explained by PC 1 in the studies of Assefa et al. (1999, 2000, 2001a, b), most of the traits responsible for variation in PC 1 showed similarity with the current study. In addition, another experiment of Assefa et al. (2003) with seventeen traits of 60 tef germplasm population showed similarity in both percent variation explained, and the traits contributing to the variation in PC 1. However, the first PC in the studies of Adnew et al. (2005) and Jifar et al. (2015) explained relatively high proportion of the variation than that in this study.

Unlike, the first PC, most yield related traits like grain yield, total biomass, straw yield, harvest index and lodging index contributed to about 16% of the gross variation accounted for by the second PC (Table 6). This is line with results of the second PC of Assefa et al. (2000). However, slightly larger variability was reported by Assefa (1999, 2001b, 2003) in other studies, whereas Assefa et al. (2001a) and Adnew et al. (2005) reported that the second PC, respectively explained 7.1% more and 5.6% less variability than that in the current study. Furthermore, about 9, 8 and 6% of the total genotype variance was explained on the basis of the third, fourth and fifth PCs, respectively (Table 6). The former was largely due to the variations in phenological traits (that is, days to maturity and grain filling period), lodging index and number of primary panicle branches, whereas, number of total and fertile tillers were the primary

Table 6. Eigenvectors and eigenvalues of the first five principal components for 18 traits of 70 tef genotypes evaluated at Debre Zeit and Holetta during the 2015 main cropping season.

Traits	PC1	PC2	PC3	PC4	PC5
Days to heading	-0.223	-0.001	-0.159	-0.074	-0.401
Days to maturity	-0.229	0.157	-0.539	-0.117	-0.042
Grain filling period	-0.163	0.19	-0.57	-0.103	0.153
Plant height	-0.328	-0.077	0.196	-0.002	0.09
Panicle length	-0.295	-0.109	0.157	0.054	0.129
Culm length	-0.298	-0.043	0.192	-0.039	0.049
Number of spikletes per panicle	-0.286	-0.114	0.193	-0.13	-0.076
Number of primary panicle branches	-0.259	0.087	0.232	-0.146	0.062
First basal culm diameter	-0.305	0.182	0.109	-0.099	0.169
Second basal culm diameter	-0.311	0.127	0.122	-0.186	0.12
Lodging index	0.099	-0.33	-0.245	0.019	0.318
Number of total tillers	0.193	-0.184	0.029	-0.634	-0.046
Number of fertile tillers	0.200	-0.169	0.063	-0.632	-0.059
Thousand seed weight	-0.123	-0.023	-0.136	-0.179	0.639
Total biomass	-0.202	-0.456	-0.132	0.052	-0.152
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Straw yield	-0.233	-0.389	-0.144	0.002	-0.235
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Percent of total variation explained	39.8	16	9.2	8.2	6.2
Cumulative percent of total variance explained	39.8	55.8	65.1	73.3	79.5

contributors to the variation explained by PC4. Likewise, the contribution of PC5 resulted chiefly from variations in characters like thousand seed weight, days to heading, harvest index, lodging index, and straw yield.

Conclusion

The grouping of tef genotypes into twelve clusters at 73% similarity level confirmed the existence of important trait variability among tef genotypes that could be recommended for further evaluation and regarding conservation of the indigenous tef genetic resources in Ethiopia, unclear patterns of genotypes grouping in respect to their origin in this experiment showed the importance to address each tef growing zones of the country. Height related traits (that is plant height, panicle length and culm length), first and second basal culm internode diameters and number of spiklets and primary branches per main panicle contributed more for the 40% variation explained by the first PC. In addition, most of tef germplasm lines which were included in the two big clusters (3 and 5) had best performance with regard to most important traits under consideration. Moreover, the higher mean values of most yield related traits of Oro-ACC#8-L30 (C-8) and earliness in maturity, higher tiller number and harvest index of "*Tseday*"(C-12), in line with their large genetic distance with most of the other clusters could make them source of elite materials for future use.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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