

*Full Length Research Paper*

# **Genetic variability of some yield and yield related traits in recombinant inbred lines of tef [*Eragrostis tef* (Zucc.) Trotter] at Laelay Maichew District, Northern Ethiopia**

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**Tef [*Eragrostis tef* (Zucc.) Trotter] is a tetraploid almanac plant which belongs to the grass family, Poaceae and plays a vital role in the Ethiopian national food. In this study, thirty-four  $F_2$  derived  $F_7$  recombinant tef inbred lines, two standard (Kora and Quncho) and one local checks were field evaluated for genetic variability in grain yield and yield related characters at Axum Agricultural Research Center in 2014 cropping season. Triplicated randomized complete block design was used. Data were collected on fourteen yield and yield related traits and the analysis of variance revealed that genotypes varied significantly for all traits studied except thousand kernel weight. Highest genotypic coefficient of variation (GCV) was computed for biomass yield followed by panicle yield, plant height and grain yield, in contrast, lowest GCV was noted for number of fertile tillers per plant, days to heading, days to maturity and lodging index, whereas the highest phenotypic coefficient of variation (PCV) was recorded for panicle yield, plant height, biomass production rate per day and biomass yield. The highest broad sense heritability values were recorded for plant height, biomass production rate per day, biomass yield, days to 50% heading and grain yield. The highest genetic advance as percent of mean was recorded for biomass production rate per day, biomass yield, grain yield and grain yield production rate per day, while the lowest genetic advance as a percent of mean was computed for number of productive tillers per plant, panicle length, days to heading and panicle weight. The overall study indicated that there were variations in magnitude of variability in traits for the genotypes studied which showed smooth selection for further improvement in tef.**

**Key words:** Genotypic coefficient of variation (GCV), genetic advance, heritability, phenotypic coefficient of variation (PCV), seed yield, variability.

## **INTRODUCTION**

Tef [*Eragrostis tef* (Zucc.) Trotter]  $2n = 4x = 40$ ] is a tetraploid plant, belonging to the family Poaceae, genus

*Eragrostis* which comprises about 350 species (Watson and Dallwitz, 1992). The center of origin and diversity of

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the tef crop is Ethiopia (Vavilov, 1951).

Tef was possibly cultivated in Ethiopia even before the introduction of emmer wheat and barley (Ebba, 1975). Early investigations of diversity showed a huge variability in majority of the traits studied in more than 100 panicle sample collections from different agro ecologies of Ethiopia (Mengesha et al., 1965). Later, Ebba (1975) characterized 35 distinct tef ecotypes and classified them based on phenology and plant morphology.

Tef cultivation as a cereal food grain is restricted to Ethiopia with an annual cultivation on 3.02 million hectares of land and a total production of 4.4 million tons with the national average standing at 1.46 t/ha (CSA, 2014). Tef is ecologically and agronomically versatile crop. It can be grown from below sea level to 3000 m above sea level, under various rainfall, temperature and soil regimes.

Tef is the most preferred crop as source of food and feed in Ethiopia. Besides, it is tolerant to drought, water-logging, and pests particularly against storage pests. Nowadays, tef has become a globally popular crop for its gluten free property that makes it conducive for people suffering from celiac disease and diabetic because of its slow release of carbohydrates.

Hence, it is regarded as a promising alternative food replacing gluten-containing cereals like wheat, barley and rye in products such as pasta, bread, beer, cookies and pancakes (Spaenij-Dekking et al., 2005). Recently, Cannarozzi et al. (2014) supported this fact with results from the genome sequence initiative. Tef has high iron content that makes it appropriate for pregnancy-related anemia (Alaunyte et al., 2012). The iron content mainly seems to play an essential role in Ethiopia, as there is absence of anemia in areas of tef consumption (BoSTID, 1996).

Despite its greater economic value and large area coverage, tef productivity is much lower as compared to its estimated potential yield level of 6 ton/ha (Ketema, 1993). The low national or regional tef productivity is mainly attributed to susceptibility to lodging, low yield of landraces under widespread cultivation, reduced agronomic management practices, biotic and environmental stresses (Ketema, 1997; Assefa et al., 2011). However, no variability has been studied on tef genotypes in the area. Hence, evaluation of different genotypes of tef is crucial for effective selection.

Generating information and understanding the nature and magnitude of variation existing among tef genotypes is a vital component of improvement programs because it provides evidence on the genetic variability of the crop and sets a base for stratified sampling of breeding populations. Tef represents a unique biodiversity component in the agriculture and food security of millions of farmers in Ethiopia. The conservation, characterization and utilization of the existing tef genetic variability are becoming increasingly important in view of the developing desires and various challenges of small-scale farmers in

Ethiopia. This is mainly because tef has remarkable genetic traits valuable for most Ethiopian farmers to cope with erratic climatic conditions, income generation for household and fulfilling concerns of food and nutritional security. Moreover, the conservation and utilization of the tef genetic resources offer a reliable basis for enhancing food security and developing crop diversification in the moisture stress and challenging agro-ecological areas of the district.

Here, an overview of the results of information generated on genetic variability for important yield and yield related traits were presented, which would help to better understand the variability at morphological level and utilize these variability in improving the crop for future breeding program through selection. In view of these, the present study was carried out with the aims to assess the characters of both genotypic and phenotypic variability and to estimate broad sense heritability (H) and genetic advance expectations from selection of the different traits.

## MATERIALS AND METHODS

### Description of the study area

The experiment was carried out at Axum Agricultural Research Center of Tigray Agricultural Research Institute (TARI) with rainfall during 2014 main cropping season. Axum Agricultural Research Center (AxARC) is suited in the northern part of Ethiopia, 1024 km North of Addis Ababa. It lies at latitude 13° 15' N and longitude 38° 34' E. It has an altitude of 2148 m.a.s.l and it receives a monomodal unevenly distributed average annual rainfall of 756.9 mm per annum. The long term mean minimum and maximum temperature is 11.2 and 27.8° C, respectively. The soil type of the study area is classified as vertisol with a pH of 7.5 to 8.3 (AxARC unpublished, 2012).

### Experimental materials

Thirty four recombinant inbred lines (RILs) of tef together with two released variety (Quncho and Kora) and one local check were used in the study. The 34 RILs were randomly taken from hundreds of RILs at the seventh filial generation from the National Tef Research Project of Debre Zeit Agricultural Research Center (DZARC).

### Experimental design and field management

The test tef genotypes were laid out in triplicated randomized complete blocks design of plots comprised of six rows of 2.5 m length and 1.2 m width (3 m<sup>2</sup>) standard plot size for variety trial with 0.2 m of row spacing. The spaces between plots and replications were 1 and 1.5 m, respectively. Sowing was done by manual drilling along the rows at a seed rate of 1.5 g per row on the basis of 25 kg/ha recommended rate. The source of P<sub>2</sub>O<sub>5</sub> and N were DAP and urea, respectively, both applied at the rate of 100 kg ha<sup>-1</sup>. All the DAP was applied at planting and urea was applied in two splits, half at the time of planting and the remaining half at tillering stage. The experimental materials were sown on the first week of July 2014, main production season. All other pre and post-planting management practices were done in accordance with the research recommendations for tef production in the area.

### Data collection

Data were obtained from fourteen quantitative traits based on plant and plot bases. Data on days to heading, days to maturity, biomass yield, grain yield, harvest index and lodging index were recorded on plot basis from the four middle rows. Derived data like harvest index, biomass production rate per day and grain yield production rate per day was calculated as a ratio of grain yield to shoot biomass, above ground biomass yield to days to physiological maturity and grain yield to physiological maturity, respectively. On the other hand, plant height, panicle length, panicle weight, number of fertile tillers per plant and thousand kernel weight were measured on previously selected and tagged ten random samples of plants from the central four middle rows of each plot. Mean values of the ten random samples of plants per plot of the four middle rows were then used for the analyses of data collected on individual plant basis.

### Data analysis

Analysis of variance was done using the procedures outlined by Gomez and Gomez (1984) with the help of SAS Computer Statistical Package version 9.1.3 (SAS Institute Inc., 2004) and variance effects were considered as significant and highly significant at  $P < 0.05$  and  $P < 0.01$ , respectively.

### Genotypic and phenotypic variance and coefficient of variation

The phenotypic and genotypic variance and coefficient of variation was estimated according to the method suggested by Burton and DeVane (1953) as follows:

$$\sigma^2_g = \frac{Mg - Me}{r}$$

Where,  $\sigma^2_p$  = phenotypic variance;  $\sigma^2_g$  = genotypic variance;  $\sigma^2_e$  = environmental variance (error mean square); Mg = mean sum square of genotypes; Me = mean sum square of error; r = number of replications.

$$\text{Phenotypic coefficient of variation, PCV} = \frac{\sqrt{\sigma^2_p}}{\bar{x}} * 100$$

$$\text{Genotypic coefficient of variation, GCV} = \frac{\sqrt{\sigma^2_g}}{\bar{x}} * 100$$

Where  $\bar{x}$  = population mean.

### Estimation of heritability in the broad sense

Heritability in broad sense was computed for each character as suggested by Allard (1960) as:

$$H^2 = \frac{\sigma^2_g}{\sigma^2_p} * 100$$

Where,  $\sigma^2_p$  = phenotypic variance,  $\sigma^2_g$  = genotypic variance,

$$\sigma^2_p = \sigma^2_g + \sigma^2_e$$

Where,  $\sigma^2_p$  = phenotypic variance;  $\sigma^2_g$  = genotypic variance;  $\sigma^2_e$  = environmental variance (error mean square).

### Estimation of expected genetic advance

The genetic advance (GA) for selection intensity (K) at 5% was calculated using the formula suggested by Allard (1960) as:

$$GA = (K) (\sigma_p) (h^2)$$

Where, GA = expected genetic advance,  $\sigma_p$  = the phenotypic standard deviation,  $H^2$  = heritability in broad sense, K = selection differential (K = 2.06 at 5% selection intensity).

$$GA \text{ (as \% of the mean)} = \frac{GA}{\bar{x}} * 100$$

Where,  $\bar{x}$  = population mean.

## RESULTS AND DISCUSSION

### Analysis of variance

Results of the analysis of variance revealed that the mean squares for genotypes were highly significant ( $p < 0.01$ ), for all traits studied except thousand kernel weight (Table 1). The range for seed yield per panicle was 1.5 to 14.5 g with mean value of 7.62 g (Table 2) indicating the presence of adequate variations among the tested genotypes. The value of coefficient of variation for most of the traits indicated good precision of the experiment. All the traits scored more than 50% estimate of  $R^2$  except thousand kernel weight (39.24%), showing the adequacy of the model in explaining the variation. In line with the current finding, Tefera et al. (2003a) reported the significant performance difference of 118 recombinant inbred lines (RILs) for days to heading, plant height, days to maturity, panicle height, panicle weight, panicle yield, lodging index, biomass yield and seed yield. Likewise, Debebe et al. (2013) observed significant difference ( $P \leq 0.01$ ) for days to maturity, days to heading, biomass yield, seed yield, harvest index and lodging index.

### Mean yield and yield component performance

As indicated in Table 3, the genotypes showed variation in phenology for days to heading ranging from 54 to 64.33 with a mean of 59.87 and days to maturity ranging from 101.67 to 117.67 with a mean of 108.1. The result showed the presence of relatively wide range of variations among the genotypes for maturity. Plaza et al. (2013) also reported wide range of variation among tef genotypes for days to heading and days to maturity with values for days to heading and days to maturity ranging from 58 to 90 days and 83 to 123 days, respectively.

Assefa et al. (2001a) also reported that days to heading and maturity ranged from 25 to 81 and 60 to 140,

**Table 1.** Description of thirty four RILs, two standard checks and one local used during the study.

Entry	Stock ID	Pedigree
1	RIL#10A	Dz-cr-387 (Quncho) x Dz-01-974 (Dukem)
2	RIL#13A	Dz-cr-387 x Dz-01-974
3	RIL#3A	Dz-cr-387 x Dz-01-974
4	RIL#65A	Dz-cr-387 x Dz-01-974
5	RIL#68A	Dz-cr-387 x Dz-01-974
6	RIL#17A	Dz-cr-387 x Dz-01-974
7	RIL#48A	Dz-cr-387 x Dz-01-974
8	RIL#19A	Dz-cr-387 x Dz-01-974
9	RIL#124A	Dz-cr-387 x Dz-01-974
10	RIL#70A	Dz-cr-387 x Dz-01-974
11	RIL#110A	Dz-cr-387 x Dz-01-974
12	RIL#121A	Dz-cr-387 x Dz-01-974
13	RIL#63A	Dz-cr-387 x Dz-01-974
14	RIL#16A	Dz-cr-387 x Dz-01-974
15	RIL#44A	Dz-cr-387 x Dz-01-974
16	RIL#50B	Dz-cr-387 x Dz-01-974
17	RIL#75B	Dz-cr-387 x Dz-01-974
18	RIL#57B	Dz-cr-387 x Dz-01-97
19	RIL#11B	Dz-cr-387 x Dz-01-974
20	RIL#5B	Dz-cr-387 x Dz-01-974
21	RIL#8B	Dz-cr-387 x Dz-01-974
22	RIL#44B	Dz-cr-387 x Dz-01-974
23	RIL#124B	Dz-cr-387 x Dz-01-974
24	RIL#113B	Dz-cr-387 x Dz-01-974
25	RIL#28B	Dz-cr-387 x Dz-01-974
26	RIL#19B	Dz-cr-387 x Dz-01-974
27	RIL#17B	Dz-cr-387 x Dz-01-974
28	RIL#45B	Dz-cr-387 x Dz-01-974
29	RIL#11C	Dz-cr-387 x Dz-01-974
30	RIL#46C	Dz-cr-387 x Dz-01-974
31	RIL#74C	Dz-cr-387 x Dz-01-974
32	RIL#3C	Dz-cr-387 x Dz-01-974
33	RIL#11D	Dz-cr-387 x Dz-01-974
34	RIL#11E	Dz-cr-387 x Dz-01-974
35	Stand. Check	Quncho (Dz-cr-387)
36	Stand. Check	Kora
37	Local check	Tsaeda zezew

respectively.

Among the genotypes, RIL#44A, with a maturity period of 101.6 days was found to be the earliest, while RIL#44C, with a maturity period of 117.67 days was found to be the latest. Among 37 genotypes, 56.7% showed days to maturity below the grand mean, signifying earliness of these genotypes in their maturity period as compared to the others. On the other hand, as compared to the standard check variety (Quncho) 5.4% of the genotypes showed early maturity. This suggested the higher chance of selecting early genotypes which can tolerate terminal moisture stress, which is one of the

bottleneck for tef production in the study area.

In this experiment, genotypes with early heading did not show early maturity and late maturing ones did not necessarily correspond with lateness in days to heading. The result is similar to previous works of Plaza et al. (2013) and Khan (2013) who in that order in tef and wheat reported that the two traits were not similar for most of the studied materials. This might be due to the genetic factors carried by the genotypes for each trait as well as the differences of growing seasons and environments under which the materials were evaluated.

Minimum and maximum plant heights of 98.7 and

**Table 2.** Analysis of variance results for 14 traits of tef RILs studied.

Traits	Source of variation				
	Replications (df=2)	Genotypes (df=36)	Error (df=72)	CV (%)	R <sup>2</sup> (%)
Days to heading	0.009 <sup>ns</sup>	17.34**	1.194	1.83	87.89
Days to maturity	3.93*	75.78**	1.002	0.93	97.43
No. tillers/plant	0.93*	0.16**	0.084	19.54	55.96
Plant height (cm)	25.33*	71.16**	7.192	2.48	83.45
Panicle length (cm)	44.2**	9.78**	3.776	4.58	61.82
Panicle weight (g)	0.059 <sup>ns</sup>	0.05**	0.021	10.93	53.20
Panicle yield (g)	0.001 <sup>ns</sup>	0.03**	0.010	12.42	63.30
Thousand-kernel weight (g)	0.0033 <sup>ns</sup>	0.01 <sup>ns</sup>	0.005	21.07	39.24
Biomass yield (kg ha <sup>-1</sup> )	123382.8 <sup>ns</sup>	4428863.5**	158686.1	4.75	93.32
Grain yield (kg ha <sup>-1</sup> )	29663.04 <sup>ns</sup>	216104.7**	15425.341	5.23	87.59
Harvest index (%)	7.88*	10.254**	1.583	4.42	77.15
Lodging index (%)	6.387 <sup>ns</sup>	64.417**	6.424	2.96	83.44
Biomass production rate (kg ha <sup>-1</sup> day <sup>-1</sup> )	15.87 <sup>ns</sup>	410.293**	14.331	4.87	93.48
Grain yield production rate (kg ha <sup>-1</sup> day <sup>-1</sup> )	1.357 <sup>ns</sup>	22.632**	1.419	5.41	88.88

df = Degrees of freedom, \*, \*\* and ns, significant at  $P \leq 0.05$ ,  $P \leq 0.01$  and non-significant, respectively, CV (%) = coefficient of variation, R<sup>2</sup> = coefficient of determination and RILs = recombinant inbred lines.

118.33 cm were recorded for RIL#17B and RIL#44B, respectively, the mean value for plant height being 108.22 cm, RIL#3A RIL#46B and RIL#13A, showed longer plant height than the standard check, Quncho. The variation with respect to number of productive tillers per plant for tested genotypes ranged from 1.17 for RIL#17B to 2.07 for Tsaeda-Zezew (Local check). Hence, the local RIL#10A (1147.8 kg ha<sup>-1</sup>). With regard to biomass yield, 32.4% of the genotypes exceeded the overall mean (8393.5 kg ha<sup>-1</sup>) of the genotypes while genotypes exceeded 27 and 5.4% of the standard checks, Kora and Quncho, respectively. Thus, there is plenty of variability among the genotypes for selection designed for improvement of this trait.

The range for panicle weight was from 16.7 for RIL#70 to 11.03 for RIL#124A. Thus, 29.7% of the genotypes recorded higher panicle weight than the standard check, Quncho which is the most popular variety currently under production in the area. Therefore, these genotypes can be considered as source materials when increment of this parameter through breeding is needed. The mean value of panicle yield was 7.42 g, RIL#5B, RIL#48A, RIL#70A, RIL#65A and RIL#3A showed superiority for panicle yield than others. Consequently, progress of this trait can be more effective when those genotypes are considered and used in the improvement program. The computed harvest index for genotypes ranged from 22.9% for RIL#11E to 32% for RIL#11C. Genotypes RIL#11C, RIL#13A, RIL#44A and RIL#28B had greater values for harvest index than even the standard checks Kora and Quncho. The top three genotypes that performed better than the standard and local checks for grain yield, as indicated in

check should be considered together with RIL#17B when parental sources for better number of productive tillers per plant are needed. The mean value of panicle length was recorded as 42.46 cm with maximum of 39.23 cm and minimum of 46 cm for RIL#63A and RIL#113B, respectively. Maximum and minimum biomass yields were harvested from RIL#13A (6760.2 kg ha<sup>-1</sup>) and Appendix Table 1, were RIL#10A, RIL#65A and RIL#3A with grain yield of 2962.7, 2842.2 and 2816 kg ha<sup>-1</sup>, respectively.

### Genetic variance, heritability and genetic advance

Estimated variance components, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) of the 13 studied traits of tef genotypes are presented in Table 2. Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were regarded as low (<10%), moderate (10 to 20%) and high (>20%) as noted by Sivasubramanian and Menon (1973), and Deshmukh et al. (1986). Therefore, high PCV was computed for yield per panicle and plant height. PCV and GCV values were computed as moderate for traits like biomass yield, grain yield, biomass production per day and grain production rate per day. Moderate GCV values of these characters suggest the possibility of improving these traits through selection. The phenotypic coefficient of variation was relatively greater than genotypic coefficient of variation for all these characters considered. This study is in agreement with the results reported by Jifar et al. (2015) and Jifar and Likyelesh (2013). In

**Table 3.** Minimum, maximum, mean values and variance components for 13 traits of tef genotypes.

Traits	Min	Max	Mean	$\sigma_p^2$	$\sigma_g^2$	GCV (%)	PCV (%)	H <sup>2</sup> (%)	GA	GAM (%)
DH	54	64.33	59.87	6.58	5.38	3.87	4.28	81.84	4.32	7.22
DM	101.67	117.67	108.1	25.93	24.92	4.62	4.71	96.14	10.09	9.34
PH	1.17	2.07	1.48	0.11	0.03	11.49	22.29	23.52	0.16	10.82
PL	98.7	118.33	108.23	28.51	21.32	4.27	4.93	74.78	8.24	7.61
NT	39.23	46	42.46	5.78	2.00	3.32	5.65	34.63	1.71	4.04
PW	11.03	16.7	13.71	0.03	0.01	7.3	12.6	31.85	0.11	8.29
YPP	5.1	9.47	7.42	0.04	0.01	13.51	27.03	25.00	0.10	13.94
BY	6760.2	11476.8	8393.5	1582078.57	1423392.47	14.21	14.99	89.97	2334.57	27.81
GY	1867.3	2962.7	2375.4	82318.48	66893.13	10.89	12.08	81.26	480.96	20.25
HI	22.9	32	28.47	4.47	2.89	5.97	7.41	64.62	2.81	9.88
LI	72.33	93	85.72	25.76	19.33	5.13	5.92	75.06	7.86	9.17
BPR	61.54	109.6	77.81	146.32	131.99	14.77	15.55	90.21	22.52	28.94
GYPD	16.87	28.3	22.03	8.49	7.07	12.07	13.16	83.28	4.98	22.62

DH = Days to heading, DM = days to maturity, PH = plant height (cm), PL = panicle length (cm), NT = number of productive tillers per plant, PW = panicle weight per plant per plant (g), YPP = yield panicle<sup>-1</sup>(g), TKW = thousand kernel weight (g), BY = biomass yield(kg ha<sup>-1</sup>), GY = grain yield (kg ha<sup>-1</sup>), HI = harvest index (%), LI = lodging index (%), BPR = biomass production rate (kg ha<sup>-1</sup> day<sup>-1</sup>), GYPG = grain yield production rate per day (kg ha<sup>-1</sup> day<sup>-1</sup>),  $\sigma_g^2$  = genotypic variance,  $\sigma_p^2$  = phenotypic variance PCV= phenotypic coefficient of variance (%), GCV = genotypic coefficient of variance (%), H<sup>2</sup> = broad sense heritability (%), GA = genetic advance, GAM = genetic advance as a percent of mean (%) and RILs = recombinant inbred lines.

contrast to this, Chanyalew (2010) reported high GCV than PCV for biomass yield, panicle seed yield and harvest index. The magnitude of the difference between PCV and GCV in this study was low for number of tillers, days to maturity, panicle length, biomass yield, lodging index and biomass production rate per day. This showed that the environmental effects on genetic expression of these traits were low and selection based on the phenotype or genotypes would result in genetic improvement which is eminent. This is in agreement with the report by Ayalew et al. (2012) for days to maturity and harvest index. Both GCV and PCV values were moderate for plant height, panicle yield, grain yield, biomass production rate per day and grain yield production rate per day. High PCV was noted for plant height and yield per panicle, while moderate PCV but low GCV values were computed for panicle weight. Both PCV and GCV values were computed as low for days to heading, days to maturity, panicle length, lodging index, harvest index and number of tillers. This is in line with the studies reported of Admas and Belay (2011), Debebe et al. (2012) and Jifar and Gugssa (2013).

The magnitude of differences between PCV and GCV for characters like plant height and yield per panicle were relatively high. This implies greater effects of environmental factors for the phenotypic expression of these characters. This may make it difficult to improve the characters by selecting high performing genotypes. This result is in close agreement with the findings of Jifar and Gugssa (2011) who reported relatively high PCV than GCV for plant height. In contrast, low PCV and GCV values were computed for days to heading, days to

maturity, number of tillers, harvest index and lodging index.

Genotypic coefficient of variation provides information on the genetic variability present in various quantitative traits, but it is not possible to determine the extent of the variation that was heritable only from the genotypic coefficient of variation. Genetic coefficient of variation together with heritability would give clear estimate of the amount of advance to be expected from selection, Burton and De Vane (1953). According to Singh (2001), if very high or high, for example 80% or more heritability is accompanied by high genetic advance of a character, selection for such characters could be fairly feasible. This could be because of close correspondence between the genotype and the phenotype due to the relative small contribution of the environment to the phenotype. But, for characters with low heritability, for example 40% or less, selection may be considerably difficult due to the masking effect of the environment.

From the results presented in Table 2, very high estimate of heritability values were estimated for days to maturity, biomass production rate per day, biomass yield, grain yield production rate per day, days to heading (81.84%) and grain yield. This result suggested that selection of these traits could be fairly easy and advancement is possible using selection breeding This result is in line with that of Tefera et al. (2003b) and Jifar et al. (2015) who reported very high broad sense heritability estimates for days to maturity (85.59%), panicle length (96.07%) and days to heading (96.98%) in tef genotypes. On the other hand, medium heritability estimates were noted for harvest index, lodging index

and panicle length. Similar results were previously reported in tef for harvest index (78.2%), panicle length (74.78%) and lodging index (74%), by Jifar et al. (2013), Chanyalew (2010), and Ayalew et al. (2012), respectively.

Low heritability estimates were recorded for plant height, number of tillers, panicle weight and yield per panicle (Table 2) such low values indicated that improvement could be difficult for these characters through selection. Similar results showed low heritability for panicle weight and plant height as reported by Debebe et al. (2012) and for number of tillers by Chanyalew (2010).

Genetic advance as percent of mean ranged from 4.04% for number of tillers to 28.94% for biomass production rate per day. Johnson et al. (1955) classified genetic advance as percent of mean as low (<10%), moderate (10-20%) and high (>20%). Based on this classification, as presented in Table 2, traits like biomass yield, grain yield, biomass production rate per day and grain yield production rate per day recorded high genetic advance as percent of mean, while moderate genetic advance as percent of mean was recorded for plant height and panicle yield. Genetic advance under selection refers to progress in selected genotypes as compared to the base population with a single cycle of selection at a given selection intensity (Singh, 2001). Therefore, the results suggested that selecting the top 5% of the genotypes could result in genetic advance values of 4.04 to 28.94%.

Genetic advance values were low (<10%) for days to heading, days to maturity, panicle length, number of tillers, panicle weight, harvest index and lodging index (Table 2). This implies that advancement of traits in genotypic value for the new population as compared to the base population under one cycle of selection is <10% at 5% selection intensity. Similar work was reported by Jifar et al. (2013) who indicated that the genetic advance was low (<10%) for traits like days to heading (6.05%), days to maturity (0.80%), panicle length (5.18%) and lodging index (4.86%).

According to Johnson et al. (1955a), high heritability together with high genetic advances are more useful than heritability alone, implying the role of additive genes in the expression of the traits and thus it could be very effective in improvement and predicting the resultant effect on selecting the best individuals. In this study, high heritability together with high genetic advance values as percentage of the mean were observed for biomass yield, grain yield, biomass production rate per day and grain yield production rate per day. Hence, selection for such traits is likely to be effective. Similar results of high genetic advance show estimates of 39.1 and 68.6% in tef for grain yield by Jifar et al. (2015) and Admas and Belay (2011), respectively.

A relatively low heritability with low genetic advance were observed for harvest index, panicle weight and

number of tillers. The low heritability of traits may be due to the presence of non-additive type of gene action (Ali et al., 2009).

## Conclusion

The present study showed that there is a wide range of variability in the studied genotypes for most of the traits studied. Hence, progress could be achieved in seed yield through selection in tef crop.

## ABBREVIATIONS

**DH**, Days to heading; **DM**, days to maturity; **PH**, plant height (cm); **PL**, panicle length (cm); **NT**, number of productive tillers per plant; **PW**, panicle weight per plant per plant (g); **YPP**, yield panicle<sup>-1</sup>(g); **TKW**, thousand kernel weight (g); **BY**, biomass yield (kg ha<sup>-1</sup>); **GY**, grain yield (kg ha<sup>-1</sup>); **HI**, harvest index (%); **LI**, lodging index (%); **BPR**, biomass production rate (kg ha<sup>-1</sup> day<sup>-1</sup>); **GYPG**, grain yield production rate per day (kg ha<sup>-1</sup> day<sup>-1</sup>);  $\sigma^2_g$ , genotypic variance;  $\sigma^2_p$ , phenotypic variance; **PCV**, phenotypic coefficient of variance (%); **GCV**, genotypic coefficient of variance (%); **H<sup>2</sup>**, broad sense heritability (%); **GA**, genetic advance, **GAM**, genetic advance as percent of mean (%); **RILs**, recombinant inbred lines.

## CONFLICT OF INTERESTS

The author has not declared any conflict of interests.

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**Appendix 1.** Mean yield and yield components performance values of 14 traits of 37 tef genotypes tested.

Genotypes	DH	DM	PH	PL	NT	PW	PY	BYLD	GYLD	HI	LI	BPR	GYPD	TKW
Kora	58.67	116.33	112.8	39.83	1.63	11.9	6.1	10866.8	2711.8	24.9	92	93.4	23.31	0.37
Local	58	116.67	106.2	43.13	2.07	14.9	7.55	7834.2	2203.4	28.14	91.67	67.17	18.89	0.33
Quncho	57	115.33	114	43.1	1.3	14.2	8.17	8632.8	2302	26.66	89.67	84.38	22.49	0.47
RIL#10A	57	104.67	105.47	40.77	1.2	13.6	7.57	11476.8	2962.7	25.8	93	109.6	28.3	0.33
RIL#110A	63.33	105	105.87	42.87	1.7	13.17	7.27	8247.7	2340.7	28.36	84.33	78.57	22.29	0.33
RIL#113B	60	104	103.8	39.23	1.43	12.97	7.57	8032.8	2380	29.6	81.67	77.25	22.88	0.33
RIL#11B	63	115.67	112.23	39.9	1.37	11.5	5.1	7284	1952.8	26.8	82.67	62.9	16.88	0.33
RIL#11C	62.33	116	103.67	42.57	1.43	13.4	7.23	7561.8	2415.8	32.01	82.33	65.17	20.83	0.4
RIL#11D	61.67	116	110.93	42.23	1.33	13.9	6.4	8139	2353.3	28.9	90	70.16	20.28	0.37
RIL#11E	61.67	110.67	114.27	42.1	1.17	14.8	8.27	11449.3	2627.2	22.9	90	103.45	23.73	0.33
RIL#121A	63.33	108.67	110.43	43.5	1.23	13.4	8.1	8283.8	2367.2	28.55	83.33	76.24	21.78	0.37
RIL#124A	57	113c	111	43.07	1.8	11.03	5.3	8449.8	2256.2	26.8	85.67	74.8	19.96	0.27
RIL#124B	59.67	111.33	105.13	44.23	1.5	12.97	6.77	7619.5	2103.8	27.6	83	68.44	18.89	0.37
RIL#13A	59	107	102	40.17	1.6	14.3	7.8	6760.2	2118.2	31.35	92	63.19	19.79	0.33
RIL#16A	64.33	107.33	110.1	40.5	1.37	12.67	7	8647.5	2636	30.5	83.33	80.57	24.56	0.3
RIL#17A	58.67	111	104.37	41.4	1.97	13.47	7.5	8346.2	2589.2	31.02	90	75.2	23.33	0.37
RIL#17B	60	115	98.7	40.13	1.17	13.8	7.1	7089.8	2015.3	28.38	72.33	61.6	17.52	0.3
RIL#19A	58.33	105	107.33	44.77	1.27	16.13	7.3	9264	2701.3	29.15	86	88.23	25.73	0.33
RIL#19B	60.33	107	102.27	42.07	1.3	14.33	8.13	7379.3	2222	30.1	89	68.91	20.76	0.33
RIL#28B	54	110.33	112.7	43.37	1.4	13.1	6.47	7530.3	2306.8	30.6	86	68.27	20.9	0.33
RIL#3A	58	105.33	118.3	45.07	1.47	14.5	8.4	9391.3	2816	29.9	90.33	89.17	26.74	0.27
RIL#3C	62	107	110.13	42.63	1.4	14.27	8.27	9531.8	2642.3	27.8	89	89.07	24.69	0.27
RIL#44A	59.67	101.6	108.43	39.97	1.67	12.9	7.37	8353.7	2601	31.16	82.67	82.14	25.58	0.27
RIL#44B	60	103	118.33	43.03	1.5	13.4	8.07	7720	2236.2	28.9	85	74.9	21.7	0.37
RIL#45B	61.67	116.67	104.23	41.2	1.27	12.33	6.03	6810	1867.3	27.42	77.33	61.5	16.87	0.27
RIL#46C	62	117.67	115.37	45.97	1.47	12.33	6.3	8373.8	2365.6	28.32	80.33	71.16	20.1	0.3
RIL#48A	59	102.67	103.3	44.47	1.5	14.6	9.4	7224.3	2053.8	28.43	86	70.39	20.01	0.43
RIL#50B	56l	102	103.5	41.1	1.53	11.9	6.67	7150.8	2094	29.3	82.33	70.1	20.53	0.4
RIL#57B	60.33	107	103.27	40.67	1.3	12.87	7.33	8718.9	2532.3	29.05	82.67	81.49	23.67	0.33
RIL#5B	58.33	102	108.27	44.4	1.9	16.6	9.47	7749.3	2217.5	28.58	92	75.9	21.73	0.3
RIL#63A	63	102	107.6	46	1.47	13	6.47	7446.8	2140	28.74	83.33	73.03	20.98	0.33
RIL#65A	61	101.33	112.05	44.8	1.67	15.5	8.6	10347	2842.2	27.6	90.33	93.8	25.76	0.37
RIL#68A	63.67	105	102.7	41.3	1.77	13.13	7.2	8644.8	2559.7	29.6	90.67	82.4	24.38	0.4
RIL#70A	57.67	109.67	106.7	42.13	1.8	16.7	8.87	8359	2356.3	28.23	83.67	76.23	21.48	0.37
RIL#74C	58	102	110.9	43.3	1.27	13.8	7.47	9401.5	2531.3	26.9	82.67	92.19	24.8	0.33
RIL#75B	60	104.67	114.2	44	1.37	15.6	8.33	9554.3	2485.3	26.02	83.67	91.28	23.75	0.33

## Appendix 1. Contd.

RIL#8B	57.67	116	103.67	41.87	1.2	14.2	7.7	6887.5	1984.5	28.78	81.67	66.24	19.1	0.3
Mean	59.87	108.1	1.48	108.23	42.46	13.71	7.42	8393.5	2375.4	28.47	85.72	77.81	22.03	0.33
CV	1.83	0.93	19.54	2.48	4.58	10.93	12.42	21.07	4.75	5.23	4.42	2.96	4.87	21.067

DH = Days to heading, DM = days to maturity, PH = plant height (cm), PL = panicle length (cm), NT = number of productive tillers per plant, PW = panicle weight, PY = panicle yield ( $\text{g}^{-1}$ ), TKW = thousand kernel weight (g), BY = biomass yield ( $\text{kg ha}^{-1}$ ), GY = grain yield ( $\text{kg ha}^{-1}$ ), HI = harvest index (%), LI = lodging index (%), BPR = biomass production rate ( $\text{kg ha}^{-1} \text{day}^{-1}$ ) and GYPG = grain yield production rate per day ( $\text{kg ha}^{-1} \text{day}^{-1}$ )