

Full Length Research

Genetic Variability, Broad Sense Heritability and Trait Associations among Grain Yield and Yield Related Traits in Tef[Eragrostis tef (Zucc.) Trotter] Genotypes

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Tef, [Eragrostis tef (Zucc.) Trotter], is an important staple cereal crop and extensively cultivated by small scale farmers in Ethiopia. Understanding of the nature and magnitude of genetic variability and heritability and the degree of correlation among traits is important for the genetic improvement of crops through breeding. Therefore, the present study was carried out to assess the magnitude of genetic variability and broad sense heritability and trait associations among grain yield and yield related traits of tef genotypes. Twenty-two tef genotypes were evaluated in a randomized complete block design with three replications at two locations in central highland of Ethiopia. Analysis of variance revealed significant genotypic difference and genotype x environment interaction for most of evaluated traits. The genotypic coefficient of variation ranged from 1.52% for lodging index to 10.15% for panicle length while the phenotypic coefficient of variation ranged from 2.71% for lodging index to 11.21% for grain yield. Panicle length and plant height exhibited highest broad sense heritability value of 94.57% and 90.22%, respectively. Genetic advance in percent of mean were ranged from 1.76 (lodging index) to 20.33% (panicle length). High heritability combined with high genetic advance was observed for Panicle length indicates the dominance of additive gene action in governing the trait. Grain yield had a positive and significant phenotypic and genotypic correlation with grain filling period, shoot biomass and harvest index. Hence, improvement in grain yield could be achieved by selecting genotypes having longer grain filling period, higher shoot biomass and harvest index.

Key words: Tef, Genetic variability, Genetic advance, Broad sense heritability, trait association

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INTRODUCTION

Tef, Eragrostis tef (Zucc.) Trotter is the major staple cereal of Ethiopia. It is cultivated annually on more than three million hectares of land by over six million smallholder farmers, accounting one-third of the total

cereal acreage (Kebebew et al., 2015). Over the past 10 years, the area of tef cultivation in Ethiopia has increased from 1.99 million ha in 2004 (CSA, 2004) to 3.02 million ha in 2015 (CSA, 2015). Similarly, tef production and

productivity have also increased from 1.67 million tons to 4.7 million tons and 0.84 to 1.58 t/ha, respectively (CSA, 2015).

Ethiopia is both the origin and center of diversity for tef (Vavilov, 1951). *Eragrostis tef* (Zucc.) Trotter, is an allotetraploid ($2n = 4x = 40$) and belongs to the Poaceae or grass family (Tavassoli, 1986). The genus *Eragrostis* constitutes about 350 species of which only tef is cultivated for human consumption (Watson and Dallwitz, 1992).

Ethiopian farmers have cultivated tef for centuries because of various merits over other cereals. Tef cultivated under diverse range of agro-ecological conditions and performs better than other cereals under adverse and marginal conditions and fits in to various cropping and crop rotations system and useful as a catch crop and low-risk reliable crop (Kebebew et al., 2011). Other benefits of tef are; tef seed can be stored for a long time as the grains not affected by storage pests, less susceptibility to disease and insect pests and tef straw is nutritious and serves as fodder for cattle feed (Seyfu, 1997). Currently, tef has been gaining global popularity as health food because of tef is gluten-free, which is suitable for peoples suffering from gluten protein allergy known as celiac disease (Spaenij-Dekkingetal.,2005).

Despite its food, feed and health merits, the national average grain yield is about 1.6 t/ha, which is low compared to 3.5 t/ha for maize and 2.5 t/ha for wheat (CSA, 2015). This could be mainly due to susceptibility to lodging, low yield potential of local varieties used by farmers, drought and other biotic and abiotic stresses (Kebebew et al., 2011). Therefore, this necessitates development of new high yielding tef varieties combining other important traits. For the improvement of crops through breeding, it is important to understand the nature and extent of genetic variability exist in the base germplasm population. Knowledge of heritability and genetic variability is essential for carrying out selection based improvement because the breeding progress in crop improvement programs depends on the magnitude of genetic variation, heritability of a given trait in a given environment and the level of selection intensity applied (Falconer, 1989; Singh, 2002). In addition to genetic variability and heritability estimate, knowledge of association (genotypic and phenotypic correlation) existing between different traits determine the progress of selection in crop improvement programs (Falconer and Mackay, 1996). Moreover, Grain yield is a complex trait which is influenced by several component traits and direct selection for grain yield is often not effective. Thus, it is essential to study the association of yield components with yield. Therefore, the objective of the present study was to estimate the genetic variability and broad sense heritability for grain yield and yield related traits of tef genotypes and to evaluate the association between these traits.

MATERIALS AND METHODS

Experimental sites and materials

The study was conducted during the main cropping season of 2015 at Holetta and Ginchi, which are situated in central highlands of Ethiopia. Holetta is located at 09° 03' N, 38° 30' E, with an altitude of 2400 m above sea level (m asl). It receives an average annual rainfall of 1102 mm and the soil type is Nitosol. Ginchi is located at 09° 30' N, 38° 30' E and an altitude of 2200 m asl. It receives an annual average rainfall of 1139 mm and the soil type is black Vertisol. A total of Twenty- two tef genotypes, including 17 germplasm lines (accessions), four standard checks and a local check were used in this study (Table 1). All the genotypes except the local and standard checks were obtained from Ethiopian Biodiversity Institute (EIB). EIB is responsible for germplasm collection and maintenance. The four standard checks were DZ-CR-387 (Quncho), DZ-01-196 and DZ-01-354, popular tef varieties released by the national tef research program for high potential areas in Ethiopia while DZ-CR-37 an improved variety released for moisture-stress environments.

Experimental design and management

The experimental design was a randomized complete block with three replications. The plot size was 2 m x 2 m with 0.2 m between rows and 1 m between plots. Sowing was done at the recommended period for each location (July 15 at Holetta and July 25 at Ginchi). Seeds were drilled along the 10 rows of each plot at the rate of 15 kg ha⁻¹. Fertilizer was applied according to recommendation for each location (60 kg ha⁻¹ P₂O₅ and 60 kg ha⁻¹ N at Ginchi and 60 kg ha⁻¹ P₂O₅ and 40 kg ha⁻¹ N at Holetta). All other cultural management practices were done as per recommended of the respective test locations.

Data collection and Statistical analysis

Data were recorded for days to heading, grain filling period, days to maturity, shoot biomass (t/ha), grain yield (t/ha), lodging index (%) and harvest index (%) on whole plot base. Lodging index was expressed following the method described by Caldicott and Nuttall (1979), while harvest index was calculated as a ratio of the grain yield to the above ground shoot biomass. Grain filling period was determined as the difference between days to maturity and days to heading. On the other hand, data were measured from five randomly selected plants from each plot on plant height (cm) and panicle length (cm).

Data of plot means were analyzed using the Genes program (computational application in genetics and

Table 1. List of tef genotypes used in the study

NO	Genotypes
1	HO-TFS-805
2	HO-TFS-1526
3	HO-TFS-1385
4	HO-TFS-1553
5	HO-TFS-5486A1
6	HO-TFS-5464A1
7	HO-TFS-831
8	HO-TFS-1449
9	HO-TFS-787
10	HO-TFS-807
11	HO-TFS-905
12	HO-TFS-992
13	HO-TFS-806
14	HO-TFS-1321
15	HO-TFS-725
16	HO-TFS-1375
17	HO-TFS-5477 A1
18	DZ-CR-37
19	DZ-CR-387(QUNCHO)
20	DZ-01-354
21	DZ-01-196
22	LOCAL CHECK

statistics) (Cruz, 2016) following the analysis of variance and covariance of randomized complete block design as per Gomez and Gomez (1984). Hartley's (1950) F-max ratio was used to test the homogeneity of error variances before analyzing the combined data.

The statistical model used for ANOVA is: $Y_{ijk} = \mu + G_i + E_j + GE_{ij} + B_k(j) + \epsilon_{ijk}$. Where, Y_{ijk} =observed value of genotype i in block k of environment (location) j , μ = grand mean, G_i = effect of genotype i , E_j = effect of environment j , GE_{ij} = interaction effect between genotype i and location j , $B_k(j)$ = the effect of block k within location (environment) j , ϵ_{ijk} = error (residual) effect of genotype i in block k of environment j .

Phenotypic and genotypic coefficients of variations, genetic advance as percent of mean and heritability in broad sense were estimated using the formula suggested by Allard (1960). Phenotypic and genotypic correlation coefficients were estimated from the components of variance and covariance based on the method described by Singh and Chaudhary (1996), using the Genes program (Cruz, 2016). Principal component analysis was

made based on the mean values using the PROC PRINCOMP procedure of SAS statistical software version 9.3 (SAS Institute, 2011).

RESULTS AND DISCUSSION

Analysis of variance (ANOVA)

The combined analysis of variance across the two locations showed significant differences among genotypes for all traits except lodging index (Table 2). The presence of significant genetic variations for grain yield and other agronomic traits suggested the possibility of developing better tef varieties by exploiting the variability existing in tef germplasm. In line with present studies, several investigators previously reported significant genotypic differences for these traits in tef (Chekol et al., 2016; Habte et al., 2015; Wondesen et al., 2012; Habtamuet et al., 2011; Solomon et al., 2010; Hailu et al., 2003; Kebebew et al., 2000). Similarly, high genetic

Table 2. Analysis of variance for grain yield and yield related traits of 22 tef genotypes evaluated across two locations.

Source	DF	DH	GFP	DM	PH	PL	LI	SB	GY	HI
Location(L)	1	5422.09**	211.28**	7774.01**	1012.60**	15.07	390.37**	712.61**	31.61**	459.13**
Replication/L	4	17.65	45.83*	97.95**	34.06	3.84	397.87**	13.54**	0.82**	1.28
Genotypes (G)	21	91.19**	126.31**	131.87**	392.29**	80.97**	39.71	3.40**	0.36**	46.05**
G x L	21	22.03**	45.95**	31.45**	38.36*	4.4	27.18	1.20*	0.10**	10.28**
Error	84	8.44	14.63	10.37	18.69	3.94	24.77	0.6	0.05	3.96
Mean		54.38	59.05	113.43	95.32	35.2	95.01	8.15	2.19	27.66
CV		5.34	6.48	2.84	4.54	5.64	5.24	9.5	10.66	7.19

DF = Degrees of freedom, DH=days to heading (days), GFP= grain filling period (days), DM =days to maturity (days), PH= plant height (cm), PL= panicle length (cm), LI =lodging index (%), SB= shoot biomass (t/ha), GY= grain yield (t/ha), HI =harvest index (%), * and ** significant at $P<0.05$ and $P<0.01$, respectively

variability in Ethiopian tef germplasm accessions was reported in Kebebew et al. (2001). Location and genotype x location interaction effect were significant for most of the traits studied. Significant genotype x location effect showed differential performances of the genotypes across the locations. Significant location and genotype x location interaction effect for different traits in tef was reported by Wondesen et al. (2012) and Habte et al. (2015). Mean values of genotypes for different agronomic traits are given in Table 3. Grain yield for genotypes ranged from 1.80 to 2.83 t /ha with a mean of 2.19 t /ha. HO-TFS-1449 gave higher grain yield (2.83 t /ha) than the standard check DZ-01-354 (2.53 t/ha), DZ-CR-387 (2.47 t/ha), DZ-01-196 (2.40 t/ha) and DZ-CR-37 (2.53 t/ha). The local check showed lower grain yield of 2.07t/ha. Similarly, the shoot biomass yield ranged from 6.93 t/ha - 10.03 t/ha with a mean of 8.15 t/ha. Mean days to maturity was 113 with a range of 103 – 121 days whereas days to heading ranged from 45 to 61 with a mean of 54 days. Genotype HO-TFS-1449 was comparable with standard checks with respect to phenology and agronomic traits suggest the potential of the genotype for future commercial release. In general, the range of values observed for grain yield and yield related traits in present study were within the range reported by Kebebew et al. (2011).

Estimates of coefficient of variation

Knowledge on the relative magnitude of coefficient of variation, heritability and genetic advance is useful since it provides an opportunity to the plant breeder to utilize his skill and art in making useful selections from genetic variability present in germplasms. Estimates of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation, components of variance, broad-sense heritability and genetic advance as percent of mean for the nine traits are presented in Table 4. Estimates of GCV ranged from 1.52 % (lodging index) to

10.15 % (panicle length) while the PCV estimates ranged from 2.71 % (lodging index) to 11.21% (grain yield). Grain yield had GCV values of 9.45 %. Panicle length, grain yield and harvest index revealed a relatively high GCV and PCV value which indicating the opportunity of manipulating these traits through selection. Similar to the present finding, Habte et al. (2015) reported higher estimates of GCV and PCV for panicle length, grain yield and harvest index. On the other hand, relatively low GCV estimates were observed for lodging index and days to maturity indicating that selection is less effective for these characters.

This is in agreement with the findings of Hailu et al. (2003). Similarly, Chekol et al. (2016), Kebebew et al. (2001) and Fufa et al. (1999) reported lower GCV value for days to maturity. The magnitude of PCV in the present study was slightly higher than GCV for all the traits studied indicating that there was little influence of environmental factors on phenotypic expression of most traits. The same results were found previously (Habte et al., 2015; Habte and Likyelesh, 2013; Wondesen et al., 2012). In contrast to the present study, large differences between GCV and PCV values for panicle length, harvest index, plant height grain yield and shoot biomass reported by Solomon et al. (2010).

Broad sense heritability and genetic advance

In the present study, the broad sense heritability (h^2) estimates for 9 traits ranged from 31.55% for lodging index to 94.57% for panicle length. High broad sense heritability estimates was recorded for panicle length followed by plant height (90.22%).

Habte et al. (2015) reported high heritability value for panicle length and plant height. Relatively high heritability estimate also found for panicle length compared to other traits by different authors (Hailu et al., 1990, 2003; Kebebew et al., 1999, 2001). High heritability value show high proportion of variation in a trait that is genetic and

Table 3. Mean grain yield and agronomic traits of the 22 tef genotypes across two locations

Genotypes	DH	GFP	DM	PH	PL	LI	SB	GY	HI
HO-TFS-805	60.17	52.17	112.33	99.70	37.27	98.17	8.43	1.95	24.23
HO-TFS-807	54.83	55.17	110.00	93.90	34.10	92.83	7.47	1.80	24.56
HO-TFS-905	45.50	62.17	107.67	79.03	29.00	91.83	6.93	2.22	32.26
HO-TFS-992	57.33	56.83	114.17	98.23	33.47	98.00	7.95	2.22	28.49
HO-TFS-806	61.17	53.50	114.67	104.43	38.03	98.67	8.18	1.85	23.75
HO-TFS-1321	55.33	53.50	108.83	88.83	30.80	97.00	8.15	2.37	29.94
HO-TFS-725	56.33	55.33	111.67	88.27	29.90	94.67	9.17	2.12	23.74
HO-TFS-1375	51.33	62.00	113.33	83.63	31.13	95.83	7.27	2.10	29.62
HO-TFS-5477 A1	57.50	61.50	119.00	101.50	37.87	97.00	8.22	2.02	25.03
HO-TFS-1526	51.33	58.67	110.00	88.37	33.13	97.00	7.60	2.18	28.99
HO-TFS-1385	54.67	61.33	116.00	94.97	33.70	97.00	8.07	2.20	27.88
HO-TFS-1553	53.50	54.17	107.67	85.83	32.50	91.33	7.72	2.17	28.58
HO-TFS-5486A1	56.83	58.67	115.50	93.90	33.20	93.17	6.97	1.88	27.69
HO-TFS-5464A1	53.50	64.67	118.17	102.13	39.93	96.00	8.75	2.38	27.71
HO-TFS-831	54.50	53.50	108.00	95.57	35.00	91.83	8.18	2.07	25.39
HO-TFS-1449	54.67	66.50	121.17	97.13	37.50	94.83	9.10	2.83	31.86
HO-TFS-787	54.83	60.17	115.00	106.13	40.17	89.50	8.52	2.03	24.50
DZ-CR-37	45.83	57.50	103.33	87.47	32.57	96.00	7.58	2.35	32.44
DZ-CR-387	59.33	57.00	116.33	112.33	41.57	97.17	10.03	2.47	25.65
DZ-01-354	53.33	68.17	121.50	98.73	38.83	96.33	8.70	2.53	29.94
DZ-01-196	53.50	63.33	116.83	102.87	40.30	93.83	8.63	2.40	29.45
LOCAL CHECK	51.00	63.33	114.33	94.10	34.53	92.17	7.60	2.07	26.89
Mean	54.38	59.05	113.43	95.32	35.2	95.01	8.15	2.19	27.66
Minimum	45.5	52.17	103.33	79.03	29	89.5	6.93	1.80	23.74
Maximum	61.17	68.17	121.5	112.33	41.57	98.67	10.03	2.83	32.66
LSD (5 %)	3.34	4.39	3.7	4.96	2.28	5.71	0.89	0.27	2.28

Table 4. Estimates of variance components, correlation coefficients, broad sense heritability, and genetic advance as percent of the mean for 9 traits in 22 tef genotype evaluated

Trait	σ^2_p	σ^2_g	σ^2_{gl}	σ^2_ϵ	PCV(%)	GCV(%)	h^2 (%)	GAM (%)
Days to heading	15.20	11.53	4.53	8.44	7.17	6.24	75.84	11.2
Grain filling period	21.05	13.39	10.44	14.63	7.77	6.2	63.62	10.18
Days to maturity	21.98	16.74	7.03	10.37	4.13	3.61	76.15	6.48
Plant height(cm)	65.38	58.99	6.56	18.69	8.48	8.06	90.22	15.77
Panicle length(cm)	13.49	12.76	0.15	3.94	10.43	10.15	94.57	20.33
Loding index(%)	6.62	2.09	0.80	24.77	2.71	1.52	31.55	1.76
Shoot biomass(t/ha)	0.57	0.37	0.20	0.60	9.24	7.43	64.68	12.31
Grain yield(t/ha)	0.06	0.04	0.02	0.05	11.21	9.45	71.04	16.4
Harvest index(%)	7.68	5.96	2.11	3.96	10.02	8.83	77.6	15.99

σ^2_p = Phenotypic variance, σ^2_g =genotypic variance, σ^2_{gl} =genotype \times location variance, σ^2_ϵ = error variance, PCV=phenotypic coefficients of variation, GCV= genetic coefficients of variation, h^2 = estimates of heritability in percent and GAM= genetic advance as percent of the mean.

Table 5. Estimates of phenotypic (above diagonal) and genotypic (below diagonal) correlation coefficients among 9 traits of 22 tef genotypes

Traits	DH	DM	PH	PL	LI	SB	GY	HI	GFP
DH	1	0.44*	0.67**	0.46*	0.40	0.50*	-0.26	-0.72**	-0.40
DM	0.54*	1	0.63**	0.66**	0.23	0.50*	0.32	-0.13	0.65**
PH	0.71**	0.68**	1	0.92**	0.23	0.68**	0.08	-0.51*	0.07
PL	0.51*	0.74**	0.97**	1	0.12	0.65**	0.23	-0.32	0.29
LI	0.87**	0.42*	0.51*	0.08	1	0.27	0.16	-0.01	-0.10
SB	0.53*	0.59**	0.76**	0.82**	0.47*	1	0.51**	-0.30	0.08
GY	-0.29	0.37	0.07	0.27	0.13	0.53*	1	0.66**	0.55*
HI	-0.76**	-0.07	-0.54*	-0.35	-0.11	-0.24	0.74**	1	0.49*
GFP	-0.33	0.62**	0.10	0.35	-0.32	0.17	0.68**	0.63**	1

DH=days to heading (days), GFP= grain filling period (days), DM =days to maturity (days), PH= plant height (cm), PL= panicle length (cm), LI= lodging index (%), SB= shoot biomass (t/ha), GY= grain yield (t/ha), HI= harvest index (%),* and ** significant at $P<0.05$ and $P<0.01$, respectively

improvement of the trait can be made based on phenotypic performance. In the contrary, Abel et al. (2012) found lower values heritability for panicle length and plant height indicates the value of heritability for a trait is specific for a given population in a given environment. Lodging index had relatively the lowest value of heritability (31.55%) indicating difficulty of improving this trait through direct selection. Lower heritability value for lodging index was reported by Hailu et al. (2003) and Solomon et al. (2009). Large effect of environment, dominance and epistatic variance cause low heritability estimate (Panse, 1957). In the current study, environmental variance for lodging index was larger than genotypic variance. Moderate heritability estimate observed for harvest index (77.60%), days to maturity (76.15%), days to heading (75.84%), grain yield (71.04%), shoot biomass (64.68%) and days to grain filling period (63.62%). Similarly, Habtamu et al. (2011) found intermediate heritability values for days to heading, days to maturity, grain filling period and grain yield for tef landraces.

The estimated of genetic advance as percent of mean in the present study was relatively high (>20%) for panicle length (20.33%). Moderate genetic advance as percent of mean (10 - 20%) were recorded for traits such as grain yield (16.40%), harvest index (15.97%), plant height (15.77%), shoot biomass (12.31%), days to heading (11.20%) and days to grain filling period (10.18%). On the other hand, low level of genetic advance (<10%) obtained for lodging index (1.76%) and days to maturity (6.48%). Johnson et al. (1955) suggested that heritability estimates combined with genetic advance would be more useful in predicting selection for superior genotypes than heritability estimates alone. In the present study, high estimate of heritability and genetic advance as percent of mean were observed

only for panicle length indicating its amenability for improvement. In tef germplasm lines, Kebebew et al. (2000) reported relatively high values of heritability and genetic advance estimates for panicle length than the other characters.

On the other hand, moderate heritability and genetic advance as percent of mean were recorded for plant height, harvest index, days to heading, grain yield shoot biomass and days to grain filling period while moderate heritability but low genetic advance as percent of mean was observed for days to maturity. According to Panse (1957), traits combining high heritability and genetic advance are predominantly controlled by additive gene action. Hence, high estimates of heritability and genetic advance as percent of mean for panicle length in this study indicate the preponderance of additive gene action in controlling the expression of the trait and the improvement of this trait can be made through direct phenotypic selection.

Genotypic and phenotypic correlations among traits

Estimates of genetic and phenotypic correlation coefficients among the 9 traits are presented in Table 5. Correlation study showed relatively higher positive and significant genotypic and phenotypic association of grain filling period, shoot biomass and harvest index with grain yield indicating dependent genetic control between grain yield and these traits. This indicates that selecting for longer grain filling period, larger shoot biomass and harvest index would increase grain yield. Positive and significant genotypic and phenotypic correlation of grain yield with grain filling period, shoot biomass and harvest index is consistent with earlier reports of Habte et al. (2015) and Habtamu et al. (2011). Similarly, Mizan et al.

Table 6. Eigenvectors and values of the first three principal components for 22 tef genotypes

Trait	Eigenvectors		
	PC1	PC2	PC3
Days to heading	0.383	-0.329	0.166
Days to maturity	0.387	0.251	-0.168
Plant height	0.477	-0.042	-0.133
Panicle length	0.444	0.103	-0.234
Lodging index	0.183	-0.012	0.770
Shoot biomass	0.408	0.103	0.193
Grain yield	0.093	0.531	0.305
Harvest index	-0.255	0.485	0.225
Grain filling period	0.071	0.536	-0.312
Eigenvalue	3.882	2.593	1.128
proportion of variance explained	0.431	0.288	0.125
Cumulative proportion of variance explained	0.431	0.719	0.845

(2017) and Wondesen et al. (2012) reported a significant positive genotypic correlation of grain yield with harvest index and shoot biomass. However, grain yield showed positive and low associations both phenotypically and genetically with plant height, panicle length, days to maturity and lodging index. Panicle length which is an important component of yield exhibited a strong positive association with days to heading, days to maturity, plant height and shoot biomass indicating the possibility of simultaneous improvement of panicle length and these characters.

Lodging index had significant positive genetic association with days to heading, days to maturity and plant height indicating that late matured and taller tef genotypes are prone to lodging. Previous studies have mentioned a significant and positive genetic correlation between lodging index and days to heading and between lodging index and days to maturity (Habte et al., 2017). Similarly, Demeke et al. (2013) reported a positive and significant genetic association of lodging index with plant height. In the contrary, Habte et al. (2015) and Solomon et al. (2010) observed that lodging index was correlated negatively with days to heading, days to maturity and plant height. Correlation between grain yield and lodging index was non-significantly positive, indicating the independent genetic control between them. Therefore, high grain yield could be combined with high lodging index and improvement in lodging would not have any adverse effect on grain yield. The highest negative phenotypic and genetic correlation obtained occurred between harvest index and days to heading, indicating that simultaneous improvement of these two characters may not be possible. Chekol et al. (2016) also found these two traits to be highly negatively associated.

Principal component analysis

Eigenvectors and eigenvalues of the first three principal components of the 9 traits are presented in Table 6. The first three principal components (PCs) with eigenvalue greater than unity explained about 84.5% of the total phenotypic variation among the 22 tef genotypes involving 9 traits. The proportion of variation explained by the first three principal components in the present study (84.5%) was higher than the previous reports of Kebebew et al. (2001), Kebebew et al. (2003), Temesgen et al. (2005), Plaza-Wüthrich et al. (2013), Habte et al. (2015) and Habte et al. (2017) who reported a value of 64.7%, 68.67, 74.66, 71.03%, 78.3% and 69.1% for the first three principal components with eigenvalue greater than one, respectively.

The first principal component (PC1) accounted for 43.1% of the total variation in tef genotypes. Plant height (0.477) contributed higher to the total variation followed by panicle length (0.444), shoot biomass (0.408), days to maturity (0.387) and days to heading (0.383) had the highest loadings in PC1 indicating that these traits explain the largest proportion of the variance in the data set and made a significant contribution to PC axis. In agreement with the current study, Kebebew et al. (2003), Habte et al. (2015) and Habte et al. (2017) also reported that about 40%, 44.7% and 41.3%, respectively, of total variation explained by PC1. The second principal component accounted for 28.8% of the total variance existing in the genotypes and was mainly due to the variations in grain filling period, grain yield and harvest index. The third principal component contributed 12.5% of the total variation in the genotypes resulted largely from variations in lodging index, grain yield and harvest index.

CONCLUSION

The present study revealed presence of remarkable genetic variability among the tef genotypes. Thus, there is an opportunity of exploiting the existing variability in tef improvement programs through selection and hybridization. Higher genotypic coefficient variation and broad sense heritability coupled with higher genetic advance observed for panicle length indicated the ease of phenotypic selection for the improvement of this trait. Correlation analysis showed that grain yield had a positive and significant phenotypic and genotypic association with grain filling period, shoot biomass, and harvest index. Hence, improvement in grain yield could be achieved by selecting genotypes possessing longer grain filling period, higher shoot biomass and harvest index. Generally, higher genotypic correlation coefficients than phenotypic correlation coefficients were observed in the present study indicating inherent association among the traits.

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