Genetic diversity of Tef [Eragrostis Tef) Zucc. Trotter] Genotypes Based on Cluster and Principal Component Analyses for Breeding Strategies

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ABSTRACT

Knowledge on nature and magnitude of variation in tef breeding materials is of great importance to develop varieties for high yield which combine other desirable traits. Field experiment was conducted in 2015 cropping season at Maysiye, northern Ethiopia,to determine the genetic diversity among 49 tef genotypes. The genotypes were planted in triple lattice design and evaluated for 14 traits including yield, yield related traits. Genetic analyses were carried out for 12 traits for which the genotypes exhibited significant differences in analysis of variance results The 49 genotypes were grouped into five clusters based on Euclidean distance matrix grouped of which the first cluster consisted of 30, second and third clusters constructed with 8 and 9 genotypes, respectively. The other two clusters were consisted of one genotype. Each genotypes within and between clusters showed wide range of Euclidean distances and clusters consisting of genotypes with desirable traits suggested the higher chance of developing varieties. Moreover, the nine genotypes in the third cluster had the most desirable traits in the study area. Four principal components (PCs) were extracted about 78.46% of the entire variation of tef genotypes variance ranged from 9.59 to 38.93%. Therefore, further evaluation of these genotypes across locations and seasons can be recommended to recommend the best performing ones to the study area.

Keywords: Cluster, Euclidean distance, *principal components (PCs)*

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Introduction

Tef, [Eragrostis tef (Zucc.) Trotter] which has genetic origin and center diversity in Ethiopia (Vavilov, 1951). Tef is an important staple cereal crop in Ethiopia occupying more than three million hectare of land. It is first in area coverage but second and last in production and productivity respectively, from cereals under production in Ethiopia. It is grown by over 6.6 million households, and constitutes the major staple food grain for over 50 million Ethiopians (CSA, 2015).Tef has remarkable genetic traits useful for most Ethiopian farmers to cope with erratic climatic conditions, generate household income, and fulfilling nutritional needs (Assefa et al., 2015).Tef is also considered to be a healthy food since its grain is free of gluten (SpaenijDekking et al., 2005). In addition to this, it has relatively few disease and insect pest problems; at least, in its major production belts (Kebebew, 2009).This implies that tef is very important in the overall national food security of the country (Kebebew et al., 2013).

In centeral Zone, tef ranks first in area coverage and production, but low in productivity. Even though tef has numerous merits and considerable economic significance in Ethiopia, the national average grain yield of tef is relatively low (1575 kg ha-^{1}) (CSA, 2015). However, Tareke *et al*. (2013) reported that the tef yields of 4000 kg ha^{-1} and 2500 kg ha^{-1} on research fields and on farmers' fields, respectively.

Tef's major yield limiting factors are the low yield potential of landrace tef, lack of cultivars tolerant to lodging, drought and pests (Assefa *et al.*, 2011). The presence of diverse genotypes in tef is a good opportunity to select genotypes for traits of interest. However, it is necessary to have good knowledge of nature and magnitude of variation existing in available plant breeding materials (Khan *et al.,* 2010; Kotal *et al.,* 2010).

Dissimilarity will always exist among individuals in a population and assessing the origin and magnitude of variability is the key to success in a crop improvement program (Poehlman, 1979; Welsh, 1981). The genetic distance thus reflects the expected mean number of changes per site that have occurred, since two sequences diverged from their common ancestor. Euclidean distance developed by Sneath and Sokal (1973), has been used to classify the divergent genotypes into different groups. According to Habte *et al*. (2015) tef genotypes were clustered in to seven.

The diversity of tef genotypes cannot be reduced into a few numbers of groups (Mengesha *et al*., 1965). The genetic improvement through hybridization and selection depends on the extent o f genetic diversity between parents. Crossing for desirable traits can be successful between clusters with the highest and the lowest divergent cluster (Ayalneh *et al*. ,2012).

Principal component analysis (PCA) can be used to reduce the dimensions of a data set. Dimension reduction is analogous to being philosophically reductionist: It reduces the data down into its basic components, stripping away any unnecessary parts. Standardization of features will have an effect on the outcome of a PCA (assuming that the variables are originally not standardized). Theoretically, the corresponding PC has inherently more information than would any single variable alone (Iezzoni and Pritts, 1991).

The principal components is used to interpreted based on finding which variables are most strongly correlated with each component i.e, which of these numbers are larger in magnitude, the further from zero in either positive or negative direction. Having correlation value above 0.5 is deemed important (Aremu, 2011). According to Habtamu *et al*. (2011) Eigenvalues greater than one were only for the first three PCs, which together explained 75% of the observed variation. Plaza-Wüthrich *et al.*(2013) observed four principal components (PCs), having eigenvalues between 5.16 and 1.12. According to Habte *et al*. (2015) report the first three principal components (PCs) with eigenvalue greater than one contributed for 78.3 % of the entire phenotypic variation observed among the 36 tef genotypes. The aim of the present of study was to determine the genetic diversity among 49 tef genotypes.

MATERIALS AND METHODS

The field experiment was carried out at Axum Agricultural Research Center (AxARC) during 2015 main cropping season at the substation Maysiye (14^0 6'43'' North and 38^0 36 '41 '' East, altitude of 2200 masl) in Tahitaey Maichew district, in central zone of Tigray, Ethiopia. The substation is located 17 km west of Axum town. Axum is located at 241 km from Mekelle and 1024 km from Addis Ababa. The annual rainfall received by the experimental site during the main cropping season was 613.92 mm. Moreover, the mean average annual minimum and maximum temperature was 12.16 ^oC and 26.78 ^oC respectively. The area is characterized by monomodal rainfall pattern that the main rainy season, locally called *kiremty*, extends from July to end of August.

The experimental material consisted of 32-released tef varieties, 12 candidate genotypes, three accessions and two local check farmers' cultivars obtained from Deber Zeit Agricultural Research Center (DZARC), Axum Agriculture Research Centers and farmers, respectively. The materials were sown in the third week of July, 2015. The experiment was laid out in 7x7 triple lattice designs. Each genotype was sown in three rows spaced at 0.2m on 2m x 0.6m plot size, while plots, blocks and replications were spaced at 1m, 0.5m and 1.5m, respectively.

In accordance with the recommended tef seed rate of 10 kg/ha (AxARC, 2013/14), 1.2 g of seeds per plot was hand-drilled in rows .Fertilizer rates of 60 kg N and 40 kg P_2O_5 $ha^{-1}$was used (Seyfu, 1997). The first urea application was made two weeks after seed germination and the second split was applied two weeks later after the first application. All other cultural crop management practices were applied as per the recommendation for tef production.

Data Collected

Data were collected on 14 traits. The data on days to 50% emergency, days to heading, days to maturity, lodging index, above ground biomass and grain yield were collected on plot basis. Data for plant height, panicle length, peduncle length, productive tiller and culm length were collected on the basis of randomly selected ten plants from the three rows. In addition to this thousand seed weight was measured by taking randomly 1000 seed from each plot. Whereas, grain filling period and harvest index were obtained from others measured data.

- Days to emergence:- The numbers of days taken from sowing to 50% of seedlings emerged in each plot.

- Days to heading: - Number of days from 50% of the emergence plants in the plots to 50% plants in the plots showed panicle emergence.

- Days to maturity:-Number of days from emergence of 50% plant on the plot to the day of 90% plants in the plot reached physiological maturity.
- Grain filling period:- The period from heading to maturity.

Data collected based on ten randomly selected individual plants

- Plant height (cm):-Height of ten randomly selected plants from the whole plot measured from ground level to the tip of the main shoot panicle at maturity and the average were considered for statistical analysis. Plant height was divided into culm and panicle length
- Panicle length (cm):- Panicle length from the base of the panicle to the tip of panicle and with ten randomly selected panicles averaging for statistical analysis
- Culm length (cm):- Plant height minus the panicle length of the plant.
- Peduncle length (cm**):-** The inter-nod of near to the panicle.
- Productive tillers:- plants raised from base o the main plant which give grain yield.
- Lodging index (%):- Lodging was estimated using the method of Caldicott and Nutall (1979) which gives an index based on both the degree (angle of leaning) on a 0-5 scale and severity percent for each degree of lodging. Where zero indicates plants in upright position and five for plants lying flat on the ground for each plot

  $$\text{Lodging index} = \frac{\text{Sum(Lodging scores or degree X the respective percentage area lodged)}}{5}$$

- Above ground biomass (kg ha^{-1}):- The total above ground biomass for the entire plot. After ten days of sun drying.
- Grain yield (kg ha^{-1}):- The weight of the grain harvested from entire plot.
- 1000-seed weight:-The weight of 1000 kernels sampled from the each plot.
- Harvest index (%):- The ratio of grain yield to above ground biomass of the entire plot.

$$\text{Harvest Index (\%)} = \frac{\text{Grain yield}}{\text{Above Ground Biomass}} * 100$$

Genetic Distance and Clustering

Cluster analysis was made using Euclidean Distance and UPGMA method. Statistical clustering analyses were performed using the SPSS 16.0 statistical package. Euclidean distance (ED) was computed from all data collected for tef genotypes after standardization (Z score) as described by (Sneath and Sokal, 1973),

$$EDjk = \sqrt{\sum_{i=1}^{n}(Xij - Xik)2}$$

where ,

EDjk = distance between tef genotypes j and k; xij and xik = phenotype traits values of the i^{th} character for the genotypes j and k, respectively; and n = number of phenotype traits used to calculate the distance.

The results of cluster analysis were presented in the form of dendrogram. In addition, mean ED was calculated for each tef genotypes by averaging of a particular genotype to the other varieties and genotype. Linkage method or measuring association between clusters was calculated by average linkage i.e this method involves looking at the distance between all pairs and averages all of these distances. This also called UPGMA Unweighted Pair Group Mean Averaging. The calculated average distance (ED) was used to estimate which varieties and genotype(s) is closest or distant to others.

Principal Component Analysis

Principal component analysis was performed using the SPSS 16.0 statistical package and method of correlation matrix. The data were standardized to mean zero and variance of one before computing principal component analysis.

RESULTS AND DISCUSSION

Analysis of Variance

The analysis of variance results for the 14 traits of 49 tef genotypes are presented in Table 1.The results showed the presence of highly significant ($P \leq 0.01$) differences among tef genotypes; for,days to heading, plant height, panicle length, culm length, grain filling period, productive tiller, days to maturity, grain yield, above ground biomass, lodging index, thousand seed weight and harvest index. However, there were no statistical significant differences among genotypes for days to 50% emergence and peduncle length. The analysis of variance results showed the presence of considerable variations among the 49 tef genotypes for most of the traits suggesting the higher chance of obtaining the genotype(s) for trait of interest.

Different authors also reported considerable genetic variability for grain yield and its components in tef (Seyfu, 1993; Kebebew *et al*., 2000, 2001, 2002; Habtamu *et al*., 2011; Plaza-Wüthrich *et al*. 2013; Motuma *et al*., 2015). However, the results of the present study is in contrast to the findings of Habtamu *et al*. (2011) who reported non-significant differences among tef genotypes tested in east Gojam for yield, panicle length, biomass yield and harvest index. Kebebew *et al*. (2001) repoted non-significant difference among tef genotypes for peduncle length in a combine analysis over locations. On the other hand, Motuma *et al*. (2015) reported significant differences among tef genotypes for peduncle length which was in contrast to the current study results. The presence of variations among genotypes for most of the traits indicates the potential to improve the crop through selection.

Table 1. Mean squares from analysis of variances for 14 traits of 49 tef genotypes tested at Maysiye in 2015

Source of variation	Mean square						R^2(%)	RE to RCBD (%)	CV(%)
	Replication (2)	Treatments(48)		Block with in reps (adj)(18)	Error				
		Un-adj	Adj		Intra block(78)	RCBD(96)			
Days to 50% emergency	4.5782ns	2.237	2.40ns	5.5676	2.92	3.4185	41	107.40	27.51
Grain filling period	44.45**	56.53	53.45**	7.2945	7.27	7.27	81	100.00	6.76
Days to heading	44.78**	90.26	90.29**	9.3095	8.97	9.04	85	100.02	6.81
Days to maturity	18.12*	32.31	31.54**	4.7542	5.12	5.06	79	98.6406	2.63
Plant height(cm)	180.6**	63.65	62.82**	18.6983	18.49	18.53	68	100.00	4.91
Panicle length(cm)	42.57*	38.57	36.03**	7.4763	9.88	9.43	70	95.4287	7.43
Peduncle length (cm)	0.80ns	2.765	2.61ns	0.8576	1.76	1.59	47	90.3440	8.14
Culm length(cm)	70.62**	27.23	26.36**	21.1397	13.490	14.92	54	103.60	8.28
Lodging index(%)	202.64ns	264.71	247.68**	72.6784	100.84	95.56	62	94.7632	34.35
Productive tillers	0.112ns	3.73	3.63**	0.668	0.66	0.661	74	100.00	24.54
Grain yield(kg ha^{-1})	393954*	259848	245521.22**	166522	110676	121147	57	102.99	17.75
Thousand seed weight(g)	0.01ns	0.0186	0.01**	0.007940	0.008	0.01	50	99.0858	25.73
Above ground biomass(kg/ha)	1538699ns	4719736	4659012.7**	1140450	1346059	1307508	67	97.1360	12.75
Harvest index(%)	49.91**	22.783	21.43**	11.0395	9.40	9.7154	59	100.47	14.180

ns, *, and **, non significant, significant at $P \leq 0.05$ and $P \leq 0.01$, respectively. Number in parenthesis represent degree of freedom. Un.adj and adj = unadjusted and adjusted mean squares, respectively RCBD= Randomized completed block design, RE to RCBD =Relative efficiency to randomized completed block design CV= Coefficient of variation, R^2 (%)= R-square by percent

Genetic Divergence Analysis

Cluster Analysis of Genotypes

Genetic relationships among 49 tef genotypes, based on 12 quantitative traits in the form of dendrogram using Unweighted Pair-group Method with Arithmetic Means (UPGMA) are presented in Figure 1 and the mean values for each cluster is presented in Table 4. Clustering resulted in the formation of five groups. The first cluster consisted of 30 or 61.224% of the tested genotypes, whereas, the third cluster consists nine (18.367%) of the tested tef genotypes. The second cluster contained of eight (16.326%) genotypes, however, the fourth and fifth clusters were solitary (ungrouped clusters) that were constructed each with single genotype (2.04%). The 32 released tef varieties (released 1970 to 2014 year of release) included in the experiment distributed in all clusters, and the 13 inbred lines of tef were grouped in cluster I and II the standard checks Quncho and Kora grouped in cluster IV and cluster II, respectively. On the other hand, the local check was grouped under cluster III. This indicating the released varieties had wide genetic distance to be clustered in different groups.

Cluster one which consisted majority of the genotypes had wide range of mean values differences for most of the traits. This cluster was characterized by long days to heading, days to maturity, high plant height, panicle length. Therefore, the cluster is containing genotypes with traits that are not desirable in the study area since the area is experienced erratic rain fall and terminal droughts (the main cropping season start late and the rainfall stop before the expected end of the season). However, there is a possibility of selecting genotypes from the cluster since the cluster was subdivided into many sub-groups depending on similarity of genotypes for different traits in sub-group and differences with other sub-groups members. The second cluster was characterized with intermediate days to heading, days to maturity, plant height, lodging index, productive tillers and grain yield.

The third cluster was characterized by short days to heading, days to maturity and maximum number productive tillers with higher grain yield. This cluster consisted of genotypes that had most of the desirable traits, which that can be considered in selection of tef genotypes/varieties for the study area. For the study area, tef genotypes with short days to heading and days to maturity having higher grain yield were preferable. The genotypes in this cluster had mean plant height lower than mean plant height of three clusters and consequently had lower mean above ground biomass yield than four clusters mean values. In the study area, tef is not only needed for grain yield but also highly valuable for animal feed, and used to reinforce mud and plaster the walls of tukuls and local grain storage facilities called *gotera.* Therefore, the above ground biomass yield of this cluster genotypes might need to be improved through hybridization (crossing of genotypes with others having highest plant height). Habte *et al*.(2015) studied tef genotypes and he found only one tef genotype that had the characteristics of cluster three genotypes.

From the 49-tef genotypes, Quncho, Holetta-key were ungrouped. This might be due to that Quncho had the highest and Holetta Key had the lowest mean above ground biomass. Quncho that had highest mean values for above ground biomass, plant height, days to heading and culm length. On the other hand Holetta Key was one of ungrouped genotype that had low mean values for grain yield, above ground biomass and days to heading.

The extent of diversity present between genotypes determines the extent of improvement gained through selection and hybridization. The more divergent the two genotypes are the more will be the probability of improving through selection and hybridization. For instances, genotypes in cluster three were characterized by early maturing and short grain filling period but had low mean values for above ground biomass, therefore, it is possible to cross with Quncho characterized by high above ground biomass but long maturing and grain filling period. The most desirable traits in this study area were short days to heading, days to maturity and maximum number of productive tillers with higher grain yield and genotypes under cluster three were characterized with these traits. Therefore, these genotypes can be considered for further evaluation to select the best genotypes that can be recommended as variety in the study area where erratic rainfall and terminal drought are the major constraints of tef production. The clustering of tef genotypes explained the homogeneity of the characters within the cluster and heterogeneity of characters between clusters of tef genotypes. Thus, it can be used to identify characters of interest from one cluster and to make crossing with genotypes in other clusters that had contrasting characters. Even though, the clustering of this study showed the similarity and difference within and between clusters and the tef genotypes grouped under five clusters depending on the mean values for the studied traits, it might not be same from season to season as Kebebew *et al*.(1999) reported tef is complex crop.

The genetic distances and clustering of tef genotypes were also studied by other workers. The researchers used different tef genotypes both in number and genetic background. Among the researchers that deal with clustering of tef genotypes, some authors reported the tef genotypes were classified into six clusters (Kebebew *et al.*, 2000; Ayalnhe *et al*., 2012; Habtamu *et al.*, 2011; Plaza-Wüthrich *et al*., 2013). Some of these authors showed that from their clusters was containing genotypes characterized with short average of days to heading, days to maturity and short plant height and panicle length that had similarity with cluster third in the present study. But Habtamu *et al*. (2011) reported result of clustering different from the current study result that the improved varieties Quncho and Estub were grouped under one cluster.

Table 2. Range, mean performance and standard deviation of five clusters consisting 49 tef genotypes for 12 traits as at tested at Maysiye in 2015

Traits	Cluster I			Cluster II			Cluster III			Cluster IV	Cluster V
	Range	Mean	SD	Range	Mean	SD	Range	Mean	SD	Mean	Means
DH	48.67-38.33	43.95	2.60	56-47	52.67	2.99	43-31.33	37.58	3.18	52.00	37.54
DM	89.67-80.33	85.74	2.30	88-82.33	85.10	1.94	83.33-74.67	79.45	2.42	87.67	82.02
PH	93.83-81.2	87.88	3.11	97.9-85.5	91.38	4.16	85.63-77.5	81.99	2.92	99.10	81.72
PAN	47.3-39	42.67	2.15	47.17-40.13	43.96	2.82	38.93-32.86	36.06	2.28	47.33	40.00
CL	50.93-39.5	45.28	2.85	51.67-44.9	47.46	2.52	51.73-41.67	46.13	2.93	51.77	40.00
GF	45.33-37	41.76	2.43	36-29.33	32.20	2.59	44-39.67	41.88	1.48	35.67	44.48
LD	46.53-12	28.49	8.29	25.67-16	20.63	3.47	55.33-21.33	34.75	12.64	19.67	34.94
PRT	36.67-21.33	29.86	3.87	33-21.67	25.23	4.40	70-36	52.76	11.20	33.00	41.79
GY	2335.6-1385.8	1920.48	274.55	2151.1-1573.6	1818.24	198.53	2377.2-2017.5	2183.20	127.27	2130.80	1011.10
BIO	10555.6-6222.2	8836.80	1100.49	10555.6-7777.8	9022.22	1081.24	10555.6-8333.3	9343.43	667.71	11444.40	4369.20
HI	27.79-14.13	21.83	3.00	22.25-14.47	19.76	2.50	25.27-20.17	22.91	1.61	20.63	23.40
TSW	0.5-0.233	0.35	0.07	0.5-0.27	0.36	0.07	0.27-0.5	0.34	0.06	0.53	0.30

DH=days to heading, DM=days to maturity, PH=plant height, PANL=panicle length, CL=culm length GF=grain filling period LD=lodging index, PRT=productive tiller, GY=grain yield, BIOM= above ground biomass, HI=harvest index and TSW=thousand seed weight, SD=standard deviation,

Table 3. List of genotypes in five clusters grouped at cut point five distance for 12 traits as tested at Maysiye in 2015

Cluster	Number of genotype	Genotype
Cluster I	30	Gibe, Me hare, Zobel, Etsub, Menagesha, Laketch, Ajora, Genete, *RIL -65* , RIL157, Gimbichu, Magna, Gola, 9441, Wellenkomi, *RIL-107,* Gerado, Dukem, Dega Tef, Yilmana, Guduru, *RIL-96, RIL-129A,* Asgori, Key Tena , Koye, Ambo Toke, Ziquala, Boset and Melko
Cluster II	8	*RIL-190, RIL-101C, RIL-86, RIL-109A,* Kora, *RIL-52, RIL-15A and RIL-91Ap*
Cluster III	9	Tsedey, Amarach, Simada, Zezew, Acc. 13 AJ, Acc.17-WJ, Dima, Zagre and Enatit
Cluster IV	1	DZ-Cr-387RIL355 (Quncho)
Cluster V	1	DZ-01-2053(Holetta Key)

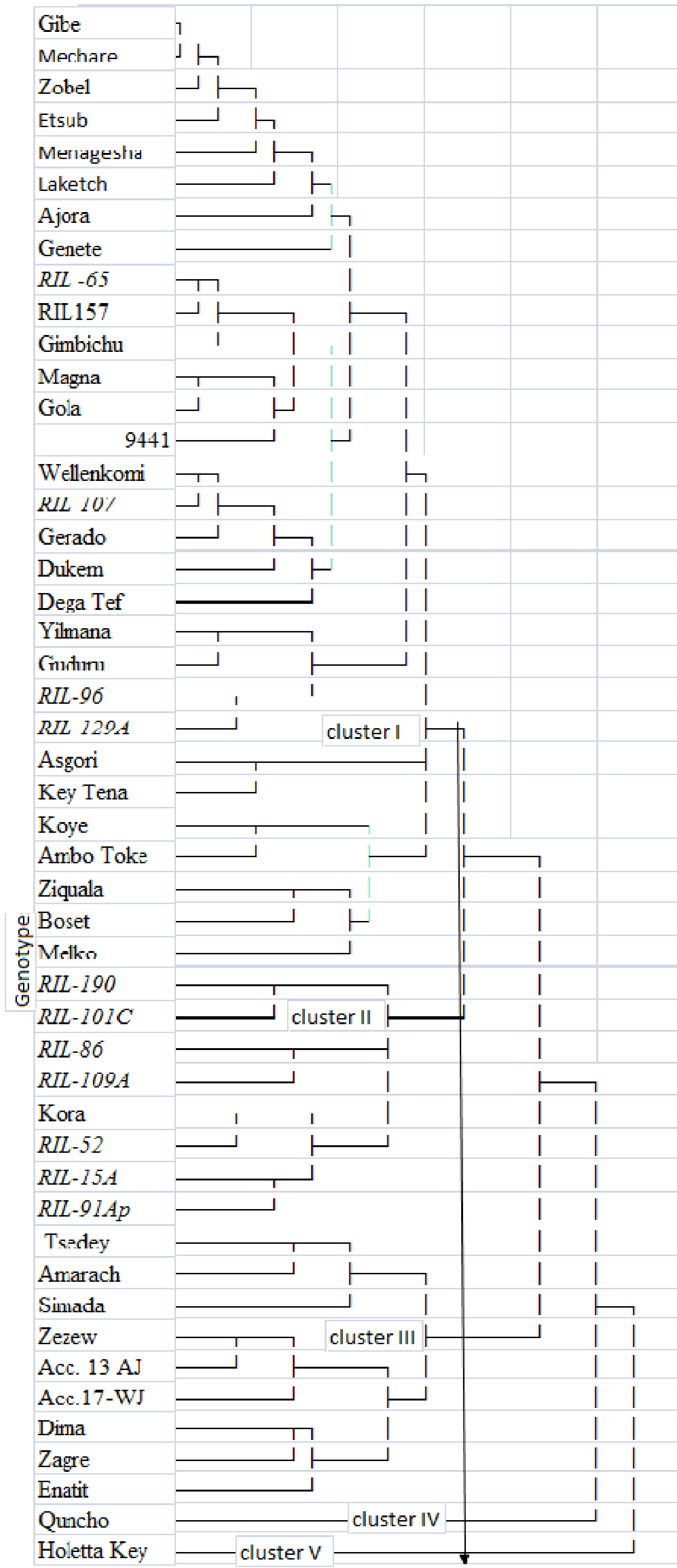
Gibe
Mechare
Zobel
Etsub
Menagesha
Laketch
Ajora
Genete
RIL -65
RIL157
Gimbichu
Magna
Gola
9441
Wellenkomi
RIL 107
Gerado
Dukem
Dega Tef
Yilmana
Guduru
RIL-96
RIL 129A
Asgori
Key Tena
Koye
Ambo Toke
Ziquala
Boset
Melko
RIL-190
RIL-101C
RIL-86
RIL-109A
Kora
RIL-52
RIL-15A
RIL-91Ap
Tsedey
Amarach
Simada
Zezew
Acc. 13 AJ
Acc.17-WJ
Dima
Zagre
Enatit
Quncho
Holetta Key
Genotype
cluster I
cluster II
cluster III
cluster IV
cluster V

Figure 1. Dendrogram generated based on UPGMA clustering method depicting relationship among 49 tef genotypes based on 12 traits.

Genetic Distance

There are various measures to express dissimilarity between pairs of objects. Euclidean distance (or straight-line distance) is the most commonly used(Annoymous, n.d). The genetic distances among 49 tef genotypes were estimated using Euclidean distance and are presented in Appendix Table 2. The summary of genetic distances within clusters is presented in Table 4. Euclidean distance ranged from 3.82 to 4.13 with mean and standard deviation of 0.77 and 1.12, respectively. The most distant genotypes were *RIL-101C* and PGRC/E 205396 (Ajora) (7.6). The lowest genetic distance was computed between Acc. 205953 (Mechare) and DZ-Cr-255 (Gibe) (1.36) .The maximum dissimilarity showed that there is a genetic distance between the pair tef genotypes. While, the minimum dissimilarity indicates the presence of few variation between the tef genotypes. Relatively it was observed wide range of genetic distance in pairs of tef genotypes with *RIL-101C* that indicating the divergence this genotype might be important for the development of tef variety through hybridization. The source of high divergence of *RIL-101C* might be due to its highest days to heading and maturity as compared to other tef genotypes(appendixes table 2).

On the basis of mean Euclidean distance of clusters, cluster II (4.125) followed by cluster I (3.936) had relatively high mean with standard deviation of 1.12 and 1.03, respectively, indicating genotypes grouped under these clusters had relatively wide range of distances than other clusters (Table 4). Genotypes grouped in cluster three (3.82) with lowest standard deviation of 0.77 indicating members were close each other and the cluster was closet to other clusters. The genotypes with high and low mean Euclidean distances suggested they were genetically most distant and not genetically closest to others, respectively. This significance that crossing of genotypes from the closest genotypes might not give heterotic F_1 and narrow range of variability in the segregating F_2 population. Whereas, the crossing of genotypes from most distant to other genotypes might give heterotic F_1 and wide range of variability in the segregating F_2 population. Therefore, hybridization between the genetically diverse parents in further breeding programs may produce large variability and better recombinants in the segregating generations. In contrast to findings Ayalneh *et al*. (2012) reported highest intra cluster distance with value of 7.78. The lower intra cluster distance indicates that low chance of obtain well performing output of high bred tef material for the improvement tef production.

Table 4. Maximum, minimum, standard deviation and mean of three clusters consisted of 47 out of 49 tested tef genotypes

Cluster	Maximum	Minimum	Standard Deviation	Mean of cluster
Cluster I	7.60	1.36	1.12	3.94
Cluster II	6.31	2.35	1.03	4.13
Cluster III	5.06	2.70	0.77	3.82

Note: Cluster IV and V were solitary (ungrouped) consisted each one genotype.

Principal Component Analysis

Principal component analysis (PCA) results of 12 quantitative traits are presented in Table 5. The PCA analysis results includes the factor scores of each character among the 49 tef genotypes, eigen values, percentage total variance accounted by four principal components (PCs). The analysis resulted with four principal components (PC1 to PC4) with Eigen values ranged from 4.67 to 1.22. The four principal components accounted varied percentage total variance ranged from 9.59 to 38.93%, which accounted 78.46% of the entire phenotypic variation observed among the 49-tef genotypes. Out of the total variation, PC1 and PC4 explained the largest and smallest variation, respectively, while PC2 and PC3 accounted for 18.056 and 11.89% of the total variation, respectively. The total contribution of the four principal component axes of this study was similar to Habte *et al*. (2015) who reported only three PC that accounted for the larger proportion of phenotypic variation observed among the tef genotypes and accounted a total of 78.3 % of the entire phenotypic variation, respectively.

Principal component one consisted mainly the variation among the 49 tef test genotypes due to the variation in days to heading, days to maturity, plant height and panicle length. This suggested that these traits vary together. However, PC1 increased with only one of the values, decreasing productive tillers, grain filling period, and harvest index. Habte *et al*. (2015) stated that days to heading, days to maturity, plant height, panicle length contributed for PC1. In the PC2 grain yield, above ground biomass and culm length were positively and strongly correlated. While, PC3 contained the variation contributed much by grain filling period and thousand seed weight. Only, harvest index showed with a negative correlation and greater loadings in PC4.

The present investigation result is in agreement with results reported by other authors. According to Habtamu *et al*.(2011) and Habte *et al*.(2015) grain yield and above ground biomass loaded in one PC. Moreover, Kebebew *et al*.(2001) reported 120 tef genotypes with four principal components and PC1 includes panicle length and productive tillers. Principal component analysis indicated that most of the variable had important in the data set for contribution to the total variation. However, grain yield, above ground biomass, culm length, lodging index and thousand seed weight showed little or no contribution for the variation in the data set for PC1. Moreover, PC2 and PC3 had less than three traits which contributed for the variation. Except harvest index no other traits were attributed for PC4.

Table 5. Principal component values of the first four principal components from principal component analysis of 12 quantitative traits of 49 tef genotypes tested in 2015 at Maysiey

Character	Eigenvectors			
	1	2	3	4
Days to heading	0.898	-0.067	-0.293	0.024
Days to maturity	0.698	-0.278	0.403	-0.189
Plant height	0.871	0.207	0.060	-0.003
Panicle length	0.747	-0.177	0.274	0.404
Culm length	0.453	0.560	-0.230	-0.479
Grain filling period	-0.609	-0.124	0.676	-0.174
Lodging index	-0.554	-0.070	0.289	-0.457
productive tillers	-0.787	0.399	-0.252	-0.100
Grain yield	-0.205	0.851	0.103	0.314
Above ground biomass	0.359	0.815	0.191	-0.107
Harvest index	-0.601	0.041	-0.091	0.567
Thousand seed weight	0.163	0.357	0.622	0.203

Eigen value	4.671	2.167	1.427	1.22
Difference	1.685	1.128	0.969	1.046
Percent of total variance explained	38.925	18.056	11.891	9.590
Cumulative percent of total variance explained	38.925	56.981	68.872	78.462

SUMMARY AND CONCLUSIONS

The 49 tef genotypes were grouped into five clusters using Unweighted Pair-group Method with Arithmetic Means (UPGMA) based on Euclidean distance matrix. Majority of the genotypes (30) were grouped in the first cluster while 9 and 8 genotypes constructed the third and second clusters, respectively. The other two clusters were consisted of each one genotype. The distance between pairs of genotypes was assessed by Euclidean distance. Genotypes in different clusters were characterized with mean values different from others for one or more traits and wide range of Euclidean distances. The higher Euclidean distances were observed between pairs of candidate tef genotypes as compared to pairs of released varieties. Most of the highest distances were observed between pairs of genotypes that include RIL101C as one member of the pairs. Generally, considerable number of genotypes showed sufficient genetic distances to launch crossing program. The result suggested crossing of genotypes with desirable traits and most distant to others could be implemented as improvement breeding method in these tef genotypes. Moreover, the seven genotypes in the third cluster had short days to heading, days to maturity and maximum number of productive tillers with higher grain yield. This suggested the importance of further evaluation of these genotypes to develop varieties fit to the study area.

Four principal components were extract more than 78 percent of total variation. The 12 traits were reduced into four to explain the total variation. The maximum variation was observed on principal component one. Days to heading, days to maturity, plant height and panicle length had the positive and strong correlation on PC1. Whereas, productive tillers also strongly and negative correlation on PC1. These extracted traits are important for selection of the genotypes with desirable traits.

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Appendix Table 1. Means of the traits from the 49 tef genotypes tested at Maysiye in 2015

S. No	Tef genotypes	DH	DM	PH	PAN	CL	GF	LD	PRT	GY	BIOM	HI	TSW
1	DZ-01-99(Asgori)	43.67^{e-i}	81.67^{b-i}	88.40^{a-d}	45.73^{ab}	42.67^{a}	38.00^{a-j}	12.67^{d}	3.30^{cde}	2335.60^{a}	9444.40^{a-d}	24.51^{a-d}	0.36^{a}
2	DZ-01-354 (Enatit)	36.33^{ij}	80.33^{e-i}	84.97^{a-d}	38.07^{a-d}	46.90^{a}	44.00^{a-d}	30.00^{a-d}	3.60^{a-d}	2298.10^{a}	9444.40^{a-d}	21.49^{a-d}	0.50^{a}
3	DZ-01-196 (Magna)	47.33^{a-h}	87.00^{a-e}	88.23^{a-d}	43.47^{a-d}	44.77^{a}	39.67^{a-g}	25.67^{a-d}	2.70^{de}	2064.70^{ab}	8888.90^{a-d}	23.28^{a-d}	0.27^{a}
4	DZ-01-787 (Wellenkomi)	45.00^{b-i}	88.33^{abc}	87.30^{a-e}	42.53^{a-e}	44.77^{a}	43.33^{a-d}	28.33^{a-d}	3.07^{de}	1832.50^{ab}	8333.30^{a-d}	21.99^{a-d}	0.40^{a}
5	DZ-Cr-44 (Menagesha	42.67^{d-i}	83.67^{a-h}	93.83^{abc}	47.30^{a}	46.53^{a}	41.00^{a-e}	25.33^{ab}	3.37^{cde}	2255.80^{a}	9444.40^{a-d}	24.08^{a-d}	0.43^{a}
6	DZ-Cr-82 (Melko)	41.00^{e-j}	86.33^{a-f}	88.10^{a-d}	45.87^{ab}	42.23^{a}	45.33^{a}	27.33^{a-d}	2.13^{e}	1385.80^{ab}	6666.70^{cde}	21.79^{a-d}	0.40^{a}
7	DZ-Cr-37(Tsedey	36.67^{ij}	79.33^{f-i}	85.63^{a-d}	37.57^{a-e}	48.07^{a}	42.67^{a-e}	49.67^{ab}	5.17^{a-d}	2085.60^{ab}	9444.40^{a-d}	22.21^{a-d}	0.37^{a}
8	DZ-Cr-255 (Gibe	42.00^{d-i}	85.00^{ab}	88.40^{a-d}	43.53^{a-d}	44.87^{a}	43.00^{a-d}	29.00^{a-d}	3.00^{de}	2286.70^{a}	10000.0^{a-d}	22.87^{a-d}	0.40^{a}
9	DZ-Cr-358 (Ziquala)	39.67^{f-j}	84.00^{a-h}	84.30^{bcd}	42.67^{a-e}	41.63^{a}	44.33^{a-d}	37.67^{a-d}	3.20^{cde}	1854.20^{ab}	7222.20^{b-e}	27.79^{a}	0.40^{a}
10	DZ-01-974 (Dukem)	42.33^{d-i}	85.67^{a-f}	86.97^{a-d}	39.97^{a-e}	47.00^{a}	43.33^{a-d}	37.68^{a-d}	2.67^{de}	1475.80^{ab}	7333.30^{b-e}	19.72^{a-d}	0.37^{a}
11	DZ-01-1281(Gerado	42.33^{d-i}	87.00^{a-f}	83.00^{cd}	39.00^{a-e}	44.00^{a}	44.67^{abc}	26.60^{a-d}	2.530^{de}	1761.20^{ab}	7777.80^{a-e}	22.89^{a-d}	0.37^{a}
12	DZ-01-1285 (Koye)	40.33^{e-j}	83.00^{a-h}	81.20^{cd}	41.70^{a-e}	39.50^{a}	42.67^{a-e}	46.53^{ab}	3.53^{cde}	1667.20^{ab}	7777.80^{a-e}	21.48^{a-d}	0.23^{a}
13	DZ-01-1681 (KeyTena)	40.67^{e-j}	80.33^{e-i}	84.27^{bcd}	42.87^{a-e}	41.40^{a}	39.67^{a-g}	12.00^{d}	3.53^{cde}	2160.80^{ab}	10000.0^{a-d}	21.81^{a-d}	0.27^{a}
14	DZ-01-899 (Gimbichu)	44.33^{b-i}	85.00^{a-h}	89.70^{a-d}	42.43^{a-e}	47.27^{a}	40.67^{a-f}	25.00^{a-d}	3.00^{de}	1882.30^{ab}	9444.40^{a-d}	20.06^{a-d}	0.30^{a}
15	DZ-01-2675 (DegaTef)	41.67^{e-i}	86.33^{a-f}	83.73^{bcd}	39.03^{a-e}	44.70^{a}	44.67^{abc}	44.33^{abc}	2.67^{de}	1908.50^{ab}	9666.70^{a-d}	19.61^{a-d}	0.33^{a}
16	DZ-Cr-387 RIL355 (Quncho)	52.00^{abc}	87.67^{a-e}	99.10^{a}	47.33^{a}	51.77^{a}	35.67^{c-j}	19.67^{bcd}	3.30^{cde}	2130.80^{ab}	11444.40^{a}	20.63^{a-d}	0.53^{a}
17	Ho-Cr-136 (Amarach)	38.67^{f-j}	78.33^{ghi}	85.53^{a-d}	33.80^{de}	51.73^{a}	39.67^{a-g}	55.33^{a}	5.87^{abc}	2177.20^{a}	8888.90^{a-d}	24.47^{a-d}	0.27^{a}
18	DZ-Cr-285 RIL295 (Simada)	31.33^{j}	74.67^{i}	80.37^{cd}	34.87^{cde}	45.50^{a}	43.33^{a-d}	43.33^{a-d}	6.37^{ab}	2139.20^{ab}	8333.30^{a-d}	24.14^{a-d}	0.37^{a}
19	DZ-01-2053 (Holetta Key	37.54^{hij}	82.02^{b-i}	81.72^{cd}	40.00^{a-e}	40.00^{a}	44.48^{a-d}	34.94^{a-d}	4.18^{b-e}	1011.10^{b}	4369.20^{e}	23.40^{a-d}	0.30^{a}
20	DZ-01-1278(Ambo Toke	43.00^{c-i}	85.00^{a-h}	83.50^{bcd}	43.00^{a-e}	40.50^{a}	42.00^{a-e}	40.33^{a-d}	2.80^{de}	1874.40^{ab}	8333.30^{a-d}	22.49^{a-d}	0.33^{a}
21	9441	44.33^{b-i}	85.00^{a-h}	86.53^{a-d}	39.13^{a-e}	47.40^{a}	40.67^{a-f}	35.33^{a-d}	2.83^{de}	2109.70^{ab}	7777.80^{a-d}	27.27^{ab}	0.30^{a}
22	DZ-01-2054 (Gola)	45.33^{b-i}	88.33^{abc}	87.30^{a-d}	43.10^{a-e}	44.57^{a}	43.00^{a-d}	33.33^{a-d}	3.33^{cde}	2091.70^{ab}	8333.30^{a-d}	25.43^{abc}	0.23^{a}
23	DZ-01-146 (Genete)	44.00^{c-i}	88.67^{ab}	88.57^{a-d}	43.23^{a-e}	45.33^{a}	44.67^{abc}	41.00^{a-d}	3.13^{cde}	1917.90^{ab}	9444.40^{a-d}	20.27^{a-d}	0.50^{a}
24	DZ-01-1821 (Zobel)	44.33^{b-i}	88.33^{abc}	90.67^{a-d}	43.30^{a-e}	47.37^{a}	44.00^{a-d}	27.33^{a-d}	3.53^{cde}	2081.10^{ab}	10000.0^{a-d}	20.81^{a-d}	0.37^{a}
25	Acc. 205953 (Mechare)	44.33^{b-i}	86.33^{a-f}	89.33^{a-d}	42.93^{a-e}	46.40^{a}	42.00^{a-d}	21.33^{bcd}	3.00^{de}	2177.20^{a}	10000.0^{a-d}	21.71^{a-d}	0.40^{a}
26	RIL273(Laketch)	45.00^{b-i}	87.67^{a-f}	91.83^{a-d}	40.90^{a-e}	50.93^{a}	42.67^{a-e}	27.33^{a-d}	2.83^{de}	2306.90^{a}	10555.6^{ab}	21.84^{a-d}	0.37^{a}
27	DZ-01-1868 (Yilmana	44.33^{b-i}	88.67^{ab}	91.63^{a-d}	42.87^{a-e}	48.77^{a}	44.33^{a-d}	20.33^{bcd}	2.53^{de}	1555.80^{ab}	9444.40^{a-d}	14.13^{d}	0.30^{a}
28	DZ-01-2423(Dima)	43.00^{c-i}	83.33^{a-h}	83.07^{cd}	38.93^{a-e}	44.00^{a}	40.33^{a-f}	34.20^{a-d}	3.87^{b-e}	2337.90^{a}	10555.6^{ab}	22.08^{a-d}	0.40^{a}
29	DZ-01-3186 (Etsub)	46.00^{a-i}	86.67^{a-f}	91.43^{a-d}	45.13^{abc}	46.30^{a}	40.67^{a-f}	30.33^{a-d}	3.10^{cde}	2129.70^{ab}	10000.0^{a-d}	21.30^{a-d}	0.47^{a}
30	DZ-01-1880 (Guduru	46.33^{a-i}	89.67^{a}	91.20^{a-d}	43.57^{a-d}	47.63^{a}	43.33^{a-d}	30.33^{a-d}	2.23^{e}	1569.20^{ab}	10000.0^{a-d}	16.14^{cd}	0.37^{a}
31	acc. 17 WJ	36.67^{ij}	78.00^{hi}	79.30^{cd}	32.87^{e}	46.63^{a}	41.33^{a-e}	24.00^{a-d}	7.00^{a}	2377.20^{a}	9444.40^{a-d}	25.27^{abc}	0.37^{a}
32	PGRC/E 205396 Ajora)	38.33^{hij}	83.33^{a-h}	89.50^{a-d}	47.20^{a}	42.30^{a}	45.00^{ab}	29.00^{a-d}	3.27^{de}	2278.90^{a}	8888.90^{a-d}	24.33^{a-d}	0.40^{a}
33	DZ-Cr-409/RIL50d (Boset)	43.33^{c-i}	82.00^{b-i}	85.33^{a-d}	41.40^{a-e}	43.93^{a}	38.67^{a-i}	24.33^{a-d}	3.20^{cde}	1633.30^{ab}	6222.20^{de}	25.92^{abc}	0.40^{a}
34	Kora	53.00^{abc}	82.33^{a-h}	93.76^{abc}	47.17^{a}	46.60^{a}	29.33^{i}	17.33^{bcd}	2.47^{de}	1797.90^{ab}	8333.30^{a-d}	22.25^{a-d}	0.33^{a}
35	Zagre (local 1)	38.33^{ghij}	80.33^{e-i}	80.37^{cd}	38.70^{a-e}	41.67^{a}	42.00^{a-e}	22.00^{bcd}	4.87^{a-e}	2017.50^{ab}	10000.0^{a-d}	20.17^{a-d}	0.40^{a}
36	Zezew(local-2)	40.33^{e-j}	81.00^{c-i}	82.07^{cd}	35.87^{b-e}	46.20^{a}	40.67^{a-f}	21.33^{bcd}	5.87^{abc}	2093.10^{ab}	8888.90^{a-d}	23.30^{a-d}	0.27^{a}
37	acc. 13 –AI	37.67^{hij}	80.67^{d-i}	77.50^{d}	34.20^{de}	43.30^{a}	43.00^{a-d}	25.67^{a-d}	4.83^{a-e}	2094.70^{ab}	8888.90^{a-d}	23.49^{a-d}	0.33^{a}

38	*RIL -65*	48.00^{a-g}	87.33^{a-e}	89.77^{a-d}	40.80^{a-e}	48.97^{a}	39.33^{a-h}	23.58^{a-d}	3.07^{de}	1999.40^{ab}	8888.90^{a-d}	22.56^{a-d}	0.27^{a}
39	*RIL-86*	50.33^{a-e}	86.33^{a-f}	86.20^{a-d}	40.13^{a-e}	46.07^{a}	36.00^{b-j}	19.33^{bcd}	2.17^{e}	2046.70^{ab}	9444.40^{a-d}	21.88^{a-d}	0.50^{a}
40	*RIL-190*	55.67^{a}	85.33^{a-h}	93.80^{abc}	43.27^{a-e}	50.53^{a}	29.67^{ij}	20.00^{bcd}	2.17^{e}	1816.90^{ab}	9444.40^{a-d}	19.13^{a-d}	0.33^{a}
41	*RIL-96*	48.67^{a-f}	87.33^{a-e}	86.23^{a-d}	42.80^{a-e}	43.43^{a}	38.67a-i	22.67^{bcd}	2.80^{de}	1629.70^{ab}	9444.40^{a-d}	17.31^{bcd}	0.37^{a}
42	*RIL-109A*	53.00^{abc}	84.67^{a-h}	90.37^{a-d}	45.33^{ab}	45.03^{a}	31.67f-j	25.67^{a-d}	2.33^{e}	2151.10^{ab}	10222.2^{a-d}	21.07^{a-d}	0.40^{a}
43	*RIL-15A*	54.33^{ab}	88.00^{a-d}	85.50^{a-d}	40.60^{a-e}	44.90^{a}	33.67^{e-j}	25.00^{a-d}	3.30^{cde}	1573.60^{ab}	7777.80^{abc}	20.20^{a-d}	0.30^{a}
44	*RIL-52*	47.00^{a-h}	82.67^{a-h}	92.93^{abc}	47.10^{a}	45.83^{a}	35.33^{d-j}	19.00^{bcd}	3.00^{de}	1665.80^{ab}	8333.30^{a-e}	20.33^{a-d}	0.33^{a}
45	*RIL-129A*	48.00^{a-g}	84.67^{a-h}	89.00^{a-d}	40.97^{a-e}	48.03^{a}	36.67^{a-j}	19.00^{bcd}	2.50^{de}	1541.10^{ab}	8888.90^{a-d}	18.20^{a-d}	0.37^{a}
46	*RIL-91Ap*	54.33^{ab}	84.67^{a-h}	89.90^{a-d}	42.50^{a-e}	47.40^{a}	30.33^{hij}	16.00^{cd}	2.17^{e}	1659.60^{ab}	7777.80^{a-e}	21.57^{a-d}	0.27^{a}
47	*RIL-101C*	56.00^{a}	86.67^{a-f}	97.90^{ab}	46.23^{ab}	51.67^{a}	30.67^{ghij}	22.33^{bcd}	2.17^{e}	1746.10^{ab}	10555.6^{ab}	14.47^{d}	0.37^{a}
48	*RIL-107*	47.67^{a-h}	87.00^{a-e}	85.57^{a-d}	40.70^{a-e}	44.87^{a}	39.33^{a-h}	25.00^{a-d}	3.23^{cde}	1841.70^{ab}	8333.30^{a-d}	22.41^{a-d}	0.33^{a}
49	RIL157	45.33^{b-i}	84.33^{a-h}	92.43^{abc}	41.97^{a-e}	50.47^{a}	39.00^{a-h}	24.33^{a-d}	3.67^{b-e}	2125.00^{ab}	9444.40^{a-d}	22.74^{a}	0.27^{a}
	MSD	10.17	7.48	14.49	10.45	12.7	9.158	32.56	2.77	1159.9	3840.4	10.42	0.3

Appendix Table 2.Euclidean distance of 49 tef genotypes measured from 14 traits and mean Euclidean distance obtained by averaging each genotype distance to other 48 tef genotypes as at tested at Maysiye in 2015

	DZ-01-354	DZ-01-196	DZ-01-787	DZ-Cr-44	DZ-Cr-82	DZ-Cr-37	DZ-Cr-255	DZ-Cr-358	DZ-01-974	DZ-01-1281	DZ-01-1285	DZ-01-1681	DZ-01-899
DZ-01-99	4.55	3.10	4.14	2.68	6.29	6.03	2.80	4.72	5.51	5.24	6.04	2.50	3.50
DZ-01-354		5.06	4.09	3.98	6.42	3.69	3.08	4.58	4.52	4.58	6.06	4.73	4.33
DZ-01-196			2.66	3.36	5.26	5.66	2.67	4.16	3.77	3.82	4.61	3.52	1.97
DZ-01-787				3.42	4.47	5.04	2.56	3.53	2.65	2.82	4.81	4.45	2.70
DZ-Cr-44					5.93	5.29	2.02	4.53	4.77	5.19	6.37	4.30	3.21
DZ-Cr-82						7.92	5.69	4.08	4.19	3.26	4.63	6.77	5.42
DZ-Cr-37							4.51	5.43	4.95	6.00	5.84	5.51	4.93
DZ-Cr-255								3.95	4.07	4.13	5.33	3.52	2.59
DZ-Cr-358									3.99	3.13	3.81	5.29	4.83
DZ-01-974										3.18	4.20	5.46	3.06
DZ-01-1281											3.93	5.22	4.10
DZ-01-1285												5.40	4.96
DZ-01-1681													3.47

Appendix Table 2(continued)

	DZ-01-2675	DZ-Cr-387	Ho-Cr-136	DZ-Cr-285	DZ-01-2053	DZ-01-1278	9441	DZ-01-2054	DZ-01-146	DZ-01-1821	Acc. 205953	RIL273	DZ-01-1868
DZ-01-99	5.48	5.73	7.85	7.43	7.83	4.27	4.20	4.10	5.23	3.88	2.81	4.41	6.05
DZ-01-354	4.26	6.32	6.00	5.17	7.38	4.57	4.60	5.49	3.88	4.03	3.55	4.41	6.06
DZ-01-196	3.72	5.78	7.09	7.68	6.81	2.91	2.75	1.75	4.26	2.65	2.47	3.53	4.38
DZ-01-787	3.38	5.56	6.88	6.96	5.81	2.69	3.46	3.11	2.36	2.23	2.51	3.84	4.02
DZ-Cr-44	5.06	4.16	7.28	7.37	7.96	4.36	4.03	4.08	3.69	2.70	2.18	3.26	5.41
DZ-Cr-82	4.81	7.81	9.60	9.27	5.36	4.47	6.09	5.51	5.50	5.74	5.67	7.29	5.55
DZ-Cr-37	4.86	7.70	2.96	3.20	6.99	4.91	4.62	5.44	4.86	4.88	5.19	5.20	6.84
DZ-Cr-255	3.57	5.06	6.67	6.65	7.42	3.16	3.39	3.30	2.88	1.93	1.36	2.79	4.89
DZ-Cr-358	4.14	7.77	7.10	6.52	4.90	2.70	3.52	3.73	4.52	4.86	4.62	6.02	6.76
DZ-01-974	2.99	6.73	6.70	7.01	5.09	3.16	3.83	4.04	3.47	3.68	3.96	4.74	3.83
DZ-01-1281	3.09	7.27	7.44	7.27	5.05	3.15	4.16	3.96	4.34	4.26	4.19	5.62	4.93
DZ-01-1285	3.38	9.13	7.19	7.00	4.65	2.70	4.98	4.23	5.80	5.72	5.83	7.09	6.22
DZ-01-1681	5.16	7.13	7.22	6.53	7.19	4.13	4.67	4.32	5.73	4.28	3.64	5.01	5.68
DZ-01-899	3.44	5.20	6.66	7.23	6.91	3.47	3.44	3.08	3.82	2.00	2.03	2.85	3.10
DZ-01-2675		7.03	6.64	7.02	6.45	2.72	4.19	3.80	3.63	3.61	3.87	4.69	4.44
DZ-Cr-387			9.26	10.09	10.62	7.26	6.89	6.91	5.16	4.48	4.34	4.44	5.87
Ho-Cr-136				3.67	7.88	6.79	5.68	6.65	7.14	6.79	7.22	6.84	8.44
DZ-Cr-285					6.94	6.58	6.46	7.34	7.24	7.31	7.39	7.81	9.04
DZ-01-2053						5.21	6.48	6.42	7.19	7.54	7.73	8.99	7.61
DZ-01-1278							3.49	2.91	3.68	3.82	3.79	5.18	5.30
9441								2.38	4.70	3.84	3.67	3.92	6.04
DZ-01-2054									4.62	3.28	3.53	4.18	5.26
DZ-01-146										2.67	3.12	3.91	4.73
DZ-01-1821											1.46	2.15	3.56
Acc. 205953												2.24	4.14
RIL273													4.64

Appendix Table 2(continued)

	DZ-01-2423	DZ-01-3186	DZ-01-1880	17 WJ	E 205396	DZ-Cr-409	Kora	Zagre	local-2	13 –AI	RIL - 65	RIL-86	RIL-190
DZ-01-99	4.08	3.69	5.68	7.53	2.95	4.15	4.31	4.22	5.62	5.37	3.91	3.88	5.49
DZ-01-354	3.09	3.78	5.56	5.97	3.81	4.70	6.79	3.34	5.12	4.12	5.07	4.30	6.87
DZ-01-196	4.04	3.32	3.94	7.96	3.54	3.88	4.00	4.92	5.46	5.37	1.77	3.83	4.38
DZ-01-787	3.66	2.63	3.26	7.33	3.21	3.41	5.16	4.37	5.25	4.92	3.02	3.46	5.29
DZ-Cr-44	4.08	2.06	4.66	7.79	2.30	4.40	4.56	4.96	6.10	6.07	3.69	3.81	5.26
DZ-Cr-82	7.30	5.47	5.45	10.36	5.58	4.63	5.86	7.07	8.41	7.75	6.09	6.33	6.59
DZ-Cr-37	3.35	5.32	6.33	4.81	4.89	5.56	7.75	4.07	3.93	3.75	5.37	6.25	7.77
DZ-Cr-255	2.62	1.95	4.06	7.07	2.01	4.29	5.25	3.81	5.30	4.81	3.24	3.37	5.53
DZ-Cr-358	4.93	4.67	6.11	7.74	3.51	2.85	6.17	5.17	6.18	5.18	5.11	5.37	7.18
DZ-01-974	4.87	4.07	3.33	8.17	4.68	3.51	5.52	5.06	5.99	5.45	3.71	4.55	5.46
DZ-01-1281	5.01	4.50	4.78	7.86	4.66	3.68	5.86	5.17	5.98	5.18	4.38	4.83	6.03
DZ-01-1285	5.69	6.06	6.03	8.55	5.34	4.81	6.62	5.51	6.48	5.62	5.62	6.85	7.26
DZ-01-1681	3.70	4.83	5.70	6.58	3.75	4.69	5.47	3.06	4.37	4.08	4.17	4.90	6.24
DZ-01-899	3.82	2.96	2.83	7.66	3.76	4.17	4.18	4.31	5.17	5.18	1.74	3.69	4.06
DZ-01-2675	4.14	4.05	3.84	8.10	4.64	5.06	6.27	4.82	6.16	5.27	4.20	5.01	5.96
DZ-Cr-387	6.34	3.53	5.06	9.84	6.16	7.20	5.22	7.46	8.39	8.79	5.37	4.54	4.51
Ho-Cr-136	5.37	7.43	8.22	4.68	7.10	7.05	8.92	6.31	4.31	5.00	6.52	8.10	8.76
DZ-Cr-285	5.17	7.70	8.87	3.25	6.47	6.56	9.57	4.83	3.90	3.60	7.58	8.20	9.97
DZ-01-2053	7.54	7.91	7.72	8.36	6.87	4.63	8.13	6.74	6.68	6.19	7.26	8.21	9.01
DZ-01-1278	3.77	3.95	4.57	7.68	3.30	3.50	5.54	4.24	5.60	4.71	4.10	4.68	6.17
9441	4.04	4.36	5.45	7.08	4.01	3.34	5.42	5.18	5.02	4.67	2.77	4.46	5.81
DZ-01-2054	4.42	4.24	4.83	7.82	3.71	4.18	5.35	5.36	5.40	5.27	2.63	5.09	5.79
DZ-01-146	3.74	2.26	3.33	7.90	3.69	4.95	6.32	4.86	6.39	5.86	4.47	3.85	6.14
DZ-01-1821	3.47	2.00	2.80	7.48	3.29	4.85	5.26	4.50	5.40	5.41	2.50	3.66	4.96
Acc. 205953	3.26	1.76	3.42	7.52	2.99	4.38	4.70	4.12	5.53	5.26	2.62	2.71	4.69
RIL273	3.90	3.02	3.88	7.82	4.38	5.74	5.78	5.35	5.95	6.00	2.73	3.76	5.15

Appendix Table 2(continued)

	RIL-96	RIL-109A	RIL-15A	RIL-52	RIL-129A	RIL-91Ap	RIL-101C	RIL-107	RIL157 (4.73)	Mean
DZ-01-99	4.47	3.50	5.02	3.48	4.49	4.83	6.74	3.68	4.47	4.52
DZ-01-354	5.15	5.56	6.30	5.65	5.07	6.85	7.72	4.49	5.15	5.77
DZ-01-196	3.17	3.39	3.16	3.11	3.48	3.52	5.78	1.78	3.17	3.40
DZ-01-787	2.76	4.39	3.59	3.87	3.46	4.73	6.24	1.76	2.76	3.73
DZ-Cr-44	4.53	3.58	5.37	3.48	4.36	5.33	6.00	3.84	4.53	4.56
DZ-Cr-82	4.78	6.59	5.77	5.29	5.70	6.00	7.57	4.85	4.78	5.70
DZ-Cr-37	6.26	6.73	6.55	6.42	6.03	7.50	8.57	5.16	6.26	6.61
DZ-Cr-255	3.74	3.68	4.89	4.04	4.10	5.41	6.38	2.96	3.74	4.33
DZ-Cr-358	5.24	5.96	5.51	5.37	5.80	6.20	8.63	3.79	5.24	5.75
DZ-01-974	3.36	5.29	3.80	4.10	3.25	4.85	6.36	2.89	3.36	4.14
DZ-01-1281	3.82	5.79	4.55	5.19	4.73	5.28	7.41	2.90	3.82	4.83
DZ-01-1285	4.98	6.58	5.26	5.73	6.03	6.25	8.50	4.38	4.98	5.85
DZ-01-1681	4.35	4.75	5.06	4.19	4.59	5.30	7.39	3.77	4.35	4.86
DZ-01-899	2.65	3.51	3.39	2.60	2.29	3.76	4.98	2.21	2.65	3.12
DZ-01-2675	3.66	5.26	4.79	5.27	4.61	5.84	6.82	3.42	3.66	4.81
DZ-Cr-387	5.50	4.17	6.41	5.14	5.14	6.07	4.06	5.89	5.50	5.32
Ho-Cr-136	8.12	8.41	7.70	8.07	7.71	8.40	9.82	6.63	8.12	8.11
DZ-Cr-285	8.24	8.97	8.38	8.36	8.14	9.27	11.05	6.97	8.24	8.62
DZ-01-2053	6.71	8.87	6.46	7.04	7.15	7.44	10.31	5.80	6.71	7.39
DZ-01-1278	3.51	4.75	4.10	4.40	4.57	5.25	7.33	2.66	3.51	4.45
9441	5.04	4.90	4.37	4.67	4.63	4.81	7.46	2.87	5.04	4.87
DZ-01-2054	4.40	4.87	4.08	4.40	4.82	4.82	7.17	2.59	4.40	4.62
DZ-01-146	3.74	4.77	5.09	5.02	4.43	6.31	6.44	3.71	3.74	4.81
DZ-01-1821	3.22	3.96	4.35	3.85	3.51	5.10	5.49	2.76	3.22	3.94
205953	3.14	3.20	4.32	3.48	3.22	4.73	5.50	2.67	3.14	3.71
RIL273	4.63	4.16	5.22	4.68	4.01	5.55	5.68	3.95	4.63	4.72

Appendix Table 2(continued)

	DZ-01-2423	DZ-01-3186	DZ-01-1880	17 WJ	E 205396	DZ-Cr-409	Kora	Zagre	local-2	13 –AI	RIL -65	RIL-86	RIL-190
DZ-01-1868	6.02	4.52	1.95	9.38	5.87	6.18	5.68	6.12	6.96	7.10	3.99	5.37	4.78
DZ-01-2423		3.69	5.25	5.28	3.66	4.99	6.54	2.71	3.93	3.27	4.21	4.01	6.54
DZ-01-3186			3.38	8.05	3.19	4.70	4.68	4.85	6.36	6.13	3.59	2.90	4.65
DZ-01-1880				9.35	5.21	5.78	5.47	5.83	7.09	6.97	3.74	4.39	4.63
17 WJ					7.21	7.39	9.87	5.19	3.02	3.73	7.62	8.13	10.02
E 205396						4.16	5.83	4.21	5.60	5.12	4.44	4.72	6.76
DZ-Cr-409							4.82	4.80	5.47	4.90	4.29	4.35	5.98
Kora								6.96	7.63	7.90	4.28	4.64	2.50
Zagre									3.73	2.62	5.17	4.87	7.33
local-2										2.35	5.08	6.44	7.80
13 –AI											5.39	5.92	8.18
RIL -65												3.81	3.97
RIL-86													4.47