Genetic Variability and Association among Grain Yield and Yield Related Traits in Tef [*Eragrostis tef* (Zucc.) Trotter] Germplasm Collections from Different Parts of Ethiopia

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Abstract

Genetic variability is a key for successful selection of better crop varieties. The present study was, therefore, conducted to determine the magnitude of genetic variation, the broad sense heritability and expected genetic advance and the association among grain yield and yield related traits of recent tef germplasm collections from different parts of Ethiopia. Seventy tef genotypes (68 germplasm collections and 2 released varieties) were evaluated in 7-by-10 alpha lattice design with two replications at Holetta and Debre Zeit Agricultural Research Centers during the main cropping season of 2015. Data were collected on 18 quantitative traits. Analysis of variance showed highly significant ($P<0.01$) genotypic differences for all quantitative traits except for thousand seed weigh and the Genotype x Environment interaction was significant for 14 of the traits. This indicates that breeding for specifically adaptable varieties would be important. The genotypic coefficients of variability (GCV) ranged from 0 to 14.87 % while phenotypic coefficient of variability (PCV) ranged from 7.88 to 31.04 %. The lowest and the highest heritability estimates were observed for grain filling period (0%) and thousand seed weight (0%), and first basal culm internode diameter (46.07%), respectively. The estimates of genetic advance as percent of mean (GAM) ranged from 0% for grain filling period and thousand seed weight to 17% for number of spikelets per panicle and first basal culm internode diameter. Diameters of the first and second basal culm internodes, and panicle length showed relatively high heritability combined with high GAM; these traits can successfully be improved through selection. Moreover, the character of correlation showed selecting longer plant, longer panicle height and high spikelet number increases grain yield, and that higher number of first and second culm internode diameters minimize lodging index.

Key words: Genotypic correlation, GCV, genetic advance, heritability, PCV, Tef

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INTRODUCTION

Tef (*Eragrostis tef* (Zucc.) Trotter) is a C4, self-pollinated, chasmogamous annual cereal crop (Seyfu Ketema, 1997). Tef owes its center of origin and diversity in Ethiopia (Vavilov, 1951). The unleavened bread made of tef flour, "*injera*", is the mainstay of the Ethiopian diet and the straw, "*chid*", is an important feed for livestock (Hailu Tefera and Peat, 1997; Hailu Tefera and Seyfu Ketema, 2001). Mekonnen Melaku *et al*. (2014) noted that the nutrient composition of tef grain has high potential to be used in foods and beverages worldwide. In addition it serves the farmer as a cash crop because both its grains and straw fetch higher market prices than that of the other cereals (Kebebew Assefa *et al.*, 1999; Kenea Yadeta *et al.*, 2001). It has long shelf life and minimal post-harvest damage since the grains are resistant to attack by storage pests (Seyfu Ketema, 1997; Kebebew Assefa *et al.*, 1999). It performs better than other cereals including maize and sorghum under moisture stress conditions and it also performs better than maize, wheat or sorghum under excess moisture (waterlogged) conditions (Hailu Tefera and Seyfu Ketema, 2001). In spite of the enormous food, feed, adaptive, nutritive, health, agronomic and economic qualities, the productivity of tef is relatively low (1.56 t/ha) (CSA, 2015) compared to other cereals. One of the major yield limiting factors is lack of cultivars tolerant to lodging which causes yield losses of up to 25%. Lodging remains the major constraint in tef production because it decreases straw yield and deteriorates the quality of both grain and straw produced. It also imposes restrictions to the use of high rates of nitrogen fertilizers. Furthermore, drought and pests play prominent role in reducing tef yield (Kebebew Assefa *et al.*, 1999; 2011; 2013).

The wide range of agro-climatic conditions in Ethiopia, generally, favors the existence of large amount of genetic diversity for characters that impart adaptation to specific environments and contribute to yield improvement of the crop. On the other hand, successful selection to develop better varieties with high grain yield is dependent on the existence of genetic variability. Therefore, estimating the existing genetic variation among landraces will enable us to determine their potential for further breeding activities (Kebebew Assefa *et al*., 2015; Tiruneh Kefyalew *et al*., 2000). In addition to genetic variability, high estimate of heritability with relatively high genetic advance value can be used as an indicator for the efficiency of the phenotype-based selection (Kebebew Assefa *et al*., 2001b). Moreover, as yield is a complex trait and its inheritance is influenced by many genes which are linked with it, assessment of its correlations with important traits facilitates selection of desired traits directly or in directly affecting it. The objectives of the current study were therefore,: to determine i) the magnitude of genetic variation, ii) the broad sense heritability and expected genetic advance and iii) the association among grain yield and yield related traits of tef germplasm recently collected from different parts of Ethiopia.

MATERIALS AND METHODS

The experiment was conducted at Holetta and Debre Zeit Agricultural Research Centers (HARC and DZARC) during the 2015/16 main cropping season. DZARC is located at 8^{o}44'N and 38^{o}58' E, and HARC is located at $9^{o\cdot}$03'N and 38^{o}30'E at an elevation of 1860 m.a.s.l and 2390 m.a.s.l., respectively. The soil of the experimental site at Holetta and Debre Zeit Research Center is Nitosol and Vertisol, respectively.

A total of 70 tef genotypes recently collected (2012-2014) by the National Tef Research Program from six zones and two released varieties ('Quncho' and 'Tsedey') were included in the present study (Table 1). These materials originated from panicles, which were sown in separate rows for purification at DZARC during the 2013 and 2014 main-cropping seasons and the 2015 off-season. The check variety 'Quncho' was released mainly for high potential areas and 'Tsedey' for low moisture areas. A 7x10 alpha lattice design with two replications and 10 blocks per replication was used at both locations. Each plot with an area of 1mx1m consisted five rows with spacing of 0.2m. All other pre- and post-planting management practices were made as per the recommendations for tef husbandry in the respective test locations.

Data collection

Data were collected on 18 quantitative traits. Out of these Days to heading; Days to maturity; Days to grain filling period; Lodging Index [following the method of Caldicott and Nuttall, (1979), who calculate lodging index as the sum of product of each scale (0-5) of lodging on 0 being erect and 5 completely lodged plant and their respective percentage divided by five]; Total biomass (g); Grain yield (g); Straw yield (g); Thousand seed weight (g); and Harvest Index (HI) were determined on whole plot basis. On the other hand, Plant height (cm); Panicle length (cm); Culm length (cm); Number of total tillers per plant; Number of fertile tillers per plant; Number of spikelets per panicle; Number of primary branches per main panicle; First basal culm internode diameter (mm) and Second basal culm internode diameter (mm) were determined on individual plant basis using five plants randomly sampled from the central parts of the middle rows of each plot.

Statistical analyses

Data of all quantitative variables were subjected to combined analysis of variance using SAS (SAS Institute, 2002). Homogeneity of error variance was tested using the F-max method of (Hartley, 1950).

To estimate the variation among the germplasm, all quantitatively measured variables were subjected to analysis of variance using SAS (SAS Institute, 2002). In the analysis, both genotype and location were considered as fixed effects. The total phenotypic variance of each of the traits were partitioned into contributions by genetic and non-genetic factors using the analysis of variance components method suggested by Singh and Chaudhury (1996). The variance components were determined from mean square values of the ANOVA for each trait according to Prasad et al (1981) as follows:

$\sigma^2G = [(MSG) - (MSE)] / r$

$\sigma^2P = [\sigma^2G + (\sigma^2E/r)]$,

where: σ^2G = Genotypic variance; σ^2P = Phenotypic variance; σ^2E = environmental variance (error mean square from the analysis of variance); MSG = mean square of genotypes; MSE = error mean square; r = number of replications.

Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) of each trait were calculated following the method suggested by Burton and Devane (1953).

PCV= $(\sqrt{\sigma^2_p}/\bar{X})$ *100

GCV= $(\sqrt{\sigma^2_g}/\bar{X})$* 100

Where: $\sigma^2_{p=}$ phenotypic variance, $\sigma^2_{g=}$ genotypic variance and $\bar{X}$= grand mean of the trait.Heritability in broad sense, genetic advance (GA) and GA as % of mean were computed as suggested by Allard (1960).

a) Heritability (H^2) = (σ^2_g/σ^2_p)*100

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

c) GA (as % of mean) = (GA/grand mean)*100

Where: GA= Genetic advance; K= A constant which at selection intensity of 5% is 2.06.

Genotypic and phenotypic correlation coefficients and their tests of significance were obtained from CANDISC procedure of SAS (SAS Institute, 2002).

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

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

*Year of release

RESULTS AND DISCUSSION

Descriptive statistics of qualitative traits

Phenological traits varied widely ranging from 38.8- 52.8 days for heading, 91.3-123.0 days for maturity and 50.0-73.3 days for grain filling (Table 2). The days to heading values of all tef genotypes in this experiment fall within Kebebew Assefa *et al*. (1999; 2000; 2001b) ranges but the maximum values of days to maturity were lower than these reports. Plant height, panicle length and culm length ranged from 74.7-115.5 cm, 26.5-44.9 cm and 47.7-72.7cm, respectively. The panicle length values in the present experiment fall within the ranges of other stated studies, except that reported by Kebebew Assefa *et al*. (2001a). Furthermore, the mean values for other traits varied from 234.9-536.5 for number of spikletes per main panicle, 17.4-32.6 for number of primary branches per main panicle, 1.3-2.9 mm for first basal culm internode diameter and 1.5 and 2.9 mm for second basal culm internode diameter. In line with the current results, Kebebew Assefa *et al*. (2001a) also reported similar mean values for number of primary branches of the main panicle. Regarding the diameters of the first and second basal culm internodes, Kebebew Assefa *et al*. (1999; 2001a&b) reported slightly lower and Habte Jifar *et al*. (2015a) found lower mean values than those recorded in the current experiment. Besides, wide ranges of lodging index values of 48.5-81.5 were noted with the low end corresponding to accessions Oro-ACC#16-L38 and Oro-ACC#9L-5 while the upper end was recorded for accession Oro-ACC#4-L18. On the other hand, studies with released tef varieties by Habte Jifar *et al*. (2015a) showed lower lodging index (10.5) as compared to the results in the current study. Moreover, the range between the lowest and the highest total biomass yielder genotypes was 9375 Kg/ha. Also 3155 Kg/ha difference in grain yield was noted between the lowest yielder Amh-ACC#11-L44 and the highest yielder genotype Oro-ACC#30-L29. Likewise, 6890Kg/ha differences in straw yield were found between the locally collected gemplasm lines Amh-ACC#1-L56 and Oro-ACC#15-L30. Lastly, among the tested tef germplasm lines, Oro-ACC#4-L25 had the lowest (22.9) and Amh-ACC#1-L51the highest (37.0) harvest index values. In comparison, the present results for tiller numbers (total and fertile) were relatively lower than those previously reported by Kebebew Assefa *et al*. (1999; 2000, 2001a&b) and harvest index were relatively higher than those formerly reported by Habte Jifar *et al*. (2015a).

Table 2.Minimum, maximum, mean and standard error (SE) for 18 traits of 70tef germplasms tested at DZARC and HARC in 2105.

Traits	Min.	Genotype	Max.	Genotype	Mean	SE (±)
DH	38.75	Amh-ACC#1-L50	52.75	Oro-ACC#7-L19, Oro-ACC#9-L38 Oro-ACC#4-L18	48.09	0.736
DM	91.25	Tsedey (DZ-Cr-37)	123.00	Amh-ACC#14-L23	109.76	1.233
GFP	50.00	Tsedey (DZ-Cr-37)	73.25	Amh-ACC#14-L23	61.67	0.659
PH (cm)	74.73	Amh-ACC#1-L56	115.46	Oro-ACC#15-L12	99.03	0.702
PL (cm)	26.49	Amh-ACC#1-L51	44.90	Oro-ACC#15-L12	36.91	0.317
CL (cm)	47.68	Amh-ACC#1-L56	72.65	Amh-ACC#8-L61	62.12	0.528
NSPP	234.90	Amh-ACC#1-L59	536.49	Oro-ACC#15-L8	395.33	6.870
NPB	17.44	Oro-ACC#4-L25	32.63	Oro-ACC#9-L37	25.52	0.313
FBCD (mm)	1.25	Oro-ACC#8-L30	2.90	Oro-ACC#11-L26	2.12	0.024
SBCD (mm)	1.53	Oro-ACC#11-L36	2.90	Oro-ACC#11-L26	2.24	0.024
LI (%)	48.50	Oro-ACC#16-L38 Oro-ACC#9L-5	81.50	Oro-ACC#4-L18	67.05	0.797
NTT	2.55	Oro-ACC#1-L37	6.75	Tsedey (DZ-Cr-37)	4.04	0.080
NFT	2.40	Oro-ACC#1-L37	6.50	Tsedey (DZ-Cr-37)	3.59	0.070
TSW (g)	0.24	Amh-ACC#8-L51 Oro-ACC#9-L45	0.36	Amh-ACC#11-L22, Amh-ACC#14-L21 Oro-ACC#4-L25	0.30	0.003
TBM (Kg/ha)	6875	Amh-ACC#11-L44	16250	Oro-ACC#15-L30	12659	1.841
GY (Kg/ha)	1921	Amh-ACC#11-L44	5076	Oro-ACC#30-L29	3690	0.586
SY (Kg/ha)	4842	Amh-ACC#1-L56	11732	Oro-ACC#15-L30	8968	1.366
HI (%)	22.88	Oro-ACC#4-L25	37.03	Amh-ACC#1-L51	29.22	0.246

DH=days to heading, DM=days to maturity, GFP=grain filling period, PH=plant height, PL=panicle length, CL=culm length, NSPP=number of spikletes per main panicle, NPB=number of primary branches per main panicle, FBCD= first basal culm internode diameter, SBCD=second basal culm internode diameter, LI=lodging index, NTT=number of total tillers, NFT=number of fertile tillers, TSW= thousand seed weight, BM= Total biomass, GY=grain yield, SY=Straw yield and HI=harvest index.

Analysis of Variance

The combined analysis of variance, across two locations revealed highly significant ($P<0.01$) variation among the tef genotypes tested for all of quantitative traits considered, except for thousand seed weight which did not exhibit significant genotype effects (Table 3). Similarly except lodging index and thousand seed weight at Holetta and thousand seed weight at Debre Zeit the individual location, the analysis of variance of all traits showed significant genotype differences (Table 4). Consequently, the presence of highly significant genetic variability among the 70 germplasm accessions for all traits indicated the possibility to exploit the variability existing in tef germplasm in future breeding programs. Supportive results to the present findings were also reported by Kebebew Assefa *et al.* (1999; 2000; 2001a&b; 2002), Ayalneh Tilahun*et al*. (2012), and Habte Jifar *et al.* (2015a&b), who also found significant genotype difference in important yield related traits.

On the other hand, 14 of the grain yield and yield related traits evaluated were significantly affected by genotype x environment interactions (Table 3). This indicated that for these traits the performance of genotypes was not consistent across the two test locations. The highly significant genotype × location interactions noted for the various traits were in agreement with the previous reports (Kebebew Assefa *et al*., 1999, 2000, 2001b, 2002; Wondewosen Shiferaw *et al*., 2012; Habte Jifar *et al*., 2015a&b). Presence of such interaction for most of the traits is in line with the current focal strategic direction of the tef breeding program (shift from wide to specific adaptation) (Kebebw Assefa *et al*., 2011). Moreover, except grain yield all traits measured in this experiment significantly ($p<0.01$) varied between locations.

Phenotypic and Genotypic Coefficients of Variation

The coefficients of variation measure the magnitude of variability present in the population (Jalal and Ahmad, 2012). In this experiment, the variances of the genotype × location interaction of 11 traits were higher than the genotypic variances. But genotypic variance of the remaining traits (plant height, panicle length, number of spikletes and primary branches per main panicle, lodging index and the diameters of the two basal culm internodes) showed either comparable or higher genotypic variation than the genotype × location interaction variances (Table 5). These were also reflected in the relatively wider gaps between the corresponding estimates the phenotypic and genotypic coefficients of variation for these traits.

The GCV values ranged from (0%) for grain filling period and thousand seed weight (where variance component due to genotypes was negative) to (14.87%) for number of fertile tillers per plant (Table 5). Similarly, low GCV values were obtained for days to maturity (2.23%) and days to heading (2.87%). This indicates that improvement of those traits through selection may not be effective in this population due to non-genetic sources of variation (Solomon Chanyalew *et al*., 2009). On the other hand, relatively high values of GCV were detected for number of spikelets per panicle (14.72 %), total number of tillers (14.59 %), first basal culm internode diameter (12.34%) and straw yield (11.10%). The lowestPCV values (7.88%) were estimated for days to heading and the highest (31.04 %) for number of fertile tillers. Apart from these, the other phenological and height related traits scored low PCV values. On the other hand, traits like number of total tillers (30.10%), grain yield (26.25%), number of spikelets per main panicle (26.08%), straw yield (24.76%), and total biomass (23.85 %) exhibited high PCV values.

In contrast to our findings, Kebebew Assefa *et al.* (2000) reported high variability in most quantitative traits considered in the experiment but, in line with the present findings, the diameters of the two basal cum internode diameters scored lower variability (7.50% and 6.02% GCV;10.60% and 9.52% PCV). Likewise, the results of Kebebew Assefa *et al*. (2001b) for GCV estimates were comparable to those found in the present study for most of the traits except for the two diameters of basal culm internodes that were lower than those found in the current experiment. Moreover, Ayalneh Tilahun *et al*. (2012) reported similar estimates of PCV and GCV for plant height, while their results were also comparable with respect to PCV values of days to heading and grain yield, and with regard to GCV values of days to maturity and culm length. However, the remaining characters showed low variability coefficients than the current study. Moreover, most of the traits considered in the current experiment showed higher GCV values than those reported by Hailu Tefera *et al*. (2003) in recombinant inbreed lines of tef. In other aspects, Solomon Chanyalew *et al*. (2009) obtained comparable PCV and GCV estimates to those reported here for traits like panicle length and lodging index, plant height and harvest index.

Table 3. Mean squares from the combined analysis of Variance for 18 traits of 70 tef genotypes

Traits	Location (DF=1)	Rep. (DF=1)	Block /Rep. (DF=18)	Genotype (DF=69)	Genotype × Loc. (DF=69)	Error (DF=121)	SEM (±)	CV (%)
DH	38282.41**	6.30ns	7.41ns	25.16**	20.29**	4.58	0.736	4.45
DM	92456.23**	284.01**	33.79ns	136.58**	135.55**	40.82	1.233	5.82
GFP	11752.13**	205.71*	42.84ns	98.28**	125.22**	41.14	0.659	10.40
PH	749.84**	35.03ns	36.19ns	276.25**	127.40**	45.54	0.702	6.81
PL	823.61**	2.17ns	6.26ns	55.97**	18.02**	9.89	0.317	8.52
CL	3145.18**	54.62ns	28.21ns	121.92**	75.46**	24.50	0.528	7.97
NSPP	559070.12**	81.48ns	6557.11ns	19989.08**	9816.62**	4827.88	6.870	17.58
NPB	1837.21**	21.14ns	18.28*	35.23**	16.26**	9.82	0.313	12.28
FBCD	2.40**	1.22**	0.053ns	0.284**	0.083ns	0.08	0.024	13.37
SBCD	7.75**	0.85**	0.091ns	0.263**	0.072ns	0.072	0.024	12.00
LI (%)	3514.51**	1064.70**	176.46ns	220.51**	138.43ns	135.57	0.797	17.37
NTT	81.01**	12.73**	0.56ns	2.93**	1.75**	0.51	0.080	17.71
NFT	26.56**	8.41 **	0.56ns	2.33**	1.46**	0.45	0.070	18.76
TSW	0.04**	0.0003ns	0.002ns	0.002ns	0.0025ns	0.002	0.003	13.99
TBM	5177.20**	432.51ns	556.01ns	1519.92**	1179.69**	382.03	1.841	15.44
GY	8.04ns	67.40ns	52.29ns	151.86**	145.93**	32.31	0.586	15.40
SY	5580.09**	157.67ns	292.90ns	850.64**	568.25**	222.29	1.366	16.63
HI (%)	300.85**	2.62ns	3.8094ns	29.62**	19.40**	5.078	0.246	7.71

DF=degree of freedom, **, * significant at 5% and 1% probability level, ns=non-significant.

Heritability and Expected Genetic advance

Heritability values ranged from 0% for grain filling period and thousand seed weight to 46.11% for first basal culm internode diameter (Table 5). According to Robinson (1966) cited in Dabholkar, (1992), Heritability estimates are classified as low (5-10%), medium (10-30%) and high (30-60%). Therefore, traits such as panicle length (46.07%), second basal culm internode diameter, panicle length (45.38 %) and plant height (37.01%) showed relatively high broad sense heritability estimates, while the values for days to maturity (6.39%) and grain yield (6.13%) were relatively low. Due mainly to the high genotype x location interactions values in the current study, most of traits exhibited low broad sense heritability estimates than those reported by Kebebew Assefa *et al*. (1999; 2000; 2001b). However, diameters of both basal culm internodes showed relatively low and similar heritability values to those previously reported by Kebebew Assefa *et al*. (2000; 2011b). In addition, compared to the other traits, Kebebew Assefa *et al.* (1999) obtained relatively low heritability for the first basal culm internode diameter. Similarly, except plant height and culm length which scored relatively low heritability estimates, most traits studied by Ayalneh Tilahun *et al*. (2012) demonstrated high heritability than those found in the present experiment. Moreover, relatively high heritability values were also reported for different comparable traits of brown-seeded tef genotypes (Habte Jifar *et al*., 2015b), released tef varieties (Habte Jifar *et al*., 2015a) and gynogenically derived tef lines (Habte Jifar and Likyelesh Gugssa, 2013). On the other hand, the heritability value obtained for harvest index in the present study was in agreement with the findings of Solomon Chanyalew *et al*. (2009). Nevertheless, a similar experiment with recombinant inbred lines of tef showed relatively lower heritability values for plant height, panicle length, lodging index and shoot biomass (Hailu Tefera *et al*., 2003).

The estimates of GA as percent of mean ranged from 0% for grain filling period and thousand seed weight to (17%) for number of spikiests per main panicle and first basal culm internode diameter (Table 5). Since, Johnson *et al.* (1955), categorize genetic advance as percent of mean (GAM) as high (>20%), moderate (10-20%) and low (0-10), second basal culm internode diameter (15.13%), number of total tillers (14.56%) and number of fertile tillers (14.68%) exhibited moderate GA estimates as percent of mean, while days to maturity (1.16), days to heading (2.16%) and grain yield (3.31 %) revealed low GA values expressed as per cent of the mean.

Table 4. Mean squares from the individual location analysis of Variance for 18 traits of 70 tef genotypes tested at Holetta and Debre zeit during the 2015 main cropping season

	Holetta							**Debre zeit**						
Traits	**Rep. (DF=1)**	**Block(Rep.) (DF=18)**	**Genotype (DF=69)**	**Error (DF=51)**	**Mean**	**SE(±)**	**CV**	**Rep. (DF=1)**	**Block(Rep.) (DF=18)**	**Genotype (DF=69)**	**Error (DF=51)**	**Mean**	**SE(±)**	**CV**
DH	0.71ns	9.98ns	29.25**	6.85	59.79	0.38	4.38	7.31ns	2.00ns	13.34**	2.37	36.40	0.26	4.23
DM	5.21ns	53.17ns	86.81**	36.94	127.94	0.69	4.75	682.01**	26.08ns	167.58**	35.96	91.59	0.94	6.55
GFP	9.78ns	57.62ns	65.74*	37.93	68.15	0.63	9.04	548.06**	29.36ns	146.04**	37.20	55.19	0.86	11.05
PH	3.15ns	11.51ns	186.35**	25.25	100.67	0.92	4.99	102.91ns	63.41ns	198.85**	67.74	97.40	1.04	8.45
PL	8.55ns	7.14ns	36.05**	6.20	35.20	0.42	7.07	0.71ns	12.08ns	36.54**	12.55	38.63	0.43	9.17
CL	1.32ns	8.51ns	81.07**	16.11	65.48	0.62	6.13	86.54ns	35.02ns	102.94**	35.97	58.77	0.76	10.20
NSPP	19426.63**	3372.23ns	12850.81**	2403.01	350.65	8.10	13.98	23148.00*	11427.78*	15821.12**	5308.93	440.02	9.75	16.56
NPB	1.15ns	5.16ns	32.88**	8.61	28.08	0.40	10.45	29.49ns	27.33**	17.29*	9.48	22.96	0.37	13.41
FBCD	0.35**	0.04ns	0.13**	0.02	2.03	0.03	7.79	4.63**	0.05ns	0.23**	0.08	2.21	0.04	12.88
SBCD	0.12*	0.03ns	0.15**	0.03	2.07	0.03	8.25	2.70**	0.14*	0.18**	0.07	2.40	0.03	11.44
LI	820.86**	237.20**	106.72ns	80.18	70.59	0.94	12.68	306.06 ns	319.98**	205.45**	105.88	63.51	1.22	16.20
NTT	9.00**	0.43ns	1.28**	0.32	3.50	0.08	16.10	4.18**	1.12*	3.09**	0.54	4.58	0.12	16.00
NFT	7.71**	0.49ns	1.16**	0.33	3.28	0.08	17.58	1.75ns	0.61ns	2.27**	0.53	3.89	0.11	18.71
TSW	0.001ns	0.001ns	0.001ns	0.001	0.29	0.003	11.90	0.000ns	0.003ns	0.003ns	0.002	0.32	0.004	15.22
TBM	1946.31**	743.16**	673.84**	295.94	130.89	2.33	13.14	5406.43**	486.01*	1576.46**	237.16	122.29	2.81	12.59
GY	158.83**	67.06**	56.09**	19.46	36.73	0.67	12.01	586.30**	48.29*	189.40**	21.64	37.07	0.96	12.55
SY	995.86*	388.34*	407.97**	185.60	94.14	1.76	14.47	2431.94**	255.55ns	802.75**	153.80	85.21	2.02	14.55
HI	0.04ns	4.01ns	12.36**	4.27	28.19	0.26	7.33	6.19ns	3.86ns	33.10**	6.27	30.26	0.40	8.28

DF=degree of freedom, **, * significant at 5% and 1% probability level, ns=non-significant.

Table 5. Components of variance, coefficient of variation, heritability, genetic advance (GA) and GA as per cent of the mean for 18 characters in 70 tef genotypes evaluated at Holetta and Debre Zeit during the 2015 main cropping season

Traits	**σ^2 l**	**σ^2 g*l**	**σ^2 e**	**σ^2 p**	**σ^2 g**	**PCV**	**GCV**	**H %**	**GA**	**GA (as % of mean)**
DH	273.30	7.85	4.59	14.35	1.91	7.88	2.87	13.29	1.04	2.16
DM	659.43	47.90	39.75	93.63	5.98	8.82	2.23	6.39	1.27	1.16
GFP	83.11	38.12	40.59	78.70	0.00	14.39	0.00	0.00	0.00	0.00
PH	4.45	41.57	44.26	136.27	50.44	11.79	7.17	37.01	8.90	8.99
PL	5.75	4.33	9.37	25.39	11.70	13.65	9.27	46.07	4.78	12.96
CL	21.93	25.41	24.65	66.77	16.71	13.15	6.58	25.03	4.21	6.78
NSPP	3923.20	2572.70	4671.10	10629.10	3385.30	26.08	14.72	31.85	67.64	17.11
NPB	13.01	3.37	9.53	18.81	5.91	16.99	9.53	31.43	2.81	11.00
FBCD	0.02	0.003	0.078	0.15	0.07	18.17	12.34	46.11	0.37	17.26
SBCD	0.06	0.01	0.07	0.13	0.06	16.18	10.90	45.38	0.34	15.13
LI (%)	24.12	0.34	137.76	159.97	21.88	18.86	6.98	13.68	3.56	5.31
NTT	0.57	0.62	0.51	1.48	0.35	30.10	14.59	23.49	0.59	14.56
NFT	0.18	0.50	0.45	1.24	0.29	31.04	14.87	22.96	0.53	14.68
TSW	0.0003	0.0004	0.0017	0.0021	0.00	15.13	0.00	0.00	0.00	0.00
TBM	28.55	399.94	379.81	911.37	131.62	23.85	9.06	14.442	8.98	7.10
GY	0.00	55.90	32.15	93.80	5.75	26.25	6.50	6.127	1.22	3.31
SY	35.80	174.24	219.77	493.09	99.08	24.76	11.10	20.094	9.19	10.25
HI (%)	2.01	7.29	4.83	15.79	3.68	13.60	6.56	23.288	1.91	6.52

σ^2 l= location variance, σ^2 g*l=genotype by location interaction variance, σ^2 e=error variance, σ^2 p=phenotypic variance, σ^2 g=genotypic variance, PCV=phenotypic coefficient of variability, GCV=genotypic coefficient of variability, H=heritability in broad sense , GA=genetic advance, DH=days to heading, DM=days to maturity, GFP=grain filling period, PH=plant height, PL=panicle length, CL=culm length, NSPP=number of spikletes per main panicle, NPB=number of primary branches per main panicle, FBCD first basal culm internode diameter, SBCD=second basal culm internode diameter, LI=lodging index, NTT=number of total tillers, NFT=number of fertile tillers, TSW= thousand seed weight, TBM= total biomass, GY=grain yield, SY=Straw yield and HI=harvest index.

On the other hand, the estimates of genetic advance (% of the mean) for days to heading and maturity found in this experiment were similar with what was reported in Hailu Tefera *et al*. (2003). In addition, the GAM values obtained for the first and second basal culm internode diameters in present investigation are in agreement with those found by Kebebew Assefa *et al*. (1999), but lower than those reported by Kebebew Assefa *et al*. (2000; 2001b). In addition, compared to the present results, Ayalneh Tilahun *et al*. (2012) obtained genetic advance (% of the mean) estimates that were similar for plant height and that were higher for panicle length. But the GAM values for both plant height and panicle length in the present study were comparable to those reported by Habte Jifar *et al*. (2015b). Accordingly, the estimated genetic advance values of number of primary branches, number of spiklets per panicle and shoot biomass in current experiment are in line with those found by Ayalneh Tilahun *et al*. (2012); Habte Jifar *et al*. (2015b) and Solomon Chanyalew *et al*. (2009). Moreover, GAM estimate for harvest index in the current study was greater than what was reported by Solomon Chanyalew *et al*. (2009) and Ayalneh Tilahun *et al*. (2012), while it was comparable with that found by Kebebew Assefa *et al*. (2001b). Moreover, compared to the findings in this study, gynogenically derived tef lines of Habte Jifar and Likyelesh (2013) showed similar genetic advance (% of the mean) estimates for days to maturity, culm length and lodging index.

Nevertheless, both heritability and genetic advance (% of mean) values of traits must show high values for effective phenotypic selection (Johnson *et al*., 1955; Ahsan*et al*., 2015). Consequently, in this study first basal culm internode diameter, second basal culm internode diameter, panicle length, number of spikletes per main panicle and number of primary branches showed high heritability combined with moderate GA values. In comparison, days to heading, days to maturity and grain filling period, thousand seed weight, grain yield, lodging index and total biomass revealed low heritability and genetic advance as percent of mean values, while most of the remaining traits depicted relatively medium heritability with moderate GAM values. Therefore, since the combinations of high heritability and GAM indicated the existence of additive gene action and lodging is the major constraint in tef (Kebebew Assefa *et al*., 2011), phenotype based selection of lodging related traits such as first and second basal culm internode diameters would appear effective to bring about improvements in the development of lodging resistant tef varieties.

Phenotypic and Genotypic Correlations

Selection criteria takes into account the information on interrelationships among agronomic characters, their relationship with grain yield and their direct influence on grain yield (Dewey and Lu, 1959). Therefore, in the present study, phenotypically**,** lodging index was correlated positively and significantly with all phenological traits i.e. total biomass, grain yield, straw yield and harvest index and culm length. On top of this, grain yield, harvest index, total and fertile number of tillers had positive and significant genotypic correlation with lodging index, indicating their role in aggravating lodging incidence. In contrary, first and second basal culm internode diameters had negative and significant correlation at both phenotypic and genotypic level with lodging index which showed their role in reducing lodging (Table 6). Similarly, number of primary branches per main panicle revealed significant and negative genotypic correlation with lodging index. On the other hand quantitative traits like total biomass, straw yield, harvest index and lodging index showed positive and highly significant (P<0.01) phenotypic and genotypic correlation with grain yield (Table 6). In the same way, positive and highly significant phenotypic correlations were observed between grain yield and other height related traits. However, apart from number of spikletes per main panicle which showed significant (P<0.01) correlation, all the remaining traits considered in this experiment did not show significant phenotypic correlation with grain yield. Likewise, plant height, panicle length, number of spikletes per main panicle also revealed significant (P<0.05) positive genotypic correlation with grain yield and those traits could serve as pointer of high yielding ability.

On other hand, excluding days to heading and grain filling period, similar phenotypic correlation of grain yield with different yield related traits was observed by Habte Jifar *et al*. (2013). But genotypically, comparable results regarding associations with grain yield were reported only for traits like days to maturity, culm length and total biomass. Moreover, among the different traits measured by Habte Jifar *et al*. (2015a), number of primary panicle branches, thousand seed weight, second basal culm internode diameter, total biomass and the above stated phenological traits showed similar phenotypic correlation with grain yield. Besides those traits, culm length and harvest index showed similar genotypic association with grain yield. Likewise, the strong and positive correlations of grain yield with yield related traits agree with the previous findings of Solomon Chanyalew *et al*. (2009) and Wondewosen Shiferaw *et al*. (2012). However, compared to the present results, the correlations of grain yield reported by Habtamu Ayalew *et al*. (2011) were not in agreement for height related and number of fertile tillers, but it was similar with total biomass and harvest index.

Table 6. Phenotypic (above diagonal) and Genotypic (below diagonal) correlation coefficient for 18 quantitative traits of 68 tef populations and two improved varieties

Variable	DH	DM	GFP	PH	PL	CL	NSPP	NPB	FBCD	SBCD	LI	NTT	NFT	TSW	TBM	GY	SY	HI
DH	1.00	0.90**	0.56**	0.20**	-0.24**	0.41**	-0.30**	0.51**	-0.15**	-0.31**	0.22**	-0.40**	-0.28**	-0.22**	0.19**	0.01ns	0.25**	-0.29**
DM	0.58**	1.00	0.87**	0.20**	-0.20**	0.40**	-0.29**	0.46**	-0.12*	-0.28**	0.20**	-0.40**	-0.29**	-0.14*	0.16**	-0.05ns	0.24**	-0.38**
GFP	0.19ns	0.91**	1.00	0.16**	-0.12*	0.29**	-0.21**	0.30**	-0.05ns	-0.17**	0.12*	-0.31**	-0.22**	-0.01ns	0.09ns	-0.09ns	0.17**	-0.38**
PH	0.44**	0.33**	0.18ns	1.00	0.71**	0.91**	0.33**	0.41**	0.36**	0.32**	0.10ns	-0.24**	-0.25**	0.07ns	0.43**	0.27**	0.46**	-0.22**
PL	0.42**	0.31**	0.16ns	0.86**	1.00	0.34**	0.56**	0.13*	0.41**	0.41**	-0.04ns	-0.07ns	-0.15**	0.12*	0.27**	0.24**	0.26**	-0.02ns
CL	0.38**	0.30**	0.16ns	0.94**	0.63**	1.00	0.11ns	0.46**	0.23**	0.18**	0.16**	-0.29**	-0.24**	0.02ns	0.41**	0.22**	0.46**	-0.28**
NSPP	0.40**	0.30**	0.15ns	0.66**	0.72**	0.52**	1.00	0.23**	0.51**	0.56**	-0.08ns	0.10ns	0.02ns	0.13*	0.24**	0.20**	0.23**	-0.04ns
NPB	0.34**	0.33**	0.22ns	0.55**	0.51**	0.48**	0.68**	1.00	0.31**	0.20**	0.07ns	-0.31**	-0.23**	-0.04ns	0.21**	0.03ns	0.26**	-0.28**
FBCD	0.40**	0.48**	0.38**	0.65**	0.55**	0.61**	0.58**	0.68**	1.00	0.81**	-0.18**	-0.13*	-0.17**	0.20**	0.06ns	-0.02ns	0.09ns	-0.21**
SBCD	0.43**	0.49**	0.38**	0.70**	0.55**	0.69**	0.62**	0.73**	0.90**	1.00	-0.22**	0.04ns	-0.02ns	0.20**	0.05ns	0.02ns	0.07ns	-0.09ns
LI	-0.12ns	-0.10ns	-0.06ns	-0.16ns	-0.06ns	-0.20ns	-0.18ns	-0.28*	-0.39**	-0.33**	1.00	-0.04ns	0.03ns	-0.11ns	0.37**	0.42**	0.32**	0.22**
NTT	-0.22ns	-0.30**	-0.25*	-0.38**	-0.36**	-0.34**	-0.22ns	-0.30**	-0.43**	-0.33**	0.24*	1.00	0.91**	0.07ns	-0.06ns	0.05ns	-0.11ns	0.26**
NFT	-0.26*	-0.34**	-0.28*	-0.40**	-0.41**	-0.32**	-0.22ns	-0.26*	-0.43**	-0.33**	0.24*	0.94**	1.00	0.03ns	-0.10ns	-0.01ns	-0.14*	0.23**
TSW	0.06ns	0.24*	0.25*	0.30**	0.29**	0.26*	0.15ns	0.12ns	0.33**	0.26*	0.06ns	-0.05ns	-0.08ns	1.00	-0.03ns	-0.04ns	-0.02ns	-0.05ns
TBM	0.33**	0.21ns	0.09ns	0.48**	0.45**	0.42**	0.50**	0.19ns	0.17ns	0.24*	0.20ns	-0.09ns	-0.12ns	0.15ns	1.00	0.86**	0.98**	-0.07ns
GY	0.09ns	-0.03ns	-0.08ns	0.23*	0.27*	0.17ns	0.28*	0.04ns	-0.05ns	0.01ns	0.39**	0.01ns	-0.03ns	0.08ns	0.85**	1.00	0.74**	0.42**
SY	0.40**	0.29**	0.15ns	0.54**	0.49**	0.49**	0.55**	0.23*	0.25*	0.31**	0.10ns	-0.12ns	-0.15ns	0.17ns	0.98**	0.72**	1.00	-0.28**
HI	-0.42**	-0.48**	-0.37**	-0.43**	-0.30**	-0.45**	-0.35**	-0.28*	-0.46**	-0.43**	0.40**	0.28*	0.28*	-0.17ns	-0.15ns	0.38**	-0.36**	1.00

*, ** **significant** at 5% and 1 % probability level, respectively. DH=days to heading, DM=days to maturity, GFP=grain filling period, PH=plant height, PL=panicle length, CL=culm length, NSPP=number of spikletes per main panicle, NPB=number of primary branches per main panicle, FBCD first basal culm diameter, SBCD=second basal culm diameter, LI=lodging index, NTT=number of total tillers, NFT=number of fertile tillers, TSW= thousand seed weight, SBM= shoot biomass, GY=grain yield, SY=Straw yield and HI=harvest index.

CONCLUSION

The present study revealed substantial variability in some yield related traits of the locally collected tef germplasm lines which can be exploited in the tef breeding program. Specifically these materials could serve as a source of lodging resistant tef varieties. Besides, the high genotype x location interactions on many of the agronomically important traits evaluated in the present study indicates that breeding for specifically adaptable varieties would be important while still exploring for widely adapted varieties. Complementary uses of phenotypic evaluations along with modern genomic tools would be important to avoid confounding effects of environment and genotype x environment interactions in genetic diversity evaluation and further studies involving diverse tef genotypes and evaluation techniques would be worth for more conclusive and comprehensive recommendations.

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