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Agro-Morphological Traits Diversity in Tef [*Eragrostis Tef* (Zucc.) Trotter] Genotypes from Various Sources

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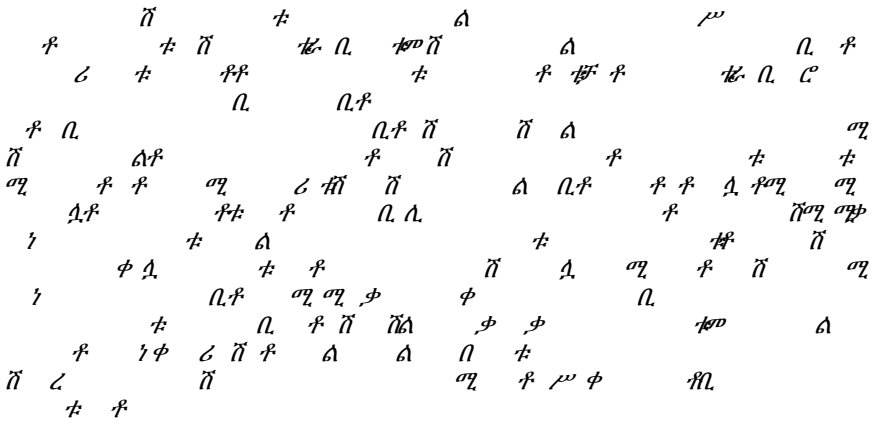

Abstract

A total of 188 tef genotypes including 144 pure lines selected from germplasm collection, 35 released varieties, eight breeding lines and their parents were evaluated in three replications at two locations in Ethiopia. The objectives were to assess the magnitude and pattern of phenotypic diversity in tef genotypes obtained from various sources in Ethiopia. Combined analysis of variance revealed highly significant ($P \leq 0.01$) differences among genotypes, locations and genotype by environment interaction for all studied traits. Thus, wide ranges of variations were observed for days to heading (40.3 to 60.8 days) and maturity (101 to 122.5 days), plant height (60.7 to 107.1 cm), panicle length (19.5 to 39.5 cm), number of fertile tillers per plant (2.1 to 5.5) and spikelet per panicle (156.7 to 441.7), 1000 kernel weights (20.7 to 33.0 mg), grain yield (3.7 to 7.3 t/ha) and lodging index (44.7 to 79.3%). Cluster analysis revealed six distinct clusters of 188 individual tef genotypes while the 14 populations were grouped into four distinct clusters. In general, existence of sufficient level of genetic variation was revealed for future use in tef improvement.

Introduction

Tef is the most important staple cereal having a dozen of agronomic, nutritional and health merits. Despite its various importance the national productivity of tef (1.66 t/ha) is still very low compared to the common cereals grown in Ethiopia (CSA, 2017). Poor dissemination of improved varieties and production packages, inability to tackle the problem of lodging are among the major factors limiting the productivity of tef.

Characterization of germplasm is the process of detecting genetic diversity existing within or among germplasm accessions using descriptor lists of morphological characters or at the level of gene expression or DNA sequences (de Vicente *et al.*, 2005). This genetic characterization, according to breeders, involves the evaluation of agronomic performance of accessions for different morpho-agronomic and physiological characters under various environmental conditions. Genetic characterization and evaluation provides essential information for germplasm utilization, establishment of core collections as well as detection of duplications in collections (Carvalho, 2004). Such characterization works are usually performed using morpho-agronomical characters, biochemical and modern molecular methods (Kebebew *et al.*, 2001c; Carvalho, 2004; de Vicente *et al.*, 2005; Zeid *et al.*, 2012; Solomon *et al.*, 2013) or combination of various approaches.

Morphological markers are the earliest markers utilized in the assessment of genetic diversity within and between populations. Even though they have low polymorphism, heritability and expression, and are vulnerable to environmental influences (Smith and Smith, 1992; Mondini *et al.*, 2009), they are simple and direct measure of phenotypes and cheap to characterize germplasm accessions.

Various studies reported the existence of wide range of variation in tef varieties (Fufa, 1998; Habte *et al.*, 2011; Habte *et al.*, 2017), cultivars (Hailu *et al.*, 1990) and germplasm accessions (Kebebew *et al.*, 2000; Kebebew *et al.*, 2001b; Kebebew *et al.*, 2001a) for days to maturity, plant height, culm and panicle length, and number of tillers per plant based on study of morpho-agronomic characters. Besides, wide range of phenotypic variability and heritability in grain yield and yield related characters were also reported (Kebebew *et al.*, 2001; Habte *et al.*, 2017). The range of values reported for phenological traits is very useful for selection of genotypes for different maturity groups and adaptation (Kebebew *et al.*, 2002a; Kebebew *et al.*, 2002b). Panicle form, seed and lemma color, embryo mark and basal stalk color are the major indicators of morphological variation in tef (Seyifu, 1997; Hailu and Seyifu, 2001). Genotypes with very loose panicle have been identified to have the highest yield and wider adaptation compared to the

other panicle forms (Hailu, 1988). Cluster and principal component analysis have also revealed the existence of variation in tef (Temesgen *et al.*, 2005; Kebebew *et al.*

This experiment was laid in randomized complete block design with three replications. Each genotype was grown on two rows of 0.5 m length in each plot at a spacing of 0.2 m between genotypes, 0.4 m between rows and 1.5 m between replications. During the crop growing period, all agronomic and cultural practices recommended for tef production were applied at each location.

Data collection

Data were collected on days to panicle emergence, days to maturity, plant height, panicle length, culm length, peduncle length, number of culm internodes, culm diameter, number of fertile tillers per plant, shoot biomass per plot, grain yield per plot, 1000-kernel weight, the index of harvest and lodging. All data were collected on plot basis, except for plant height, panicle and peduncle length, number of culm internodes, number of spikelet, number of fertile tillers that were recorded using the average of five plants randomly tagged in each plot before flowering.

Statistical analysis

Variance homogeneity test and combined analysis of variance were performed using the general linear model (PROC GLM) procedure to determine the effect of environment (E), genotype (G) and GE interaction for the various traits of tef using SAS software (SAS, 2002). Mean separation was performed using Duncan's multiple range test at 5% probability level. Cluster analysis and principal component analysis were conducted using MINITAB software version 17.1 (MINITAB, 2007). Partitioning of the total variance into components due to genotype (σ^2_g), environment (σ^2e) and genotype by location interaction (σ^2gl) variances was performed from the analyses of variance by assuming various observed mean squares equal to their expected mean squares as suggested by Singh and Chaudhary (1985). Thus,

$$\sigma^2g = [(\sigma^2e + R\sigma^2gl + RL\sigma^2g) - (\sigma^2e + R\sigma^2gl)]/RL$$
$$\sigma^2gl = [(\sigma^2e + R\sigma^2gl) - (\sigma^2e)]/R$$
$$\sigma^2ph = \sigma^2g+\sigma^2gl/L +\sigma^2e/RL$$

Where: σ^2g = genotype variance, σ^2e= environmental variance and σ^2gl = genotype by location interaction variance and σ^2_P = phenotypic variance.

Broad-sense heritability (h^2b) was calculated as: $h^2b = \sigma^2g / [\sigma^2g+\sigma^2gl/L +\sigma^2e/RL] \times 100$

The predicted response to selection or the expected genetic advance (GA) was calculated, assuming the selection intensity of 5%, as:

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

$$GAM = (\frac{GA}{X}) \times 100$$

Where: GAM= Genetic advance as percent of mean, X= grand mean, GA = expected genetic advance from selection and K = the selection differential (K = 2.06 at 5% selection intensity) and h^2 = broad-sense heritability (Singh and Chaudhary, 1985).

Table 1. Passport description of the test genotypes

Origin/ Category	Collection Zones	No of genotypes (serial No.)	Name of genotypes (Accessions)	Altitude (m)
Lines from landrace accessions	Central Tigray	12 (1-12)	Acc. nos. 19132-2, 19132-3, 19166-1,19253-1,19253-2, 234407-1, 234407-2, 237184-1, 237205-2, 243513-1, 243513-3 & 243520-2	1350-2640
	East Gojam	12 (13-24)	Acc. nos. 9545-1, 9556-1, 19516-1, 19516-3, 55221-1, 55221-2, 212698-2, 229768-1, 229768-3, 229768-4, 55046-2 and 55046-3	1470-2650
	East Shewa	12 (25-36)	Acc. nos. 15361-3, 17335-1, 18460-0, 18466-2, 18466-3, 236963-1, 236963-2, 236965-1,236965-3,236967-1, 236967-2 and 236972-0	1657-2303
	East Tigray	12 (37-48)	Acc. nos. 15297-1, 15297-2,15299-1,15299-3,19201-1,19201-3, 19202-2, 234460-1, 234460-2, 234460-3, 242540-1 and 242540-2	1979-2632
	North Gonder	12 (49-60)	Acc.9448-1, 9448-2, 9451-2, 9469-2, 9472-2, 9472-4,19343-2, 242186-3, 242186-4, 243540-1, 243540-3 and 243540-4	1840-2208
	North Shewa	12 (61-72)	Acc. nos. 9559-1, 9559-2, 15309-2, 15309-3, 15322-1, 15322-2, 18385-2, 212482-1, 236745-2, 236746-0, 236748-2 and 236957-1	1260-2670
	North Wello	12 (73-84)	Acc. nos. 55104-3, 215196-1, 215200-1, 215200-2, 215200-3, 234356-4, 234985-2, 234993-1, 234993-3, 237148-1, 237148-5 and 243501-2	1520-2950
	South Gonder	12 (85-96)	Acc. nos. 19341-2, 19341-3, 19367-2, 19374-1, 55293-2, 212717-0, 212720-1, 225919-2, 225919-3, 225919-4, 225919-7 and 242160-1	1804-2950
	South Wello	12 (97-108)	Acc. nos. 212607-2, 212612-3, 212614-1, 212614-2, 225898-1, 242214-1, 242214-2, 243491-2, 2433497-2, 243504-1, 243504-2 and 243504-3	1550-3090
	West Gojam	12 (109-120)	Acc. nos. 19394-1, 19443-3, 19452-4, 19506-2, 19506-4, 242140-3, 242144-1, 242144-3, 242155-1, 242155-3, 55029-2 and 55029-3	1890-2735
	West Shewa	12 (121-132)	Acc. nos. 17365-1, 17371-3, 18410-1, 18410-2, 18410-3,18414-2, 18414-4, 18423-3, 236757-2, 236760-1, 236760-4 and 236760-6	1640-2674

Table 1. *Continued*

Origin/ Category	Zones	No of genotypes (serial No.)	Name of genotypes (Accessions)	Altitude (m)
	West Tigray	12 (133-144)	Acc. nos. 9419-1, 9444-2, 9444-3, 19241-1, 19241-2, 234435-2, 237236-3, 237236-4, 237239-3, 243526-2, 243526-4 and 243526-5	1260-2054
Improved varieties by breeders	Improved varieties	35 (145-179)	Enatite (DZARC), Asgori (DZARC), Magna (DZARC), Wellenkomi (DZARC), Menagesha (DZARC), Melko (DZARC), Tsedey (DZARC), Gibe (DZARC), Ziquala (DZARC), Dukem (DZARC), Holetta Key (HARC), Ambo Toke (HARC), Gerado (DZARC), Koye (DZARC), Key Tena (DZARC), Gola (SARC), Ajora (ArARC), Genete (SARC), Zobel (SARC), Dima (AARC), Yilmana (AARC), Dega Tef (DZARC), Gimbichu (DZARC), Amarach (DZARC), Quncho (DZARC), Gudurru (BARC), Gemechis (MARC), Mechare (SARC), Kena (BARC), Etsub (AARC), Laketch (SARC), Simada (DZARC), Boset (DZARC), Kora (DZARC) and Were-Kiyu (SARC	-
Lines from crosses of mutant by adapted cultivars	Breeding lines	10 (180-189)	Kaye Murri (cultivar, parent), *Kinde* (Mutant line, parent), Quncho X *Kinde* (RIL-85),Quncho X *Kinde* (RIL-91), Quncho X *Kinde* (RIL-96),*Kinde*X Kaye Murri (RIL-11),*Kinde*X Kaye Murri (RIL-302), *Kinde*X Kaye Murri (RIL-44), *Kinde*X Kaye Murri (RIL-69) and *Kinde*X Kaye Murri (RIL-81)	-

DZARC, HARC, SARC, ArARC, AARC, BARC and MARC refer to the Debre Zeit, Holetta, Sirinka, Areka, Adet, Bako and Melkassa Agricultural Research Centers, respectively.

Results and Discussion

Combined analysis of variance revealed highly significant ($P \leq 0.01$) differences among the different factors for the studied traits (Table 2). Thus, the mean square due to genotypes was significant for all traits while that of location was also significant for all traits except for culm length. Similarly, the mean square due to G *X* E interaction was also highly significant ($P \leq 0.01$) for most of the studied traits except plant height, peduncle length, number of total and fertile tillers ($P > 0.05$). The fact that the G *X* E interaction was significant shows the differential performance of genotypes across different environments (Table 2).

Table 2. Combined ANOVA across two locations for 16 traits of 188 tef genotypes

Trait	Loc	Rep (loc)	Geno	GXE	Error
DH	298350.2***	86.8***	97.9***	31.9***	5.47
DM	510085.3***	41.3***	92.85***	63.9***	7.86
GFP	27415.5***	90.4***	98.7***	71.3***	9.34
PH	2313.89***	137.5***	392.4***	13.5ns	13.48
PL	1429.7***	54.2***	101.0***	2.0ns	5.64
CL	0.32ns	17.8ns	219.2***	15.5**	11.92
Pdl	362.0***	145.0***	36.6***	0.8ns	3.85
SCD	159.9***	0.37***	0.14***	0.10***	0.04
TT	140.2***	17.5***	2.41***	0.02ns	0.47
FT	73.1***	8.9***	2.14***	0.02ns	0.43
SPK	6432547.4***	3120.3**	21514.7***	13205.3***	896.7
SBM	36895.1***	23.4***	89.0***	56.4***	1.09
GY	666.1***	0.57***	2.5***	1.6***	0.05
HI	2574.4***	0.72ns	29.1***	27.8***	0.41
TKW	364.0***	32.2***	24.4***	22.2***	6.41
LG	4036.4***	669.0***	201.0***	242.8***	21.33

Abbreviations: DH: days to heading; DM: days to maturity; GFP: grain filling period; PH: plant height; PL: panicle length; CL: culm length; Pdl: peduncle length; SCD: second culm diameter; TT: number of total tillers; FT: number of fertile tillers; SPK: number of spikelet; SBM: shoot biomass; GY: grain yield; HI: harvest index; TKW: thousand kernel weight; LG: lodging index. *,** significantly different at 5 and 1%, respectively.

Patterns of quantitative traits variation in tef

In this study, a wider range of variations were observed for all quantitative traits of the 188 tef genotypes evaluated at two locations (Table 3). For instance, the days to heading and maturity ranged from 40.3 to 60.8 and 101 to 122.5 days, respectively. Kebebew *et al*. (2001a), on the other hand, reported values ranging from 37 - 46 and 83-101 for days to heading and maturity, respectively, based on study conducted using germplasm collections whereas, Hailu *et al*. (1990) reported a range of 82-113 for days to maturity. Such variations are very essential to augment the efforts to develop varieties fitting to various agro-ecologies and cropping systems to increase tef production and productivity in Ethiopia. Thus, it enables breeders to develop variety that can escape late season drought by focusing on traits related g on l 37

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- 427.4 for number of spikelet per panicles and 16.9-28.8% for harvest index (Kebebew *et al*., 2001a). In the present study, thousand kernel weights and grain yield ranged from 20.7 mg to 33.0 mg and 3.7 to 7.3 t/ha respectively. The wide variation observed for plant height, culm diameter and tillering capacity in this study indicates the possibility to combat the problem of lodging. Similarly, the variation in number of spikelet per panicle, harvest index, thousand kernel weight, biomass and grain yield imply the possibility to develop varieties with better grain yield and/or other biological yields. Besides, the value of lodging percent ranged from 44.7 to 79.3 showing the possibility to make selection for lodging resistance among the studied genotypes (Table 3).

Table 3. Range, mean and Standard error (SE) of mean for 13 different traits of tef genotypes (based on average of 188 genotypes from 14 populations)

Variable	Range				Mean± SE
	Minimum		Maximum		
	Value	Genotype	Value	Genotype	
Days to heading	40.3	Simada	60.8	Acc. 236760-6	51.1±0.30
Days to maturity	101	Acc. 212614-2	122.5	Melko	114.0±0.29
Plant height (cm)	62.7	Acc. 19506-4	107.1	Acc. 212698-2	85.9±0.59
Panicle height (cm)	19.5	Acc. 55221-1	39.5	Acc. 18460-0	30.4±0.30
Peduncle length (cm)	12.5	Acc. 237205-2	26	Acc. 242160-1	18.9±0.18
Culm diameter (mm)	1.2	Acc. 19506-4	2.1	Acc. 243491-2	1.5±0.01
Number of fertile tillers	2.1	Acc. 243540-3	5.5	Acc. 242186-4	3.2±0.04
Number of spikelet per panicle	156.7	Acc. 236760-4	441.7	Acc. 15309-3	312.5±4.37
Shoot biomass (kg/ha)	15.8	RIL-11	36.7	Acc. 237184-1	26.3±0.28
Grain yield (kg/ha)	3.7	RIL-302	7.3	RIL-91	5.6±0.05
Harvest index (%)	14.7	Acc. 237205-2	24.3	Acc. 234407-2	21.73±0.10
Thousand kernel weights (mg)	20.7	Acc. 243513-1	33	Acc. 19241-1	26.7±0.15
Lodging index	44.7	Key Murri	79.3	Acc. 242155-3	67.2±0.42

Estimates of variance components, heritability and genetic advance

PCV and GCV values below 10%, 10% - 20% and above 20% are considered to be low, intermediate, and high, respectively (Khorgade *et al*., 1985). In this study, the values for PCV ranged from 3.45 % for days to maturity to 19.16% for number of spikelet per panicle while GCV ranged from 0.0 for lodging index to 16.96 for number of fertile tillers (Table 4). Thus, 33.3 % and 66.7% of the studied traits had low PCV and GCV values, respectively, while the rest traits had intermediate PCV and GCV. Thus, panicle length, peduncle length, number of fertile tillers and spikelet per panicle had intermediate values of both GCV and PCV while second culm diameter, yield of shoot biomass and grain had intermediate value at PCV level only. The range of value estimated for GCV and PCV in this study is in line with the previous reports of 6.1 to 40.2% for PCV and 3.0 to 22.1% for GCV (Kebebew *et al*., 1999), 4.3 to 21.7 for PCV and 4.0 to 20.3% for GCV (Habte *et al*., 2015a) while it is far below the previous report of 2 to 58% for PCV and less than 1 to 35% for GCV (Kebebew *et al*., 2000). Heritability and genetic advance are

important factors determining the success of selection in breeding programs. Estimates of heritability (h^2) in this study ranged from near zero for lodging index to 96.6% for plant height (Table 4). Hence, the highest heritability estimates were for plant height (96.6%), panicle length (95.1%), peduncle length (91.1%), and number of fertile tillers per plant (83.7%), respectively. Such high heritability indicates high proportion of genetic variance that could be inherited and would be exploited by breeders to select superior genotypes based on phenotypic performance (Peter *et al*., 2008; Tazeen *et al*., 2009, Mulugeta *et al*., 2017). Lodging index, 1000-kernel weight, days to maturity, grain yield and second culm diameter, however, had relatively low heritability value (below 40%). Estimates of genetic advance as percent of mean ranged from 0% for lodging index to 31.96 % for number of fertile tillers (Table 4). Singh (2000) suggested the importance of considering heritability along with genetic advance. In this study, highest heritability coupled with high genetic advance were estimated for plant height (96.6%, 18.8%), panicle length (95.1%, 26.4%), peduncle length (91.1%, 24.6%) and number of fertile tillers per plant (83.7%, 31.9%). This indicates that additive gene action plays a key role in controlling the expression and existence of high expected genetic gain through selection.

Principal component analysis

The principal component analysis (PCA) based on 12 quantitative traits of 188 tef genotypes from various origin was assessed and is presented (Table 5). In this study, the first three PCs with eigen value greater than unity contributed for 59.4% of the total variation. Thus, PC1, PC2 and PC3 accounted for 32.9%, 15.8% and 11.4% of the total variation, respectively. All traits other than peduncle length and 1000-kernel weight contributed for most of the variation in PC_1 (Table 5) whereas the variation in PC_2 was mainly due to grain yield and shoot biomass, lodging index and peduncle length. Furthermore, peduncle length, 1000-kernel weights, days to heading and grain yield, respectively, were the major traits for the variation in PC_3.

Table 4. Estimates of variance components, heritability and genetic advance for 188 tef genotypes evaluated at two locations

Trait	gσ^2	glσ^2	lσ^2	eσ^2	Phσ^2	σPh	σg	GCV (%)	PCV (%)	H^2	GA	GAM	Grand mean
DH	11.00	8.81	528.42	5.47	16.32	4.04	3.32	6.49	7.91	67.42	5.61	10.98	51.09
DM	4.82	18.69	905.30	7.86	15.48	3.93	2.20	1.93	3.45	31.15	2.52	2.21	114.0
PH	63.14	0.02	3.86	13.48	65.40	8.09	7.95	9.25	9.42	96.55	16.1	18.73	85.86
PL	16.01	0.0	2.44	4.91	16.83	4.10	4.00	13.2	13.5	95.14	8.04	26.43	30.42
PdL	5.56	0.0	0.38	3.25	6.10	2.47	2.36	12.5	13.1	91.12	4.64	24.56	18.88
SCD	0.01	0.02	0.28	0.04	0.03	0.16	0.10	6.54	10.7	37.50	0.12	7.56	1.53
FT	0.30	0.0	0.11	0.35	0.36	0.60	0.55	17.0	18.5	83.72	1.03	31.94	3.23
SPK	1384.9	4102.9	11376.3	896.7	3585. 8	59.9	37.2	11.9	19.2	38.62	47.6	15.25	312.5
SBM	5.44	18.42	65.23	1.09	14.83	3.85	2.33	8.85	14.6	36.68	2.91	11.04	26.34
GY	0.14	0.53	1.18	0.05	0.41	0.64	0.37	6.73	11.6	33.87	0.45	8.17	5.56
TKW	0.37	5.26	0.56	6.41	4.07	2.02	0.61	2.28	7.55	9.09	0.37	1.40	26.72
LI	0.0	66.85	5.62	21.33	36.98	6.08	0.00	0.00	0.06	0.00	0.00	0.00	67.15

Abbreviations: DH: days to heading; DM: days to maturity; PH: plant height; PL: panicle length; Pdl: peduncle length; SCD: second culm diameter; FT: number of fertile tillers; SPK: number of spikelet; SBM: shoot biomass; GY: grain yield; TKW: thousand kernel weight; LI: lodging index. σ^2g=genotypic variance, σ^2ph=phenotypic variance, σ^2e = error variance, lσ^2 = environmental variance, σ^2gxl=variance of genotype x environment interaction, r intra class=intra class correlation, GCV (%) = percent genotypic coefficient of variation, PCV (%) = percent phenotypic coefficient of variation, H^2= broad sense heritability, GA=genetic advance, GAM=genetic advance as percent of mean

Principal component analysis based on 14 predetermined populations, on the other hand, revealed that the first PCs with eigen value greater than one accounted for 75.8% of the total variations. In this analysis, PC1, PC2 and PC3 contributed for 39.5%, 21.6% and 14.7% of the total variations (Table 5), respectively. Thus, the majority of variations in PC1 were due to lodging index, panicle length, shoot biomass, days to maturity, plant height and grain yield whereas those in PC_2 were due to peduncle length, culm diameter, shoot biomass and plant height. On the other hand, the variation in PC3 was due to number of spikelet per panicle, 1000-kernel weight and number of fertile tillers. In the present study, the variation explained based on individual genotypes was very small whereas variation explained based on populations was comparable to the previous report of 81% total variance for germplasm collected from south and western Ethiopia (Kebebew *et al*., 2003). On the other hand, Habte *et al* (2015a) reported 78.3% of the total variation based on 36 brown seeded tef genotypes while the present result is far below the 85% reported for 28 semi dwarf tef genotypes based on the first five PCs (Habte *et al*., 2017). The variation in PC1 was due to all studied traits other than peduncle length and 1000-kernel weight whereas that of PC2 was due to grain yield, shoot biomass, lodging index and peduncle length. However, grain yield, 1000-kernel weight and days to heading were the major traits contributing to the variation in PC3 (Table 6). Various authors also reported the contribution of different phenotypic traits to each PCs in tef (Kebebew *et al*., 2003; Dagnachew *et al*., 2011; Habte *et al*., 2013; Plaza *et al*., 2013; Habte *et al*., 2015a and b; Habte *et al*., 2017).

Table 5. Principal component analysis for 12 quantitative traits of 188 tef genotypes from various origins

Variable	PC1	PC2	PC3
Days to heading	0.323	-0.05	-0.468
Days to maturity	0.368	-0.196	-0.088
Plant height	0.443	0.051	0.113
Plant height	0.359	0.213	-0.046
Peduncle length	0.076	-0.39	0.52
Culm diameter	0.387	-0.244	0.091
Fertile tillers	-0.217	0.112	-0.262
Spikelet per panicle	0.338	0.013	-0.1
Shoot biomass	0.267	0.478	0.052
Grain yield	0.142	0.513	0.399
Thousand kernel weights	0.004	-0.135	0.473
Lodging index	-0.16	0.42	0.127
Eigenvalue	3.866	1.893	1.371
Proportion	0.322	0.158	0.114
Cumulative	32.2	48.0	59.4

Table 6. Principal component analysis of 12 traits of tef genotypes based on 14 predetermined populations of germplasm collections

Variable	PC1	PC2	PC3
Days to heading	0.177	0.297	0.271
Days to maturity	0.366	0.142	0.196
Plant height	0.36	-0.311	0.102
Panicle length	0.375	-0.281	0.091
Peduncle length	-0.001	-0.556	-0.098
Culm diameter	0.265	-0.4	0.05
Fertile tillers	-0.235	0.073	0.451
Spikelet per panicle	-0.042	-0.269	0.628
Shoot biomass	0.372	0.338	0.016
Grain yield	0.352	0.129	0.061
1000- kernel weights	0.174	-0.084	-0.506
Lodging index	0.38	0.177	-0.029
Eigenvalue	4.736	2.589	1.768
Proportion	0.395	0.216	0.147
Cumulative	0.395	0.61	0.758

Cluster analysis

Cluster of individual tef genotypes

Cluster analysis based on 12 standardized traits of 188 individual tef genotypes from various sources resulted in the formation of six distinct clusters consisting of 19 to 50 genotypes. Similar number of clusters were reported previously by different authors using germplasm collections (Kebebew *et al*, 2001a, 2003), released tef varieties (Habte *et al*., 2015b), brown seeded tef genotypes (Habte *et al*., 2015a). Cluster I and V consisted of 26 genotypes whereas cluster II, III, IV and VI consisted of 32, 19, 35 and 50 genotypes, respectively (Table 7, 8; Fig. 1). The first cluster consisted of 26 genotypes from 11 pre-determined populations with the majorities from Central Tigray (5) North Gonder (3), North Wello (3), West Gojam (3) and improved varieties (3). Cluster II, on the other hand, consisted of 32 genotypes from 11 populations whereby the majority of the genotypes were from populations of breeding lines (7) improved varieties (5), West Gojam (4) and East Gojam (3). Cluster III consisted of 19 genotypes whereby, the majorities were from populations of North Wello (4) followed by North Shewa (3), Central Tigray (2), South Gonder (2) and West Tigray (2) In cluster IV, genotypes from populations of improved varieties (7), South Wello (5) North Gonder (4), North Shewa (3) and South Gonder (3) covered the majority. Cluster -V consisted of 26 genotypes from 13 populations, with the majority from improved varieties (7) and East Shewa (5). Cluster-VI, on the other hand, consisted of the largest number of genotypes from all predetermined populations except the breeding lines. Thus, the highest number of genotypes

were from improved varieties (12) followed by East Tigray (6), West Shewa (6) and East Gojam (5) populations.

Based on cluster mean, genotypes in cluster-I had the highest number of fertile tillers while it had the least peduncle length. Genotypes in cluster-II, however, were characterized to have the shortest days to heading and maturity, plant height and panicle length, least value of second culm diameter, number of spikelet per panicle and shoot biomass and the highest value of lodging index. Cluster-III had the highest value of days to maturity, peduncle length and 1000-kernel weight and the lowest value of lodging index with moderate values for all remaining studied traits. Cluster-IV, furthermore, had the least value for grain yield and 1000-kernel weight while it had the longest days heading with moderate values for the remaining traits. Surprisingly, cluster-V had the highest values for five of the twelve studied traits while it had the least value for number of fertile tillers only. Genotypes in cluster-VI, were found to have the highest value of grain yield and average values of all studied traits (Table 8). Thus, breeders dealing with high yield should use genotypes in cluster VI whereas those dealing with early maturity should focus on genotypes in cluster-II. Besides, in variability creation, excellent level of genetic variability and high heterosis can be obtained when crossing is to be made between cluster 2 and 5 followed by cluster 1 & 3, Cluster 2 & 3 and cluster 1 & 5, respectively (Table 9).

Table 7. Clustering of 188 tef genotypes into six clusters using mean of 12 morpho-agronomic characters

Cluster	No of genotypes	Name of genotypes
C1	26	Acc. 19166-1, 19253-1, 234407-2, 243513-3, 243520-2, 19516-1, 55221-1, 18466-3, 236972-0, 234460-3, 9448-1, 242186-4, 243540-1, 15322-1, 212482-1, 215200-1, 237148-1, 243501-2, 19506-4, 242140-3, 55029-2, 18410-2, 237236-4, Holeta Key, Key Tena, Yilmana
C2	32	Acc. 243513-1, 55221-2, 229768-3, 55046-3, 242540-2, 9472-4, 15309-2, 234993-1, 19341-2, 225919-3, 212614-2, 225898-1, 19394-1, 19452-4, 242155-1, 242155-3, 17365-1, 236760-1, 9444-2, 234435-2, Asgori, Tseday, Amarach, Simada, Boset, *Kaye Murri,* RIL-85, RIL-91, RIL-96, RIL-11, RIL-302 and RIL-69
C3	19	Acc. 19132-2, 19132-3, 236965-1, 19202-2, 9559-1, 9559-2, 236746-0, 55104-3, 215200-2, 234985-2, 234993-3, 19341-3, 19374-1, 242214-1, 242144-1, 237236-3, 237239-3, Magna and RIL-81.
C4	35	Acc.234407-1, 237205-2, 19516-3, 18466-2, 19201-1, 242540-1, 9448-2, 9469-2, 9472-2, 243540-3, 15309-3, 18385-2, 236745-2, 215196-1, 234356-4, 212717-0, 225919-2, 225919-7, 212607-2, 212612-3, 2433497-2, 243504-1, 243504-3 and 19443-3, 18423-3, 236757-2, 19241-1, 243526-2, Holenkomi, Melko, Gibe, Gerado, Dega Tef, Gemechis and Kena
C5	26	Acc.19253-2, 55046-2, 15361-3, 17335-1, 18460-0, 236963-1, 236965-3, 19201-3, 9451-2, 242186-3, 15322-2, 19367-2, 212720-1, 242214-2, 19506-2, 18414-4, 9444-3, 243526-5, Genet, Zobel, Quncho, Guduru, Etsub, Laketch, *Kinde* and Kora
C6	50	Acc.237184-1, 9545-1, 9556-1, 212698-2, 229768-1, 229768-4, 236963-2, 236967-1, 236967-2, 15297-1, 15297-2, 15299-1, 15299-3, 234460-1, 234460-2, 19343-2, 243540-4, 236748-2, 236957-1, 215200-3, 237148-5, 55293-2, 225919-4, 242160-1, 212614-1, 243491-2, 243504-2, 242144-3, 55029-3, 17371-3, 18410-1, 18410-3, 18414-2, 236760-4, 236760-6, 9419-1, 19241-2, 243526-4, Enatit, Menagesha, Ziquala, Dukem, Ambo-Toke, Koye, Gola, Ajora, Dima, Gimbichu, Mechare and Workiyu

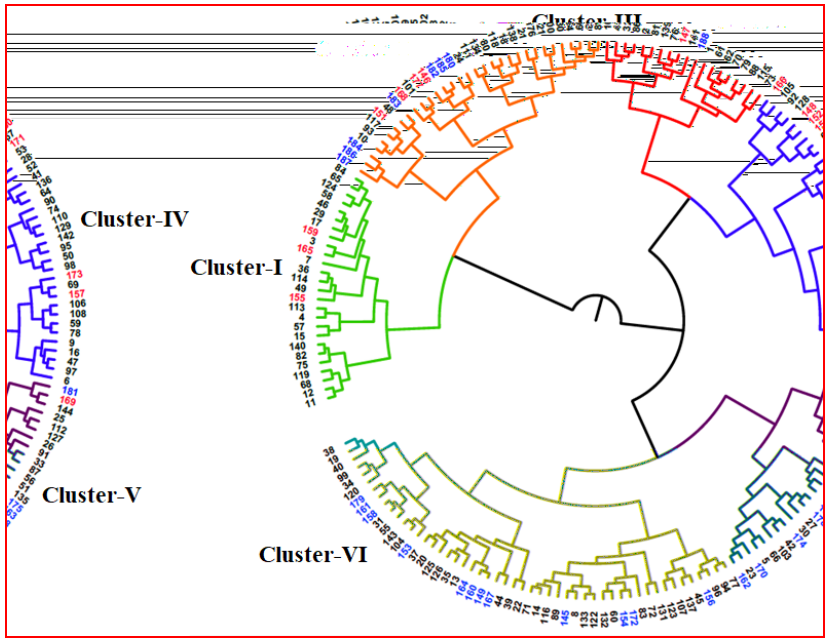

Figure 1. Dendrogram based on Ward Method showing the genetic relationship among 188 tef genotypes from various sources: in Ethiopia using 12 major traits. Genotypes and their collection zones are described as 1-12 (central Tigray), 13-24 (East Gojam), 25-36 (East Shewa), 37- 48 (East Tigray), 49-60 (North Gonder), 61-72 (North Shewa), 73-84 (North Wello), 85-96 (South Gonder), 97-108 (South Wello), 109-120 (West Gojam), 121-132 (West Shewa) and 133-144 (West Tigray). Improved varieties (145-179) and breeding lines (180-189) are written in red and blue color, respectively.

Table 8. Cluster means of 12 quantitative traits of 188 tef genotypes

Trait	Cluster mean					
	I	II	III	IV	V	VI
Days to heading	50.86	47.23	52.21	54.45	54.14	49.33
Days to maturity	111.97	108.92	116.32	116.17	115.51	115.22
Plant height (cm)	80.16	77.54	84.74	87.97	95.01	88.33
Panicle length(cm)	29.25	26.40	25.60	32.33	34.42	32.03
Peduncle length(cm)	16.16	18.88	22.06	18.19	18.85	19.58
Culm diameter(mm)	1.42	1.41	1.65	1.58	1.70	1.54
Number of fertile tillers	3.87	3.36	2.91	3.38	2.85	3.02
Number of spikelet per panicle	275.93	266.89	308.84	368.52	379.65	350.94
Shoot biomass (kg/ha)	27.57	23.53	24.17	24.99	28.99	27.87
Grain yield(kg/ha)	5.78	5.38	5.08	4.92	5.87	6.02
Thousand kernel weights	26.60	26.59	28.11	26.09	27.01	26.62
Lodging index	68.69	69.50	62.72	67.44	63.88	68.04

Table 9. Distance among six clusters of 188 tef genotypes

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6
Cluster1	0					
Cluster2	9.73	0				
Cluster3	30.67**	26.65**	0			
Cluster4	12.51	20.96	17.14	0		
Cluster5	25.34**	38.98**	19.17	12.23	0	
Cluster6	12.97	19.55	16.07	9.63	6.81	0

Clustering of tef population

Clustering based on 14 populations of tef from various sources resulted in the formation of four distinct clusters (Fig. 2). The number of genotypes in each cluster ranged from one genotype in cluster-IV to six genotypes in cluster-III while the first and second cluster consisted of three and four genotypes, respectively. In this study, the breeding lines remained solitary whereas the population of improved varieties was grouped with populations from East, West and North Shewa, North Gonder and West Tigray zones. The grouping of populations from different parts of Shewa zones is due to geographic proximity along the three zones. Cluster-I consisted of three populations (Central Tigray, North Wello and West Gojam) whereas, cluster-II consisted of four populations (East Gojam, East Tigray, South Gonder and South Wello zone). The grouping of Central Tigray population with West Gojam populations could be due to seed movement by trans human. Thus, populations from adjacent zones and/or distant origin were clustered together may be due to geographic proximity and/or trans human seed exchange. In this population clustering, the largest inter cluster distance was found between Cluster 3 and 4 followed by Cluster 2 and 4, and 1 and 4 to provide best level of genetic recombination (Table 10).

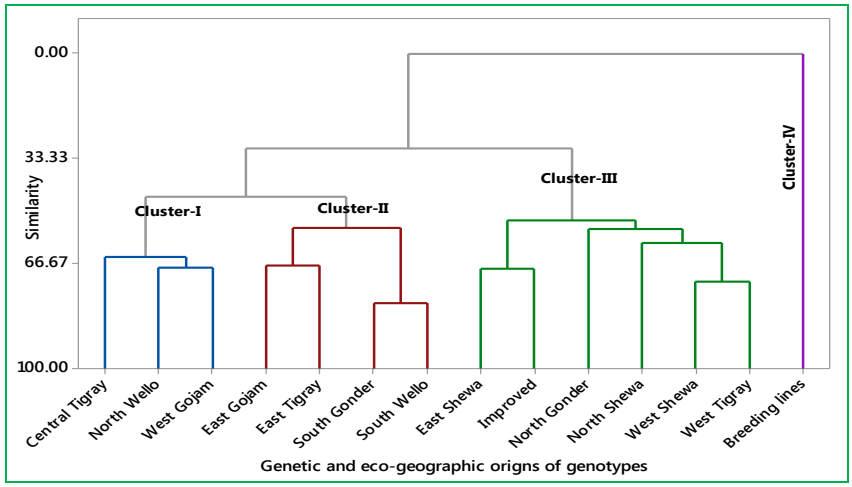

Figure 2. Clustering pattern of the 14 populations based on various sources of origins

Table 10. Distance among four clusters of 188 tef genotypes

	Cluster 1	Cluster 2	Cluster 3	Cluster 4
Cluster 1	0			
Cluster 2	3.21	0		
Cluster 3	3.84	2.97	0	
Cluster 4	6.08	7.01	7.78	0

Conclusion

Though tef is the most important indigenous cereal with various uses, its productivity is still far below its expected genetic potential and that of other major cereal crops grown in Ethiopia. Genetic characterization and evaluation of indigenous germplasm resources are very essential towards development of new tef varieties with traits of interest. In the present study, assessment of agro-morphological trait diversity in tef genotypes from various sources revealed the existence of wide range of trait variations for yield and yield related traits, phenological traits and morphological traits. Especially, genotypes with the highest mean grain yield, shoot biomass, 1000-kernel weight, number of spikelet per panicle and fertile tillers per plant were identified among collections from West Shewa and Central Tigray zones. Such variation could, therefore, be used in future tef breeding to develop varieties useful to combat the effect of climate change and to increase tef productivity.

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