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Genetic variability, Heritability and Association of Traits in Released tef [*Eragrostis tef* (Zucc.)Trotter] Varieties Evaluated in Southwestern and Central Ethiopia

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Abstract

Nineteen released tef varieties and two landraces were evaluated in Completely Randomized Block Design with three replications at Debre Zeit and Jimma Agricultural Research Centers during the 2007/08 cropping season. The objectives were to assess the extent of genetic variability; to estimate the variance and broad sense heritability for the various traits, and to examine the phenotypic and genotypic correlation for grain yield and yield related traits in released tef varieties. The mean squares due to genotype and genotype by environment interaction were highly significant (P≤0.01) for all traits while that due to locations were highly significant (P≤0.01) for thirteen of the fifteen traits. The phenotypic variance value was higher than genotypic variance for all the traits and genotypic and phenotypic coefficient of variation ranged from 5.06 to 20.47% and 5.91 to 21.66%, respectively. Similarly, broad sense heritability ranged from 47.9 to, 92.9%. Expected genetic advance and genetic advance as percent of the mean respectively varied from 0.04 to 56.84 and 7.21% 29.65%. Grain yield showed positive and significant (P<0.01) phenotypic and genotypic correlation with shoot biomass yield and harvest index only. Lodging index, however, had shown significant phenotypic and genotypic association with most of the traits in the current study. In general, wider phenotypic variability in terms of plant morphology, phenology and yield attribute were observed in the current study that would help to utilize in the future breeding works.

Key words: *Eragrostis tef*, Genotypes, Variability, Varieties

Introduction

Tef [*Eragrostis tef* (Zucc.) Trotter] is an allotetraploid plant with a base chromosome number of 10 ($2n = 4x = 40$) (Jones *et al*., 1978; Tavassoli, 1986). It is a C4, self-pollinated chasmogamous annual cereal bearing both the stamens and pistils in the same floret (Seyfu, 1997). The center of origin and diversity of tef is in Ethiopia (Vavilov, 1951) where it is primarily grown as a staple cereal (Amanda and Doyle, 2003). It is the only cultivated cereal in the genus *Eragrostis* which consists of 350 species (Hailu and Seyfu, 2001; Hailu *et al*, 2003). Tef crop exhibits high level of phenotypic plasticity in phenology and agronomic traits depending on the environment where it is grown. Tef days to heading and to maturity and grain yield per plant, for instance, ranges from 25 to 81 and 60 to140 days and 0.78 to 5.96 gram per plant respectively (Kebebew *et al*., 2001). The grain yield and quality also vary with the soil type, climate,

season and varieties. Therefore, better tef grain yield and quality is obtained when grown on black soils and at an altitude range of 1800-2400m a. s. l. and areas receiving annual rainfall of 750-850mm (Seyfu, 1993).

Tef is an excellent source of human food and livestock feed that provide better market prices for its grain and straw than all other cereals grown in Ethiopia. It is a gluten free cereal (Spaenij-Dekking *et al.,* 2005), tolerant to moisture stresses, suitable for double cropping and has long shelf life and low post harvest pest problem (Seyfu, 1993)

It is ranked first in area coverage and second to maize in total volume of grain production in Ethiopia (CSA, 2012). However, national average yield is very low (below 1.3 t/ha) when compared to other cereals, (CSA, 2012). Nevertheless, it was reported that the use of appropriate tef technologies can increase tef yield to over 4.5 t/ha (Hailu and Seyfu, 2001). According to MoA (2012), over 33 varieties had been developed and released for commercial use in Ethiopia.

Knowing the genetic variability existing among released tef varieties enable breeders to utilize the genetic potential for further breeding and avoid the suspected redundancy. A considerable genetic variation, heritability, genetic advance and correlation among different traits of tef germplasm had been reported (Kebebew *et al.*, 2001) and released varieties (Yifru and Hailu, 2005; Habte *et al.*, 2011). However, previous studies conducted on released varieties by Yifru and Hailu (2005) and Habte *et al* (2011) did not include released varieties after 1995 and the high potential tef growing central region of Ethiopia. Hence, both reports have some limitations. The objectives of the current study, therefore, were: 1) to assess the extent of genetic variability among released tef varieties, 2) to estimate the genotypic and phenotypic variances and broad sense heritability and 3) to examine the phenotypic and genotypic correlation coefficients for grain yield and yield related traits in released tef varieties under two environments.

Materials and Methods

Description of experimental sites

Two field experiments were carried out at Jimma Agricultural Research Center (8^0 44′ N, 38^0 58 E, and 1860 m. a. s. l.) and Debre Zeit Agricultural Research Center (8^0 44′ N, 38^0 58′ E, and 1753 m. a. s. l.) of the Ethiopian Institute of Agricultural Research (EIAR) during the 2007/2008 GC cropping season. The soil of the experimental site at Jimma and Debre Zeit research center is Eutric Nitosol with a pH of 5.2 and Inceptisol with pH of 6.9, respectively.

Experimental materials and design

Nineteen commercial tef varieties released before 2006 and two local landraces from around Jimma (Table 1) were evaluated in a randomized complete block design with three replications in 2007/08 cropping season. The experimental plot size was 1m x 1m ($1m^2$) and consisted of five rows. Three grams of seeds was drilled along the surface of the five rows in each plot using a seed rate of 30 kilogram per hectare.

Table 1. Description of released tef varieties used in the study

No.	Name of Varieties	Year of release	Seed color	Adaptation zone
1	DZ-01-354 (Enatite)	1970	Pale white	1600-2400
2	DZ-01-99 (Asgori)	1970	Brown	1600-2400
3	DZ-01-196 (Magna)	1970	Very white	1800-2400
4	DZ-01-787 (Holonkomi)	1978	Pale White	1600-2400
5	DZ-Cr-44(Menagesha	1982	White	1800-2500
6	DZ-Cr-82 (Melko)	1982	Pale white	1700-2000
7	DZ-Cr-37 (Tsedey)	1984	White	1600-2400
8	DZ-Cr-255 (Gibe)	1993	White	1700-2000
9	DZ-Cr-358 (Ziquala)	1995	White	1400-2400
10	DZ-01-974 (Dukem)	1995	White	1400-2400
11	DZ-01-2053 (Holetta Key)	1999	Brown	1900-2700
12	DZ-01-1278(Ambo-Toke)	2000	White	2200-2400
13	DZ-01-1281(Gerado)	2002	White	1850
14	DZ-01-1285 (Koye)	2002	White	1900-2200
15	DZ-01-1681(Key Tena)	2002	Brown	1600-1900
16	DZ-01-2675 (Dega Tef)	2005	White	1800-2500
17	DZ-01-899 (Gimbichu)	2005	White	2000-2500
18	Ho -Cr-136 (Amarach)	2006	White	Low moisture areas of rift valley
19	DZ-Cr-387 (Quncho)	2006	Very white	1800-2400
20	Dalasso*	-	mixed	Southwestern Ethiopia
21	Gomojor*	-	mixed	Southwestern Ethiopia

** Both are local landraces from Jimma area*

Phosphorus and nitrogen fertilizer was applied at the rate of 60 KgP_2O_5 and 40 KgN per hectare fertilizer. Di-ammonium phosphate (DAP) was the source of P_2O_5, while N was obtained from both DAP and Urea. DAP was applied at planting while Urea was top dressed at tillering stage.

The plants in each row were thinned four weeks after planting to have 20 plants per row at an intra-row spacing of five centimeters. All other crop management practices were applied as per the recommendation and standard procedure for each location. Five randomly selected plants from the central rows of each plot were tagged on the main shoots at early tillering for assessment of all plant related data.

Data collection

Data was collected on fifteen phenological and morpho-agronomic traits. Days to heading and maturity, biomass and grain yield (g/m^2), thousand seed weight (g), harvest index (%) and lodging index (%) were assessed on plot basis. On the other hand plant height (cm), length of culm and panicle (cm), number of fertile tillers per plant and spikelet per panicle, were assessed on a single plant basis.

Statistical analysis and partitioning of the variance components

All measured data were subjected to the analysis of variance (ANOVA) to assess the differences among the genotypes under investigation using the SAS program software (SAS, 2002). Significance of variability test was made at 5 and 1% probability level.

The total phenotypic variance of each trait was partitioned into contribution due to genetic and non-genetic factors using the variance component method based on the combined analyses of the two test locations as per the method suggested in Kebebew *et al.,* (1999):

$$Vg = [MsG - \frac{(MSGL - MSE)}{r} - MSE]/rl \; ;$$

$$VP = Vg + \frac{Vgl}{r} + \frac{Ve}{rl}$$

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 also calculated following the method of Burton and de Vane (1953).

$$PCV = (\frac{\sqrt{\sigma^2 P}}{X}) \times 100 \; ;$$

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

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 (GAM), assuming selection of the superior 5% of the genotypes were estimated following the procedure elaborated by Singh and Chaudhary (1996):

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

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

Where: K is a constant with a value of 2.06 at selection intensity of 5%;

$\sqrt{\sigma^2 P}$ = Square root of phenotypic variance and h^2= heritability in broad sense.

Traits association

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

$$rP_{xy} = \frac{P\,\mathrm{cov}_{xy}}{\sqrt{\sigma^2 p_x \times \sigma^2 p_y}};$$

$$rg_{xy} = \frac{G\,\mathrm{cov}_{xy}}{\sqrt{\sigma^2 g_x \times \sigma^2 g_y}}$$

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; $\sigma^2 p_x$ and $\sigma^2 p_y$ is the phenotypic variance for trait X and Y, respectively

Results and Discussion

The combined analyses of variance results of two locations for the investigated traits are presented in Table 2. The result showed that the mean squares due to location were highly significant (P≤0.01) for all traits except shoot biomass yield per plot and thousand seed weight (P≤0.05), indicating that there are differences between the two environments to examine the genetic performance of tef genotypes. The mean square due to genotypes and that of genotype by environment interactions were also highly significant (P≤0.01) for all traits under investigation. The significant variation observed among genotypes implied the presence of substantial variation among genotypes, which give an opportunity for plant breeders to improve those traits through breeding. On the other hand, the significant genotype by location interaction for all the traits in this study indicated that some genotypes perform differently under different environment. Similar results had been reported for the combined analysis of variance across two locations, which collaborates the findings regarding most of the traits in the present study (Solomon *et al.*, 2009; Ayalneh *et al.*, 2012; Wendeweson *et al.*, 2012).

Descriptive statistics of quantitative traits

Means, range and standard deviation of each trait of the test genotypes were computed and are presented in Table 2. The mean grain yield of the genotypes ranged from 61.76 to 296 g/ m² for genotype DZ-01-196 and DZ-01-354, respectively. Likewise, the shoot biomass yield also ranged from 290 g/m² for genotype DZ-01-196 to 475 g/m² for DZ-01-974. Furthermore, thousand seed weight ranged from 0.25g to o.42 g for genotype DZ-01-196 and genotype DZ-01-1285,

respectively. From this result, one can understand that those varieties having loose type of panicle (DZ-01=974, DZ-01-1285 and DZ-01-354) are high yielders as compared to the semi compact varieties like DZ-01-196. This finding is in line with Hailu (1988). On the other hand, shorter days to grain filling and maturity were observed for Ho-Cr-136 while longer days to grain filling and maturity were recorded for genotype DZ-01-354. This is due to the inherent differences in the genetic makeup of the two varieties since the former variety was an escape type developed and released for moisture stress areas while DZ-01-354 was meant to serve the high potential areas with relaxed growing season. Thus, the result obtained in the present study is still in the range previously reported (Kebebew *et al.*, 2001). The minimum and maximum number of fertile tillers per plant was recorded for DZ-Cr-82 and DZ-cr-37, respectively. DZ-01-2053 was found to have the shortest plant height (43.4cm) and panicle length (18.9cm) while the longest plant height (96.6cm) and panicle length (41cm) was recorded for DZ-01-2675 and DZ-Cr-82 respectively (Table 3). This is a good indication that most white seeded varieties have usually longer plant height and panicle length as compared to the brown seeded varieties like DZ-01-2053 (Holetta red). In general, higher phenotypic variability in terms of plant morphology, phenology and yield attribute were observed which agrees with the works of Kebebew *et al.*, (2001) and Habte *et al.*, (2011).

Table 2. Mean square values for combined analysis of variance of 21 tef genotypes

Variable	Mean square					
	Loc (df=1)	Rep (df=2)	Genotype (df=20)	Loc*Genotype (df=20)	Error (df =82)	CV (%)
DPE	224**	0.63ns	53.99**	13.82**	2.29	2.88
DGF	48.29**	0.60ns	86.77**	75.35**	3.48	4.29
DTM	6557.79**	11.01*	216.86**	81.52**	2.54	1.55
PHT (cm)	9108.26**	55.30ns	173.32**	89.61**	36.47	8.53
PL (cm)	89.29**	9.87ns	45.00**	19.80**	8.48	9.63
CL(cm)	7362.67**	18.15ns	45.81**	34.21**	13.84	9.19
NFT	22.21**	0.33ns	7.01**	1.02**	0.27	10.17
NSP	1145868.65**	479.04ns	10641.25**	7112.25**	1083.5	11.03
PBM	20.84**	5.07ns	29.97**	12.94**	4.54	11.32
SBD	1.14**	0.02ns	0.16**	0.04**	0.02	12.93
SBM	470.19ns	341.32ns	5230.05**	447.42*	341.23	3.97
GYP	566.17**	33.38ns	1568.39**	240.09**	62.11	7.75
HI	0.005**	0.0003ns	0.0047**	0.0008**	0.0003	6.38
TSW	0.0018ns	0.0006ns	0.004**	0.0017**	0.0006	7.74
LI	65303.91**	5.31ns	115.04**	67.27**	16.92	9.71

DF=degrees of freedom; ns = Non significant; *, ** significant at P≤0.05 and P≤0.1, respectively, 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), NFT=No. fertile tillers/plant, NSP=No. spikelet per main panicle, PBM= Panicle branches per main stem, SBD= Second basal culm diameter, SBM= Shoot biomass yield (t/ha), Grain yield (t/ha), HI= Harvest index, TSW=Thousand seed weight, LI=Lodging index in percentage

Table 3. Ranges, means and standard deviations for 15 traits of 13 selected released tef varieties

Traits	Range of values for genotypes					
	Minimum		Maximum		Mean	Standard deviation (±)
	Value	Genotype	Value	Genotype		
DPE	45.00	DZ-Cr-37	59.00	DZ-01-787	52.51	3.76
DGF	28.00	Ho-Cr-136	57.00	DZ-01-354	43.46	5.35
DTM	87.00	Ho-Cr-136	121.00	DZ-01-354	102.60	10.10
PHT	43.38	DZ-01-2053	96.60	DZ-01-2675	70.83	11.82
PL	18.88	DZ-01-2053	41.00	DZ-Cr-82	30.25	4.10
CL	22.13	DZ-01-2675	60.00	DZ-Cr-387	40.48	9.00
NFT	2.77	DZ-Cr-82	9.80	DZ-Cr-37	5.06	4.00
NSP	86.80	DZ-01-196	513.80	DZ-Cr-387	298.50	112.81
PBM	10.80	DZ-Cr-37	26.60	DZ-Cr-387	18.82	3.18
SBCD	0.42	DZ-01-2053	3.16	DZ-Cr-387	1.09	0.23
SBM)	290.0	DZ-01-196	475.00	DZ-01-974	391.40	32.78
GYP	61.76	DZ-01-196	147.70	DZ-01-354	101.73	18.31
HI	0.20	DZ-01-1285	0.33	HO-Cr-136	0.26	0.03
TSW)	0.25	DZ-01-196	0.42	DZ-01-1285	0.33	0.04
LI	10.47	DZ-01-899	79.00	DZ-01-974	42.36	23.72

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), NFT=No. fertile tillers/plant, NSP=No. spikelet per main panicle, PBM= Panicle branches per main stem, SBD= Second basal culm diameter, SBM= Shoot biomass yield (t/ha), Grain yield (t/ha), HI= Harvest index, TSW=Thousand seed weight, LI=Lodging index (%).

Estimates of phenotypic and genotypic variation

The estimates of the genotypic and phenotypic variance, genotypic (GCV) and phenotypic (PCV) coefficient of variability, broad sense heritability (h^2), genetic advance (GA) & genetic advance as per cent of mean (GAM) are presented in Table 4. The estimated phenotypic variance ranged from 0.0007 for thousand seed weight to 2108.47 for number of spikelet per panicle. Similarly, the lowest and highest genotypic variance of 0.0005 and 1258.03 was also estimated for the above two traits respectively. On the other hand, GCV values of greater than 10% were observed for number of fertile tiller per plant (20.47%), grain yield per plot (15.26%), SBCD (13.65 %), NSP (11.88%), PBM (10.32%) and harvest index (10.27%) while the remaining traits had a value less than10%. Similarly, number of fertile tiller per plant, grain yield per plot, SBCD, NSP, PBM, lodging index and harvest index had PCV values greater than 10% while values for the remaining traits were below 10%. Maximum PCV was observed for number of fertile tillers per plant (21.66%) followed by grain yield per plot (16.19%), number of spikelet per panicle (15.38%) and second basal culm diameter (15.11%). Unlike the present study, Kebebew *et al.* (2000) had reported a PCV and GCV values of less than five percent for SBCD. The higher PCV and GCV values observed for some of the traits could be an evidence for the existence of wide range of variation to improve those traits. The lower GCV for phenological traits and culm length, however, suggests the difficulty of manipulating these traits. In general, PCV values in the current study were higher than GCV values for all traits indicating that the environmental effect was higher for the expression of the traits under investigation.

The estimates of heritability indicated that higher values were recorded for shoot biomass (92.85%), fertile tillers number (89.39%), grain yield/m^2 (88.89%), harvest index (86.95%), days to panicle emergence (82.75) and second basal culm diameter (81.16) (Table 4). Similarly, high heritability values were reported previously for days to panicle emergence (Kebebew *et al.*, 2001; Tilahun *et al.*, 2012). On the other hand, the minimum heritability value estimated in this study was 53.6 and 47.9% for days to grain filling and culm length respectively.

High heritability along with high genetic advance is an important factor to predict the resultant effect for selecting the best genotypes. High expected genetic advance estimates were obtained for shoot biomass yield per plot (56.84%), number of spikelet per panicle (56.44%) and grain yield per plot (30.16%). Unlike the present findings, estimates of genetic advance ranging from less than 1% to 21% had been reported by Kebebew *et al.*,

(2000), and from less than 2% to 23% (Kebebew *et al.*, 2001).

High estimates of both heritability and genetic advance values were recorded for shoot biomass yield and grain yield per plot suggesting the possibility of improving tef grain yield through direct selection for both traits. On the other hand, number of fertile tiller per plant, harvest index and days to panicle emergence had average broad sense heritability value coupled with low expected genetic advance. Conversely, number of spikelet per panicle in the current study had moderately low broad sense heritability value accompanied with higher genetic advance value.

Table 4. Estimates of σ^2g σ^2p σ^2ge σ^2e, GCV, PCV, h^2, GA and GAM) in tef genotypes

Traits	σ^2g	σ^2ge	σ^2e	σ^2p	GCV (%)	PCV (%)	H (%)	GA	GAM (%)
DPE	7.98	3.84	2.29	9.64	5.38	5.91	82.75	5.29	10.08
DGF	9.89	23.96	3.48	18.45	7.24	9.88	53.58	4.74	10.91
DTM	31.33	26.33	2.54	40.53	5.46	6.20	77.30	10.14	9.88
PHT (cm)	19.86	17.71	36.47	31.84	6.29	7.97	62.37	7.25	10.23
PL (cm)	5.46	3.77	8.48	8.13	7.72	9.43	67.15	3.94	13.04
CL (cm)	4.20	6.79	13.84	8.77	5.06	7.31	47.87	2.92	7.21
NFT	1.08	0.25	0.27	1.21	20.47	21.66	89.39	2.03	39.88
NSP	1258.03	2009.58	1083.50	2108.47	11.88	15.38	59.67	56.44	18.91
PBM	3.77	2.80	4.54	5.46	10.32	12.42	69.06	3.32	17.67
SBD	0.02	0.01	0.02	0.03	13.61	15.11	81.16	0.28	25.27
SBM (gm/m^2)	820.02	68.73	241.23	883.13	7.32	7.59	92.85	56.84	14.52
GYP (gm/m^2)	241.16	59.33	62.11	271.29	15.26	16.19	88.89	30.16	29.65
HI	0.0007	0.0002	0.0003	0.0008	10.27	11.02	86.95	0.05	19.73
TSW (gm)	0.0005	0.0003	0.0006	0.0007	6.91	8.28	69.70	0.04	11.88
LI (%)	13.56	16.78	16.92	21.97	8.69	11.07	61.70	5.96	14.06

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), NFT=No. fertile tillers/plant, NSP=No. spikelet per main panicle, PBM= Panicle branches per main stem, SBD= Second basal culm diameter, SBM= Shoot biomass yield (t/ha), Grain yield (t/ha), HI= Harvest index, TSW=Thousand seed weight, LI=Lodging index in percentage

Higher genetic advance as the percent of mean values were obtained for number of fertile tillers per plant (39.9), grain yield per plot (29.7%) and second basal culm diameter (25.3%). The GA as percent of mean values in the current study (7.2% for culm length to 39.9% for number of fertile tillers per plant) is far higher than the previous report that was just under 21% (Kebebew *et al.* 2000).

Association of grain yield and related traits

Estimation of the degree of genotypic and phenotypic correlation of grain yield and yield components is very important to utilize the available genetic variability through selection

(Singh *et al.*, 1998). The phenotypic and genotypic correlations for morpho-agronomic traits are presented in Table 5. Grain yield per plot showed positive and significant ($P<0.01$) phenotypic and genotypic correlation with shoot biomass yield per plot and harvest index, implying that improving these traits could result in high grain yield. On the other hand, grain yield per plot showed negative but non-significant correlation with days to grain filling, days to maturity, panicle length, second basal culm diameter and thousand seed weight. This finding is contrary to Habte *et al.*, (2011) that reported positive and highly significant genotypic and phenotypic correlation for grain yield with both days to panicle emergence and maturity. Moreover, the insignificant association observed between grain yield and that of days to maturity and days to panicle emergence is in line with the previous findings of Yifru and Hailu (2005). Shoot biomass yield had shown non-significant association with all traits except grain yield per plot and harvest index. Meanwhile lodging index showed significant phenotypic and genotypic association with nine and seven of the fifteen traits under the current study, respectively. Days to panicle emergence also showed significant positive correlation with most of the traits ; days to grain filling, days to maturity, plant height, culm and panicle length, spikelet per panicle and panicle branch per main stem at both phenotypic and genotypic level. This finding agrees with the result of Temesgen *et al.* (2005).

Maximum genotypic and phenotypic correlation values were observed between grain yield per plot and harvest index (r_g=91, r_p=90) followed by days to maturity and days to panicle emergence (r_g=0.90, r_p=73), culm length and plant height (r_g=87, r_p=0.90) and plant height and panicle length (r_g=0.88, r_p=70). This indicates a great possibility of making simultaneous improvement for those pairs of traits having higher genotypic correlations.

Table 5. Genotypic and Phenotypic Correlation Coefficient for 15 traits of 21 tef genotypes

Variable	DPE	DGF	DTM	PHT	PL	CL	FT	SPK	PBMS	SBCD	SBM	GYP	HI	TSW	LI
DPE	1	0.57**	0.90**	0.62**	0.70**	0.46*	-0.46*	0.62**	0.72**	0.38ns	0.17ns	-0.08ns	-0.22ns	0.14ns	-0.62**
DGF	0.26**	1	0.53*	0.19ns	0.49*	-0.11ns	-0.10ns	0.25ns	0.27ns	0.35ns	0.07ns	-0.05ns	-0.12ns	0.44*	-0.42ns
DTM	0.73**	0.20*	1	0.46*	0.60**	0.25ns	-0.53*	0.61**	0.67**	0.31ns	0.11ns	-0.19ns	-0.35ns	0.30ns	-0.54*
PHT	0.44**	0.002ns	0.67**	1	0.88**	0.87**	-0.45*	0.66**	0.68**	0.61**	0.16ns	-0.01ns	-0.12ns	0.06ns	-0.48*
PL	0.41**	0.16ns	0.38**	0.70**	1	0.56**	-0.42ns	0.75**	0.71**	0.58**	0.26ns	0.09ns	-0.04ns	0.32ns	-0.50*
CL	0.39**	-0.06ns	0.69**	0.90**	0.42**	1	-0.31ns	0.45*	0.52*	0.48*	0.11ns	-0.02ns	-0.11ns	-0.22ns	-0.32ns
FT	-0.19*	-0.01ns	-0.04ns	0.13ns	-0.07ns	0.24**	1	-0.51*	-0.53*	-0.28ns	0.15ns	0.24ns	0.24ns	-0.20ns	0.33ns
SPK	0.46**	-0.02ns	0.74**	0.81**	0.46**	0.83**	0.17ns	1	0.76**	0.61**	0.25ns	0.10ns	0.005ns	0.31ns	-0.48*
PBMS	0.37**	0.20**	0.19*	0.28**	0.46**	0.11ns	-0.29**	0.20*	1	0.58**	0.25ns	0.09ns	-0.03ns	0.28ns	-0.45*
SBCD	-0.10ns	0.30**	-0.10ns	-0.06ns	0.22*	-0.19*	-22*	-0.18**	0.38**	1	0.14ns	0.01ns	-0.08ns	0.21ns	-0.46*
SBM	0.13ns	-0.02ns	-0.01ns	-0.02ns	0.07ns	-0.05ns	0.09ns	0.01ns	0.16ns	0.09ns	1	0.80**	0.48*	-0.01ns	0.14ns
GYP	0.02ns	-0.14ns	-0.05ns	0.004ns	-0.01ns	0.04ns	0.21*	0.12ns	0.03ns	-0.08ns	0.76**	1	0.91**	-0.30ns	0.36ns
HI	-0.06ns	-0.17ns	-0.06ns	0.02ns	-0.04ns	0.08ns	0.23*	0.17ns	-0.06ns	-0.15*	0.41**	0.90**	1	-0.42ns	0.43ns
TSW	0.14ns	0.20*	0.24**	0.13ns	0.23*	0.05ns	-0.03ns	0.18*	0.21*	0.10ns	0.02ns	-0.14ns	-0.18*	1	-0.14ns
LI	0.24**	-0.15ns	0.63**	0.68**	0.17ns	0.82**	0.39**	0.80**	-0.17ns	-0.44**	-0.04ns	0.16ns	0.25**	0.09ns	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), NFT=No. fertile tillers/plant, NSP=No. spikelet per main panicle, PBM= Panicle branches per main stem, SBD= Second basal culm diameter, SBM= Shoot biomass yield (t/ha), Grain yield (t/ha), HI= Harvest index, TSW=Thousand seed weight, LI=Lodging index in percentage

Conclusion

These study findings showed the presence of considerable variations among 19 released tef varieties for all traits tested which gives an opportunity to plant breeders for the improvement of these traits. High estimates of broad sense heritability accompanied by high genetic advance values were recorded for shoot biomass yield and grain yield per plot suggesting the possibility of improving tef grain yield through direct selection for the two traits. Besides, the positive genotypic and phenotypic correlation of shoot biomass yield per plot and harvest index traits with that of grain yield per plot suggests a common genetic/physiological basis among these traits and the possibility of simultaneous improvement of the traits. Biomass and harvest index can, therefore, be considered as a suitable selection criteria for the development of high yielding tef varieties.

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