ORIGINAL ARTICLE

Variation in Major Traits of Gynogenically derived Tef [*Eragrostis tef* (Zucc.)Trotter] lines Evaluated in the Central highlands of Ethiopia

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ABSTRACT

Field experiments were conducted using 36 tef genotypes in a 6*6 simple lattice design at three testing locations in Ethiopian during 2011 main cropping season. The objectives were to assess the variation in major quantitative traits of tef genotypes, and to examine the phenotypic and genotypic correlation among those traits. The mean square due to genotypes was significantly (P<0.01) higher for all traits except days to maturity and grain yield per hectare. Besides, mean square due to location was also highly significant for all traits of the test genotypes while that due to genotype x location interactions were not significant (P<0.05) for all traits except plant height. Genotypic and phenotypic coefficient of variation ranged from 0.28 to 19.19 and 1.01 to 20.53%, respectively, and broad sense heritability ranged from 8 to 87%. Estimate of expected genetic advance was relatively very low while genetic advance as percent of the mean within the range of 0.39 to 28.21%. Grain yield showed significant (P<0.01) genotypic correlation with shoot biomass yield, harvest index, days to panicle emergence and to grain filling period only. Cluster analysis grouped the entire test genotypes into seven distinct clusters. The first five principal components with Eigen value greater than one accounted for 88.9% of the entire diversity among the test genotypes based on the ten quantitative traits. In general, considerable variations that will be utilized for future breeding works were detected among the test tef genotypes for all traits under investigation.

***Key words*:** tef, traits, variation, yield

INTRODUCTION

Tef [*Eragrostis tef* (Zucc) Trotter] is the most important cereal crop in Ethiopia. It is a C_4 self-pollinated chasmogamous annual cereal bearing both the stamens and pistils in the same floret (Seyfu, 1997). It is the only cultivated cereal in the genus *Eragrostis* which consists of 350 species (Hailu and Seyfu, 2001; Hailu *et al,* 2003). It exhibits high level of phenotypic plasticity in phenology and agronomic traits. Its days to heading and to maturity and grain yield per plant, for instance, ranges from 25 to 81 and 60 to 140 days and 0.78 to 5.96 gram per plant, respectively (Kebebew *et al*., 2001). The soil type, climate, season and varieties we use are among the major factors affecting tef grain yield and quality. Tef, therefore, gives better grain yield and quality when grown on black soils in areas between altitude range of 1800 to 2400m a. s. l. and receiving annual rainfall of 750 to 850mm (Seyfu, 1993).

Tef is the most preferred cereal in Ethiopia due to excellent quality grain and straw, its gluten free nature (Spaenij-Dekking *et al.,* 2005), tolerance to moisture stresses, suitability for double cropping and its long shelf life and low post harvest pest problem (Seyfu, 1993). It ranks first in area coverage and second to maize in total grain production in Ethiopia (CSA, 2012). It is annually cultivated by over six million small-scale farmers on 28% of the total area allocated to cereal crops (CSA, 2012). However, its national average yield is below 1.3 t/ha which is very low as compared to other cereal (CSA, 2012). Nevertheless, it is possible to increase the yield over 4.5 t/ha by using improved varieties and management practices (Hailu and Seyfu, 2001). The major constraints of tef production are lodging, drought and the wider use of low yielding landrace cultivars (Kebebew *et al*., 2011). Lodging, the displacement of the plant from the upright position due to wind and rain, is found to reduce grain yield by about 17% (Seyfu, 1993) and affect the quality of the seed in terms of germination energy and capacity, colour and nutritional value. Several efforts are being made to generate high yield and lodging tolerant varieties and crop production technology packages among which the use of conventional breeding, modern molecular tools as well as different aspects of genetic transformation can be mentioned. Through the use of those tools, several genotypes have been developed and evaluated at different stages of breeding schemes.

Haploid induction, for instance, has potential application for crop breeding as it enables to get true bred lines in a single step and cut generations of breeding. Haploid or doubled haploid (DH) plant production for tef was first invented by Likyelesh *et al. (*2006) from un-pollinated ovary culture, (which is known as 'gynogenesis' of variety DZ-01-196. The technique was then verified by extending experiments on gynogenic culture of F_1 hybrids from varietal crosses to achieve best hybrid vigor at a single step. The test genotypes in the present study were, thus, randomly selected from the putative tef double haploids lines derived from gynogenic culture experiment conducted at Holeta Research Center.

Knowledge of the variability, heritability and genetic advance of economically important traits as well as understanding the association among those traits of the genotypes developed through different approaches are critical in crop improvement and selection. The objectives of the present study were to identify the variability and heritability estimates, to see the grouping or clustering of the test genotypes and to examine the

phenotypic and genotypic association of economically important quantitative traits of tef genotypes developed through gynogenesis (plant regeneration from unpollinated pistils).

MATERIALS AND METHODS

Description of experimental sites

Three field experiments were carried out at Holeta Research Center, Ginchi sub center and Adadi testing site of the Ethiopian Institute of Agricultural Research (EIAR) during the 2011 main season. Holeta and Ginchi are located at about 30 and 60 kilo meters to the western direction from Addis Ababa while Adadi is located at about 70 kilo meters south of Addis Ababa. The description of geographic, climatic and soil condition of the three experimental locations are shown on Table 1.

Experimental materials and Design

Twenty nine randomly selected putative DH gynogenic lines from the F_1 hybrids, four from the culture of sole cultivar, DZ-01-196, (named as '196 gyno') and two standard and one local check from each respective location (Table 2) were evaluated in a 6*6 simple lattice design. A 2m x 2m plot was used at 1m and 2m spacing between plots and replications respectively. Twelve grams of seeds was broadcasted in each plot. Regarding fertilizer, 60 Kg P_2O_5 and 40 Kg N per hectare was used in the form of Di ammonium phosphate (DAP) and Urea, respectively. DAP was applied at planting while Urea was top dressed at tillering stage. All cultural crop management practices were applied as per the recommendation for each location.

Table 1. Geographic and climatic descriptions of the three experimental sites in the Central Highland of Ethiopia

Items	Locations		
	Holeta	Ginchi	Adadi
Latitude	09°03′ N	09°30′ N	08°31′ N
Longitude	38°30′ E	38°30′ E	38°13′ E
Altitude(m.a.s.l.)	2400	2200	2383
MAR (mm)	1102	1139	1105
MAT (°C)	14.5	16.3	16.9
Soil type	Light red	Black Vertisol	Light brown
Soil pH	6.32	6.18	7.62

Source: Gemechu, 2012 MAR= Mean Annual Rainfall, MAT= Mean Annual Temperature

Table 2. Description of tef genotypes included in the current study

No	Genotype	Source
1	354 x 196 p# 63 S#8	HARC
2	354 x 196 p# 61 S#1	HARC
3	Alba x 196 p# 169 S#6	HARC
4	354 x 196 p# 48 S#5	HARC
5	354 x 196 p# 13 S#1	HARC
6	196 gyno p# 27 S#1	HARC
7	354 x 196 p# 102 S#8	HARC
8	Albax196 p# 7 S#1	HARC
9	196 gyno P#31S#1	HARC
10	354 x 196 p# 84 S#6	HARC
11	354 x 196p#122 S#3	HARC
12	196 gyno p# 96 S#5	HARC
13	Alba x 196p# 141 S#7	HARC
14	Alba x 196p#17S#2	HARC
15	Alba x 196 p# 173 S#3	HARC
16	Alba x 196 p# 175 S#1	HARC
17	Alba x 196 p# 147 S#8	HARC
18	Alba x 196 p# 145 S#1	HARC
19	354 x 196 p# 74 S#9	HARC
20	Alba x 196 p# 176 S#6	HARC
21	Alba x 196 p# 177 S#10	HARC
22	354 x 196 p# 118 S#4	HARC
23	Alba x196 p#176 S#7	HARC
24	354X196 p# 105 S#5	HARC
25	354 x 196 p# 81 S#2	HARC
26	354 x Cr-37 p# 24 S#5	HARC
27	354 x196 p# 71 S#8	HARC
28	196 gyno p# 116 S#6	HARC
29	Alba x196 P#165 S#1	HARC
30	Alba x 196 p#175 S#4	HARC
31	354 x 196 p# 73 S#4	HARC
32	DZ-01-354*	DZARC
33	Quncho *	DZARC
34	Local Check	HARC
35	354 x 196 p#68 S#2	HARC
36	354 x 196 p# 119 S#6	HARC

* Standard checks
HARC =Holeta Agric. Research Center
DZA RC= D/Zeit Agric. Research Center

Statistical analysis and partitioning of the variance components

All measured data were subjected to analysis of variance (ANOVA) using the SAS program software (SAS, 2002) and the significance of variability test was made at 5 and 1% probability level. The total phenotypic variance of each of the traits was partitioned into contribution due to genetic and non genetic factors using the variance component method based on the combined analyses over two test locations as per the method suggested in Kebebew *et al.* (1999):

$$Vg = [MSG - (MSGL - MSE)/r - MSE]/rl$$

$$VP = Vg + Vgl/r + Ve/r$$

Where: *MSG*, *MSGL* and *MSE* are the mean squares of genotypes, genotype X location interaction, and experimental error; r and l are the number of replications and locations; and Vgl and Ve are genotype x location interaction and error variance estimated by $(MSGL - MSE)/r$ and *MSE*, respectively. Phenotypic (PCV) and genotypic (GCV) coefficient of variation were calculated following the method of Burton and de Vane (1953).

$$PCV = \sqrt{\sigma^2 p} / X) \times 100;$$

$$GCV = (\sqrt{\sigma^2 g} / X) \times 100$$

Where: X= the grand mean for the trait considered.

Heritability and Genetic advance

Broad-sense heritability (h^2) was calculated as the ratio of genotypic variance to phenotypic variance according to Allard (1960):

$h^2 = \frac{Vg}{Vp} \times 100$. Genetic advance in absolute unit (GA) and genetic advance as percentage of the mean, assuming selection of the superior 5% of the genotypes were estimated following the procedure elaborated by Singh and Chaudhary (1996):

$$GA = K(\sqrt{\sigma^2 p})(h^2)$$

$$GA(as\%ofmean) = \frac{GA}{X} \times 100$$

Where: K is a constant with a value of 2.06 at selection intensity of 5%;= Square root of phenotypic variance and h^2= heritability in broad sense.

Association of the traits

Phenotypic and genotypic correlation coefficients between pairs of traits were computed from the components of variance and co variances as suggested by Singh and Chaudhury (1996).

$$rp_{xy} = \frac{P\,\mathrm{cov}_{xy}}{\sqrt{(\sigma^2 P_x . \sigma^2 P_y)}}$$

$$rg_{xy} = \frac{G\,\mathrm{cov}_{xy}}{\sqrt{\sigma^2 g_x . \sigma^2 g_y}}$$ Where: r_p and r_g is the phenotypic and genotypic correlation coefficient between variables x and y, $Pcov_{xy}$ and $Gcov_{xy}$ is the phenotypic and genotypic covariance between variables x and y; $\sigma^2 g_x$ and $\sigma^2 g_y$ is the genotypic variance for trait X and Y; $\sigma^2 px$ and $\sigma^2 py$ is the phenotypic variance for trait X and Y, respectively.

Cluster and Principal Component Analysis

For both cluster analysis (CA) and principal Component analysis (PCA), mean values for the ten traits and 36 tef genotypes at three locations were used. CA grouped the test tef genotypes into genetically distinct classes using the PROC CLUSTER of SAS Version 9 (SAS, 2002) following the average linkage cluster analysis. The numbers of clusters were determined based on the Pseudo-F and Pseudo-T^2 options. On the other, PCA were employed to identify traits contributing to a large part of the total variation among the genotypes using the PROC PRINCOMP of SAS version 9 (SAS, 2002). After principal component analysis is accomplished, PCs with eigen values greater than unity were considered important to explain the observed variability.

RESULTS AND DISCUSSION

A combined analysis of variance, across three locations, revealed a non significant genotype by location interaction ($P \leq 0.05$) for all the seven traits other than plant height, culm length and shoot biomass of the 36 tef genotypes (Table 3). On the other hand, locations were highly significant ($P<0.01$) for all traits of the genotypes while highly significantly variation among genotypes was observed only for five of the ten traits under study. This result is contrary to the previous findings of Ayalneh *et al.* (2012) who reported no significant tef genotype variation for several traits including days to maturity, grain filling period, culm length and plant height. Besides, Wendeweson *et al.* (2012) reported a significant genotype by environment interaction unlike the present findings whereby no significant genotype by environment interaction was documented for all the seven traits other than plant height, culm length and shoot biomass.

Holeta location had significantly higher mean values for all traits except for days to grain filling, days to maturity and harvest index while the mean for these three traits were the highest at Ginchi as compared to the remaining two locations (Table 4). Grain yield was the highest at Holeta followed by Adadi and Ginchi; however, the highest shoot biomass was recorded for both Holeta and Adadi. Unlike mean grain yield and shoot biomass, the highest mean harvest index was recorded at Adadi. Surprisingly, shoot biomass yield was the only trait with significantly higher values at Adadi station. Mean value for lodging index was the highest at Holetta and the least at Ginchi. Early days to panicle emergence, grain filling and maturity were recorded for Adadi followed by Holetta and Ginchi locations, respectively which might be due to relatively warmer temperature at Adadi. Holetta location was identified to have the longest days to panicle emergence while the longest days to grain filling and maturity were observed at Ginchi location probably due to slow growth on the vertisols. In general, from the present findings, one can possibly say that Holeta, Ginchi and Adadi, are suitable for better grain yield, reduced lodging percent and earliness, respectively.

Estimates of phenotypic and genotypic variation

The estimates of genotypic (GCV) and phenotypic (PCV) coefficient of variability, broad sense heritability (h^2), genetic advance (GA) & genetic advance as percent of the mean (GAM) are presented on Table 5. The estimated GCV and PCV values for days to maturity and harvest index were relatively small and it ranged from 0.39 to 6.07% and 1.04 to 7.76% respectively (Table 5). The result of the current study is lower for all traits than most of the previous findings (Habte, 2008; Habte *et al.,* 2011). In general, higher PCV than GCV values was observed for all traits in the present study indicating that the environmental effect was higher for the expression of the traits under investigation.

Table 3. Mean squares values for combined analysis of variance of 36 tef genotypes evaluated at three locations in 2011.

Traits	Loc (DF=2)	Rep (DF=1)	Treat (DF=35)	Block (rep) (DF=10)	Loc* Treat (DF=70)	Error (DF=97)	Mean	CV (%)
DPE	37.95**	9.80ns	27.83**	12.21ns	8.17ns	6.45	60.95	4.17
DGF	7617.78**	75.85**	34.72**	7.66ns	11.26ns	10.68	62.80	5.20
DTM	8067.51**	31.13ns	7.80ns	7.05ns	8.88ns	9.47	123.75	2.49
PHT	1477.32**	304.00**	46.24**	10.19ns	34.75**	20.23	86.92	5.17
PL	116.76**	176.95**	9.46ns	3.78ns	8.16ns	6.91	35.15	7.48
CL	897.73**	17.09ns	32.4**	7.51ns	17.33**	10.21	51.77	6.17
SBM	234.48**	3.60ns	2.95**	3.99**	1.44*	0.93	10.57	9.11
GY	6.41**	1.96**	0.21ns	0.61**	0.17ns	0.20	2.95	15.20
HI	0.13**	0.0064ns	0.0024ns	0.0022ns	0.0013ns	0.0016	0.29	14.22
LI	12488.95**	146.69*	36.89ns	25.44ns	41.45ns	34.16	80.16	7.29

DF=degrees of freedom; ns = non significant; *, ** significant at P≤0.05 and P≤0.01, respectively
DPE=Days to panicle emergence, DGF=Days to grain filling, DTM=Days to maturity, PH=Plant height, PL=Panicle length, CL=Culm length, SBM= Shoot biomass yield, Grain yield, HI= Harvest index, LI=Lodging index

Table 4. Mean values of 10 traits for 36 tef genotypes evaluated at three locations in 2011.

Location	DPE	DGF	DTM	PHT	PL	CL	BM	GY	HI	LI
Holetta	61.8a	67.0b	128.8b	91.0a	36.6a	54.4a	11.6a	3.3a	0.29b	95.3a
Ginchi	60.6b	70.3a	130.9a	87.8b	34.6b	53.2b	8.5b	2.8b	0.33a	71.6c
Adadi	60.5b	51.1c	111.6c	82.0c	34.3b	47.8c	11.6a	2.8b	0.24c	73.6b

DPE=Days to panicle emergence, DGF=Days to grain filling, DTM=Days to maturity, PH=Plant height, PL=Panicle length, CL=Culm length, SBM= Shoot biomass yield, Grain yield, HI= Harvest index, LI=Lodging index

The highest estimates of heritability values (84.7%) was detected for grain filling period followed by days to 50% panicle emergence (82.5%) and harvest index (78.2%), respectively while days to 50% maturity showed the lowest estimate of heritability value (37.2%) in the current study (Table 5). Similar results were previously reported for days to panicle emergence on tef crop (Kebebew *et al.*, 2001; Ayalneh *et al.*, 2012). The estimate of expected genetic advance was generally very low in the current study. High genetic advance as percent of the mean (12.5%) was detected for harvest index followed by shoot biomass (11.85%) and culm length (8.1%) while the least value was estimated for days to maturity (0.8%). The result of the present finding is far below than that of Kebebew *et al.* (2001) ranging from less than 2% to 23%. This could be due to the uniformity expected in double haploid lines.

Association of the traits

The phenotypic and genotypic correlations observed for morpho-agronomic traits are presented on Table 6. All traits, except days to maturity, showed significant ($P<0.01$) phenotypic correlation with grain yield per hectare. The non significant phenotypic association observed between grain yield and days to maturity is in line with the previous findings of Yifru and Hailu (2005) and contrary to Habte *et al.*, (2011). On the other hand, there was no significant ($P\leq0.05$) genotypic association between grain yield and most of the traits except days to panicle emergence, days to grain filling, shoot biomass and harvest.

Lodging index, which is the most limiting factor of tef grain yield and quality, had shown significant phenotypic association with all traits at $p< 0.01$, and for harvest index and culm length at $p<0.05$ while days to panicle emergence and harvest index were not significant. On the other hand, this important trait had significant genotypic association with half of the ten traits under investigation. This finding is in line with the previous report (Temesgen, 2002).

On the other hand, harvest index was highly significantly associated with all traits at ($P<0.01$) and with plant height at ($P<0.05$) while days to maturity and panicle length were not significantly correlated to it

Cluster analysis

Cluster analysis was used to group the 36 tef genotypes in the current study into six genetically distinct classes based on the means of multiple traits following the average distance method using SAS statistical software program (SAS Institute 2002). The number of genotypes in each cluster ranged from one in the smallest cluster to 25 in the largest cluster group (Fig. 1). Cluster number IV, V and VI was remained solitary without grouping while largest number (25) genotypes was grouped in cluster-I followed by cluster-II and cluster III each with four genotypes per cluster. The standard check, Quncho, has remained solitary in cluster six while the other standard check, DZ-01-354, and the local check were grouped under cluster-I. Similar findings have been reported previously on the cluster number (Tadesse, 1975; Kebebew *et al.*, 2001; Temesgen, 2002; Pilaza *et al.*, 2013). Unlike Habte (2008) who reported the formation of four distinct clusters based on 18 traits of 21 tef genotypes, Tadesse (1975), Kebebew *et al.* (2001), Temesgen (2002) and Pilaza *et al.*, 2013) reported the formation of six major clusters though they have utilized different number and type of genotypes and traits for their investigation.

Principal component analysis

The principal component analysis (PCA), the relative contribution of traits towards the variation in the 36 tef genotypes were estimated and presented (Table 7). The first four principal components (PCs) with Eigen value greater than one were accounted for 88.9% of the entire diversity among the genotypes for all the 10 traits detected. The percentage contribution of the first four principal components to the gross genetic variation obtained in the current study (88.9%) is higher than the previous reports of Kebebew *et al.* (2003) 81%, Temesgen *et al.* (2005) 80.6% and Habte (2008) 85.2%. PC_1 accounted for 43.5 % of the variation among the genotypes under investigation. The variation in PC_1 was mainly due to the variation in culm length, days to grain filling, plant height and days to panicle emergence, in that order. Generally, the contribution of PC_1 obtained in this study is in line with Kebebew *et al.* (2003) 40% and Habte (2008) 43.9% while it is lower than Temesgen *et al.* (2005) 26.4%.

PC2, on the other hand, accounted for about 20.2 % of the total variation among the test genotypes. The variation in PC2 is mainly resulted from the variation in traits such as grain and biomass yield, panicle length and days to panicle emergence. Except for the days to panicle emergence and days to maturity all the rest traits showed positive polarity in this component.

Furthermore, PC3 contributed 13.3 % of the total variation in the genotypes which was mainly resulted from days to maturity, lodging index, panicle length and biomass yield in that order. Similarly, PC4 contributed for 11.9% of the total variation in the test genotypes. The main source of variation in PC4 was due to biomass yield, harvest index, panicle length and lodging index in that order.

Generally, the presence of considerable variation among tef genotypes was detected for all traits under investigation. The estimates of broad sense heritability ranged from 8% to 87 %. The expected genetic advance in the current study was relatively very low. Besides, significant genotypic correlation between grain yield and that of shoot biomass yield, days to 50% panicle emergence, days to grain filling and harvest index traits. The whole genotypes were grouped into six distinct clusters and the first four principal components with Eigen value greater than one contributed for 88.9 per cent of the total variation. The variation observed in the present study is, therefore, useful for future breeding in identifying some genotypes with better harvest index and lodging tolerance.

Table 5. Estimates GCV and PCV, H, GA and GAM for ten traits of 36 tef genotypes

Traits	GCV (%)	PCV %)	H (%)	GA	GAM (%)
Days to panicle emergence	2.93	3.56	82.5	3.69	6.05
Days to grain filling	3.52	4.15	84.7	4.55	7.25
Days to maturity	0.39	1.04	37.2	0.99	0.80
Plant height (cm)	2.60	4.00	64.9	4.65	5.35
Panicle length (cm)	2.51	4.26	59.0	1.82	5.18
Culm length (cm)	3.93	5.33	73.7	4.19	8.10
Shoot biomass (t/ha)	5.75	7.65	75.2	1.25	11.85
Grain yield (t/ha)	3.71	6.55	56.7	0.23	7.65
Harvest index	6.07	7.76	78.2	0.04	12.50
Lodging index (%)	2.36	4.16	56.8	3.90	4.86

GCV= Genotypic coefficient of variability, PCV= Phenotypic coefficient of variability, H= broad sense heritability,
GA=genetic advance in absolute and GAM=genetic advance as percent of mean

Table 6. Genotypic (upper diagonal) and Phenotypic (lower diagonal) Correlation Coefficient for 10 traits of 36 tef genotypes evaluated at three locations in the central highlands of Ethiopia

Variable	DPE	DGF	DTM	PHT	PL	CL	BM	GY	HI	LI
DPE	1	-0.87***	-0.03ns	0.52**	0.16ns	0.55**	0.05ns	-0.54***	-0.51**	-0.59***
DGF	-0.22**	1	0.52**	-0.68***	-0.14ns	-0.76***	-0.12ns	0.40*	0.45**	0.49**
DTM	0.15*	0.93**	1	-0.49**	-0.005ns	-0.60***	-0.16ns	-0.11ns	0.02ns	-0.025ns
PHT	0.21**	0.37***	0.45***	1	0.60***	0.90***	0.43**	0.001ns	-0.36*	-0.45**
PL	0.14*	0.17*	0.22**	0.71***	1	0.20ns	0.24ns	0.30ns	0.08ns	-0.33ns
CL	0.20**	0.39***	0.47***	0.90***	0.34***	1	0.40*	-0.16ns	-0.48**	-0.38*
BM	-0.02ns	-0.43***	-0.44***	0.04ns	0.11ns	-0.02ns	1	0.44**	-0.54**	-0.20ns
GY	-0.25***	0.21**	0.12ns	0.35***	0.40***	0.22**	0.45***	1	0.50**	0.17ns
HI	-0.17*	0.62***	0.56***	0.27***	0.25***	0.21**	-0.60***	0.43***	1	0.35*
LI	0.02ns	0.25***	0.26***	0.29***	0.22**	0.25***	0.35***	0.41***	-0.02ns	1

DPE=Days to panicle emergence, DGF=Days to grain filling, DTM=Days to maturity, PH=Plant height, PL=Panicle length (cm), CL=Culm length (cm), SBM= Shoot biomass yield(t/ha), Grain yield (t/ha), HI= Harvest index, LI=Lodging index in percentage

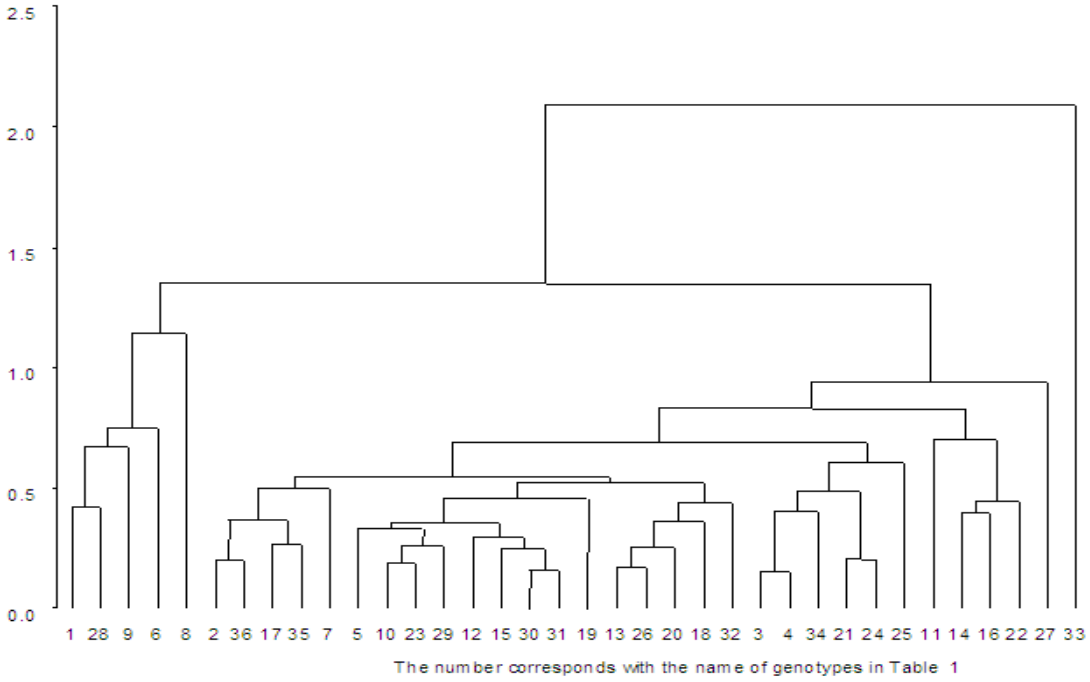

Figure1. A Dendrogram showing the average distance between clusters of 36 tef genotypes based on mean performance of 10 quantitative traits

Table 7. Eigen values and Eigenvectors of the first four principal components of 10 quantitative traits of 36 teff genotypes.

Traits	PC_1	PC_2	PC_3	PC_4
Days to panicle emergence	0.38	-0.30	0.14	0.17
Grain filling period (days)	-0.43	0.14	0.21	-0.14
Days to maturity	-0.21	-0.24	0.67	0.02
Plant height (cm)	0.42	0.26	-0.03	0.14
Panicle length (cm)	0.16	0.39	0.37	0.46
Culm length (cm)	0.43	0.12	-0.24	-0.08
Biomass yield (t/ha)	0.19	0.40	0.26	-0.58
Grain yield (t/ha)	-0.15	0.62	0.06	-0.01
Harvest Index (%)	-0.30	0.21	-0.22	0.57
Lodging index (%)	-0.30	0.06	-0.41	-0.21
Eigen value	4.35	2.02	1.33	1.19
Percent of contribution	43.5	20.2	13.3	11.9
Cumulative percentage	43.5	63.7	77.0	88.9

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