SOIL & CROP SCIENCES | RESEARCH ARTICLE

 Variance components in recombinant inbred lines of Tef [Eragrostis tef (Zucc.) Trotter L.]: Estimation and their implications in selection

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 Abstract: Tef [Eragrostis tef (Zucc.) Trotter L.] is an indigenous and important cereal crop in Ethiopia. Its improvement is dependent on the presence and magnitude of genetic variation among traits in a given environment. Forty-nine tef genotypes (RILs and checks) were evaluated in 2019 to assess the nature of genetic variability, broad sense heritability and genetic advance of traits using 7×7 simple lattice design. Analysis of variance revealed significant (P ≤ 0.05) differences among the genotypes except for thousand seed weight. About 53% of the genotypes provided higher yield than the latest improved variety (Ebba), implied that most of the studied RILs varied for grain yield. Higher phenotypic and genotypic coefficients of variation found for main shoot panicle weight, main shoot panicle grain yield, fertile tiller number and days to heading, grain-filling period, main-shoot panicle length, total-tiller number, fertile-tiller number, main-shoot panicle weight, main-shoot panicle grain yield, grain yield and harvest index, implying the presence of adequate variability within the genotypes for these traits. High values of broad sense heritability coupled with high genetic advance as percent of the mean were observed for days to heading, grain-filling period, peduncle length, fertile-tiller number and grain yield indicating the contribution of additive genes for trait expression and possibility

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 PUBLIC INTEREST STATEMENT

 Tef [Eragrostis tef (Zucc.) Trotter], is a cereals crop mainly grown for its grain as a major staple food and market crop. As an indigenous cereal crop to Ethiopia, it is well adapted to diverse climatic and soil conditions and most of the countries’ population is highly dependent on its food value; however, its productivity is extremely reduced mainly due to absence of high yielder varieties. Therefore, research towards high yielding varieties will be the primary focus. For this end, it’s phenotypic plasticity in phenology and agronomic traits will be exploited for its improvement through partitioning its variation into heritable and non heritable variation in recombinant inbred lines by using genetic parameters such as genotypic and phenotypic coefficients of variation, heritability and genetic advance for further breeding and to carry out selection based improvement.

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of traits improvement through direct selection. Generally, this considerable genetic variability among the RILs confirmed the possibility of improving tef productivity, while most of these RILs should further be studied on more test locations.

**Subjects:** Agriculture; Crop Science; Plant Biology

**Keywords:** Coefficient of variation; *Eragrostis tef*; genetic advance; heritability; recombinant inbred lines

1. **Introduction**

Tef (*Eragrostis tef* (Zucc.) Trotter L.) is self-pollinated panicle bearing crop with 0.2–1.0% out-crossing and an allotetraploid with a base chromosome number of 10 (2n = 4x = 40) and genome size of 730 Mbp (Mulu et al., 2001). Tef is a C₄ plant and an intermediate between a tropical and temperate grass (Seyfu, 1997). It is small cereal grain crop that belongs to the family Poaceae, subfamily *Eragrostioideae*, tribe *Eragrostidae* and genus *Eragrostis*. The genus *Eragrostis* comprises about 350 species among which tef is the only cultivated species (Watson & Dallwitz, 1992). A total of 14 wild *Eragrostis* species have been suggested as potential progenitors of tef (Ingram & Doyle, 2003).

Tef can be cultivated under diverse ranges of agro-ecological conditions and performs better than other cereals under adverse and marginal conditions and fits in to various cropping and crop rotation systems and useful as a catch crop and low-risk reliable crop (Kebebew et al., 2011), it excellently performs in areas with altitudes of 1800–2100 m.a.s.l., annual rainfall of 750–850 mm (growing season rainfall of 450–550 mm) and temperature ranges of 10–27°C (Seyfu, 1997). Its seed can be stored for a long time as the grain is not affected by storage pests, less susceptible to disease and insect pests and tef straw is nutritious and serves as fodder for cattle feed (Abebe, 2001).

Tef have been cultivated in Ethiopia for centuries due to various merits over other cereals. Moreover, a total production of 5.4 million tons with area coverage of 3.0 million ha has been recorded in 2019 (CSA, 2019). The Amhara Region is one of the major tef growing regions in the country with productivity of 1.81 t ha⁻¹, which is slightly more than the National average. North Gondar zone is one of the major tef growing area with 132,046 ha of land cultivated with it. Tef is one of the most important cereals grown in west Belesa district grown nearly on 21,032 ha of land (WBAO, 2019).

However, the national average grain yield of tef is still lower due to the low yield potential of landraces and local varieties used by farmers under widespread cultivation, lodging problem, drought and other biotic and abiotic stresses (Kebebew et al., 2011). These problems could be solved by developing better high yielding, stress resistant and adaptable tef varieties by exploiting the broad spectrum of trait diversity through either direct selection or intra-specific hybridization between parental lines with desirable traits (Kebebew et al., 2015). The breeding progress in crop improvement is dependent on the magnitude of genetic variation, heritability and genetic advance of traits in a given environment (Singh, 2002). Tef has high level of phenotypic plasticity in phenology and agronomic traits depending on the type of variety and environment where it is grown (Kebebew et al., 2011). Its grain yield and quality also vary with soil type, climate, season and varieties. Therefore, partitioning of the total variation into heritable and non heritable variation by using genetic parameters such as genotypic and phenotypic coefficients of variation, heritability and genetic advance is necessary in order to utilize the genetic potential for further breeding and to carry out selection based improvement.

In Ethiopia, different studies have reported the existence of adequate genetic variability, heritability and genetic advance of various traits of tef, and more than 49 improved tef varieties have
been released (MoANR, 2019). These varieties were developed by exploiting the naturally occurring diversity and this makes the released varieties lack some farmer-preferred traits, and were poorly adopted by tef growers in Ethiopia. Therefore, this necessitates development of new tef varieties with high grain yield, early maturity, lodging resistance, tolerance to moisture stress and desirable grain quality (Kebebew et al., 2013). Furthermore, though tef cross breeding have indicated a 9% yield advantage as compared to those developed through direct selection from germplasm materials, much attention have not been given to trait recombination and few studies have been conducted on estimation of genetic variability, heritability and genetic advance in tef recombinant inbred lines (Abraha et al., Abraha, et al., 2017).

More specifically, though tef is the major crop grown in West Belesa district, limited use of productive and drought tolerant varieties in the area have reduced it's productivity. Therefore, to select high yielder, drought tolerant and early maturing tef recombinant inbred lines for further breeding program, it is necessary to estimate components of variance so as to study the genetic variability, heritability and genetic advance of important traits of tef in the study area. Thus, the objectives of the present study were to estimate variance components; genetic variability, heritability and genetic advance in yield and yield related traits of tef recombinant inbred lines and their implication in selection.

2. Materials and methods

2.1. Experimental area

The field experiment was conducted at the Agricultural experimental field of the University of Gondar in Arbaya, West Belesa district (Figure 1 & Figure 2) during the main cropping season of 2019. The center is located at 81 km and 651 km from the city of Gondar and Addis Ababa respectively and it is found in Central Gondar zone of the Amhara National Regional State. The site is located at an altitude of 1680 m.a.s.l with dominant soil type of well drained black vertisol. The temperature ranges from 13.84–28.04°C to 13.07–26.75°C (WBAO, 2019).

2.2. Experimental plant materials

Forty-Nine genotypes, 42 F₆ advanced recombinant inbred lines (RILs), two recently released standard check varieties (Negus and Ebba), four parents of the RILs, namely, DZ-01-196
(Magna), HO-TFS-1486, Boset and GA-10-3 along with one local check variety were used for the study (Table 1). The 42 F₂ RIL populations were progenies from the cross of four parent varieties; DZ-01-196 × HO-TFS-1486 and Boset × GA-10-3. The cross was made by Debre Zeit Agricultural Research Center and F₂ plants were selfed and subsequent generations were advanced until they reached to the 8th generation. The two standard check varieties, Negussu and Ebba were recently released by Debre Zeit Agricultural Research Center (MoANR, 2019). Seeds of the 42 advanced lines, the four parents, and the two standard checks were obtained from Debre Zeit agricultural research center (DZARC) and the local check was included from the study area as shown in Table 1.

2.3. Experimental design and management

A 7 × 7 simple lattice design was used to lay out the 49 genotypes. Each experimental plot was 2 m² (1 m × 2 m) with five rows spaced 20 cm apart. The distance between plots and incomplete blocks was 1 m and that between replications was 1.5 m. The genotypes were allotted to plots at random with in each replication. As per the recommendation of 15 kg ha⁻¹, 3 gm plot⁻¹ of seed was each drilled along the surface of each row on a well prepared soil. The experimental materials were planted in the mid of July. The fertilizers recommended for the study area 100 kg Urea and 100 kg DAP per hectare was applied (Alemayehu et al., 2007). Full dose of DAP was applied at planting, while Urea was applied two weeks after sowing and top dressed at tillering stage. Hand weeding was done three times during the crop growth season.

2.4. Data collection

Data were collected on the basis of plot and individual plants from July 20 to 25 October 2019. For plant basis, five plants were randomly selected from the central two rows of each plot. The mean value of the sample plants from each plot was used for analysis.

2.4.1. Individual plant based traits

(1) **Plant height (PH) (cm)**: the height of five randomly taken plants from the central rows of each plot was measured from the ground level to the tip of the main shoot panicle at maturity.

(2) **Main shoot panicle length (MSPL) (cm)**: The average length of the main shoot panicle of five randomly taken plants from the central rows of each plot measured from the end of the peduncle to the tip of the panicle at maturity.

(3) **Peduncle length (PDL) (cm)**: The average length of the last apical internode of the main shoot culm of five randomly taken plants from the central rows of each plot measured from the last culm node up to the place where the panicle starts.
Table 1. List of tef recombinant inbred lines and checks used for the study

| Entry | Genotype | Parental cross (Source) | Entry | Genotype | Parental cross (Source) |
|-------|----------|-------------------------|-------|----------|-------------------------|
| 1     | RIL146   | DZ-01-196 × HO-TF-1486  | 26    | RIL52    | DZ-01-196 × HO-TF-1486  |
| 2     | RIL303   | Boset × GA-10-3         | 27    | RIL296   | Boset × GA-10-3         |
| 3     | RIL32    | DZ-01-196 × HO-TF-1486  | 28    | RIL191   | DZ-01-196 × HO-TF-1486  |
| 4     | RIL293   | Boset × GA-10-3         | 29    | RIL225   | DZ-01-196 × HO-TF-1486  |
| 5     | RIL280   | DZ-01-196 × HO-TF-1486  | 30    | RIL42    | Boset × GA-10-3         |
| 6     | RIL213   | Boset × GA-10-3         | 31    | RIL162   | DZ-01-196 × HO-TF-1486  |
| 7     | RIL58    | DZ-01-196 × HO-TF-1486  | 32    | RIL163   | Boset × GA-10-3         |
| 8     | RIL259   | DZ-01-196 × HO-TF1486   | 33    | RIL152   | DZ-01-196 × HO-TF-1486  |
| 9     | RIL134   | Boset × GA-10-3         | 34    | RIL174   | Boset × GA-10-3         |
| 10    | RIL122   | Boset × GA-10-3         | 35    | Ebba     | Kari murri × 3774-13    |
| 11    | RIL114   | Boset × GA-10-3         | 36    | RIL178   | DZ-01-196 × HO-TF-1486  |
| 12    | RIL55    | DZ-01-196 × HO-TF-1486  | 37    | RIL128   | Boset × GA-10-3         |
| 13    | RIL90    | Boset × GA-10-3         | 38    | RIL123   | DZ-01-196 × HO-TF-1486  |
| 14    | RIL281   | DZ-01-196 × HO-TF-1486  | 39    | RIL170   | Boset × GA-10-3         |
| 15    | RIL176   | DZ-01-196 × HO-TF-1486  | 40    | RIL92    | DZ-01-196 × HO-TF-1486  |
| 16    | RIL104   | Boset × GA-10-3         | 41    | RIL313   | Boset × GA-10-3         |
| 17    | RIL285   | Boset × GA-10-3         | 42    | Local    | Farmers’ variety        |
| 18    | RIL89    | Boset × GA-10-3         | 43    | RIL143   | DZ-01-196 × HO-TF-1486  |
| 19    | RIL108   | DZ-01-196 × HO-TF-1486  | 44    | RIL127   | Boset × GA-10-3         |

(Continued)
### Table 1. (Continued)

| Entry | Genotype   | Parental cross (Source) | Entry | Genotype | Parental cross (Source) |
|-------|------------|-------------------------|-------|----------|-------------------------|
| 20    | RIL240     | Boset × GA-10-3         | 45    | GA-10-3  | Mutant line             |
| 21    | RIL105     | DZ-01-196 × HO-TF-1486  | 46    | Boset    | DZ-Cr-409 RIL 50d       |
| 22    | RIL26      | DZ-01-196 × HO-TF-1486  | 47    | DZ-01-196| Land race               |
| 23    | RIL281     | DZ-01-196 × HO-TF-1486  | 48    | HO-TF-1486| Land race               |
| 24    | RIL69      | DZ-01-196 × HO-TF-1486  | 49    | Negus    | DZ-01-353 × Kay Murri   |
| 25    | RIL242     | Boset × GA-10-3         |       |          |                         |

(4) **Numbers of primary branches per main shoot panicle (NPBMP)**: The number of primary panicle branches of the main shoot was counted for five randomly taken plants from the central rows of each plot and averaged.

(5) **Number of total tillers per 0.5 m row length (TLN)**: The number of all tillers produced was assessed on randomly taken central rows of each half meter part of the plot.

(6) **Number of fertile tillers per 0.5 m row length (FTN)**: The number of panicle bearing (fertile) tillers produced was assessed on randomly taken central rows of each half meter part of the plot.

(7) **Main shoot panicle weight (MSPNW) (gm)**: Weight of the panicle on the main shoot was measured.

(8) **Main shoot panicle grain yield (MSPGY) (gm)**: Yield of the panicle grains on the main shoot was weighted.

#### 2.4.2. Plot based traits

(1) **Days to heading (DH) (days)**: The number of days from the date of seedling emergence to the date when 50% of the plants in each plot with panicle tips emerged (about 5 cm) on the main shoot was counted.

(2) **Days to physiological maturity (DM) (days)**: The number of days from the date of seedling emergence up to the date when 90% of the plants in each plot attained physiological maturity by the turning of the vegetative parts to yellow (straw) color was counted.

(3) **Grain-filling period (GFP) (days)**: The number of days from 50% panicle emergence to physiological maturity, was obtained by subtraction of the days to heading from the days to physiological maturity.

(4) **Lodging index (LI)**: It was recorded following the method of Caleicott and Nuttall (1979) as a product sum of each scale or degree of lodging (0–5) and their respective percentage divided by five. LODGING INDEX = Sum (Lodging scores or degree × the respective percentage area lodged)/5. The calculated values for lodging index is between 0 (no lodging or erect) and 100 (complete lodging).
(5) **Grain yield per plot (GY) (gm):** The mass (weight) of grain yield obtained from all plants harvested from the central rows of each plot after adjusting to a moisture content of 12.5% and was calculated to kg ha\(^{-1}\) scale.

(6) **Above ground biomass yield per plot (AGBY) (gm):** The total above ground biomass (grain + straw) was weighted for all plants harvested from the central rows of each plot after sun drying and attaining constant moisture content and was calculated to kg ha\(^{-1}\) scale.

(7) **Harvest index (HI) (%):** It was computed as the ratio of grain yield to the total above ground biomass.

(8) **Thousand-seed weight (TSW) (gm):** The mass (weight) of 1000 seeds was measured after the seeds collected from the bulk of seeds harvested from all plants in each plot and its moisture content adjusted.

### 2.5. Data analyses

#### 2.5.1. Analysis of variance

The relevant values generated on plot and plant basis were subjected to analysis of variance (ANOVA) using general linear model and lattice procedures by SAS software version 9.2 (SAS Institute, 2007). The lattice procedure was used to accurately estimate treatment effects, while general linear model procedure was used to calculate unadjusted sum squares for block, intra block error and treatment. Comparison of trait means of genotypes was done following the significance of mean squares using Duncan’s Multiple Range Test.

The Mathematical Model for Simple Lattice Design is:

\[
Y_{ijk} = \mu + G_i + B_k(j) + R_j + e_{ijk}
\]

Where \(Y_{ijk}\) = Phenotypic effect of ith genotype under jth replication and kth incomplete block within replication j, \(\mu\) = grand mean, \(G_i\) = effects of ith genotype, \(B_k(j)\) = effect of kth block within replication j, \(R_j\) = the effect of replication j, \(e_{ijk}\) = the plot residual effect or effect of random error.

Means adjusted by blocks were used when the relative efficiency of lattices was higher than 105% when compared with the RCBD. Otherwise, unadjusted means were used. Intra block error mean squares instead of RCBD error mean squares were used as a denominator in the F-test when relative efficiency of lattice designs was greater than 105% compared with the RCBD (Cochran & Cox, 1992).

#### 2.5.2. Comparison of genotypic performances

Genotypic performances were compared by using the minimum and maximum values, means and standard errors of means (SEM) from the results of ANOVA and means comparison to estimate the variability of the studied traits among genotypes.

#### 2.5.3. Estimation of phenotypic and genotypic variance components

The phenotypic and genotypic variances of each trait were estimated using the mean squares from the analysis of variance. The genotypic and phenotypic components of variances were computed as per the methods suggested by Burton and Devane (1953).

\[
\sigma^2_g = \frac{\text{Msg} - \text{Mse}}{r}
\]

Environmental variance (\(\sigma^2_e\)) = Mse
Where $\text{Msg}$ and $\text{Mse}$ are the mean squares for the genotypes and error in the analysis of variance, respectively, and $r$ is the number of replications. Then, the phenotypic variance is estimated as the sum of the genotypic and environmental variances.

\[
\text{Phenotypic variance } (\sigma^2_p) = \sigma^2_g + \sigma^2_e
\]

2.5.4. Estimation of genotypic and phenotypic coefficients of variability

The genotypic and phenotypic coefficients of variability were estimated according to the formula of Singh and Chaudhary (1977)

Genotypic Coefficient of Variation (GCV) = \frac{\sqrt{\sigma^2_g}}{\bar{x}} \times 100

Phenotypic Coefficient of Variation (PCV) = \frac{\sqrt{\sigma^2_p}}{\bar{x}} \times 100

Where $\sigma^2_g$ and $\sigma^2_p$ are genotypic and phenotypic variances, respectively.

$\bar{x}$ = population mean of the trait considered.

Phenotypic and genotypic coefficients of variation (PCV and GCV) were categorized as low (<10%), moderate (10–20%) and high (>20%) based on the method of Sivasubramanian and Menon (1973) and Deshmukh et al. (1986).

2.5.5. Estimation of broad sense heritability and genetic advance

Heritability in broad sense was computed as the proportion of the genotypic variance to the total variance (Allard, 1960). It refers to the portion of phenotypically expressed variation within a given environment and it measures the degree to which a trait can be modified by selection (Christianson & Lewis, 1982). Thus, broad sense heritability, genetic advance and genetic advance as percent of the mean were estimated using the procedure developed by Allard (1960).

Heritability in broad sense ($H^2$) = $\frac{\sigma^2_p}{\sigma^2_p + \sigma^2_e} \times 100$

\[
\sigma^2_p = \sigma^2_g + \sigma^2_e \times 100
\]

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

$\sigma^2_p$ = phenotypic variance and $\sigma^2_e$ = error variance.

Broad sense heritability values were categorized according to Johnson et al. (1955), where heritability values greater than 80% as very high, values 60–79% as moderately high, values from 40% to 59% as medium and values less than 40% were classified as low.

Then Genetic advance (GA) and genetic advance as percent of the mean (GAM) for each character was computed using the formula adopted from Johnson et al. (1955).

\[
\text{GA} = (k) (\sigma p) \times (H^2) \text{ and GAM} = \frac{\text{GA}}{\bar{x}} \times 100
\]

Where $k$ = selection differential; (at 5% selection intensity, $k = 2.06$)

$\sigma p$ = phenotypic standard deviation

$H^2$ = Broad sense heritability
\( X = \) Grand mean

Genetic advance as percent of the mean was classified following the rule of Johnson et al. (1955) as low (<10%), moderate (10–20%) and high (>20%).

3. Results and discussion

3.1. Analysis of variance

Analysis of variance (ANOVA) showed that the mean squares due to genotypes were highly significant \((P < 0.01)\) for days to heading, days to physiological maturity, grain-filling period, plant height, panicle length, tiller number, fertile tiller number, panicle weight, grain yield per panicle, grain yield, above ground biomass yield and harvest index; while peduncle length, number of primary branches per main shoot panicle and logging index showed significant \((P < 0.05)\) difference, indicating the existence of adequate variability among the 49 genotypes for pheno-morphic, yield and yield related traits studied indicating the possibility to exploit the variability for future breeding programs and the higher chance of improving the crop through selection. The reduced value of coefficient of variation for most of those traits indicated the existence of good precision in the experiment (Table 2). These findings are in agreement with Habte et al. (Habte, et al., 2015a, 2017), Chekole et al. (2016), Mizan et al. (2016), Haftamu (2018), and Worede and Tefera (2020) who found highly significant variation among those traits in study of tef genotypes.

However, some disparity that might have been resulted due to variation of genetic factors carried by the genotypes for each trait used in the study and difference in the experimental area under which the lines were evaluated were found with Habtamu et al. (2011) for fertile tillers, panicle length, biomass yield, grain yield and harvest index. Solomon et al. (2009) also found a statistically non-significant effect for panicle length that is opposite to the current result.

3.2. Mean and range of measured traits

Wide ranges of mean values (maximum and minimum values) were observed for phenological, growth and yield related traits evaluated as shown in Table 3.

3.2.1. Phenologic traits

Days to heading for genotypes ranged from 27.5 (RIL-58) to 60 (local check) with a mean of 36.96. Mean physiological maturity was 79 with a range of 67.5 (Ebba)–89.5 (local check) days whereas grain filling period ranged from 24 (RIL-69) to 53.5 (RIL105) with a mean of 42 days. The range of values observed for phenologic traits in present study were similar to the range reported by Habte et al. (Habte, et al., 2015a) and Worku (2018).

Therefore, 45.83%, 89.6% and 91.6% of the tested RILs exhibited lower mean value than the early maturing genotype Boset for days to heading, days to physiological maturity and grain filling period respectively, indicating those were earlier to head, mature and fill grains as compared to others. This might be due to the genetic factors carried by the genotypes for each trait. This suggests higher chance of selecting early maturing genotypes that can escape terminal moisture stress, which is the constraint of tef production in the study area. Those early maturing genotypes can also be employed in double cropping systems in high rainfall areas with long growing seasons. Furthermore, RIL-58 and variety Ebba that was the earliest to head and mature respectively can be suggested to be used as parental line for future tef breeding programs due to their desirable trait. The result of this research agreed with previous works of Plaza-Wuthrich et al. (2013) who reported genotypes vary for these phenologic traits.

3.2.2. Growth related traits

Plant height ranged from 58.6 to 110.5 cm with mean of 82.5 cm, total tiller number (81–143) with mean of 111.58, fertile tillers number (37.5–106) with mean of 69.8, number of primary branches
| Traits  | Mean squares | CV (%) | $R^2$ | RE of SL over RCBD |
|---------|--------------|--------|-------|-------------------|
|         | Replication  | Block (Adj.) | Genotype | Intra Block error |         |
|         | $(DF = 1)$   | $(DF = 12)$ | $(DF = 48)$ | $(DF = 36,\  \ DF_{RCBD} = 48)$ |         |
| DH      | 13.22        | 7.43    | 69.27** | 5.35              | 6.41    | 0.94 | 102.53 |
| DM      | 14.73        | 9.45    | 48.03** | 5.86              | 3.06    | 0.91 | 105.32 |
| GFP     | 0.04         | 12.49   | 84.1**  | 9.2               | 7.17    | 0.92 | 102.22 |
| PH (cm) | 989.49       | 118.6   | 196.12** | 79.91           | 10.83   | 0.79 | 103.65 |
| MSPL    | 4.54         | 20.94   | 65.79** | 15.77            | 9.9     | 0.85 | 101.91 |
| PDL     | 94.63        | 8.96    | 12.79*  | 7.31             | 15.24   | 0.72 | 101.00 |
| TLN     | 817.23       | 63.43   | 389.63** | 42.98           | 6.26    | 0.91 | 103.55 |
| FTN     | 75.46        | 102.61  | 409.19** | 89.14           | 13.7    | 0.84 | 100.48 |
| PBMP    | 1.62         | 16.7    | 15.64*  | 7.47             | 10.8    | 0.75 | 114.97 |
| MSPNW   | 0.69         | 0.4     | 0.53**  | 0.15             | 19.6    | 0.77 | 122.38 |
| MSPGY   | 0.00004      | 0.073   | 0.299** | 0.081           | 15.6    | 0.78 | 96.73  |
| LI      | 210.42       | 64.52   | 82*     | 41.56            | 14.9    | 0.72 | 104.51 |
| GY      | 1981.62      | 24.459  | 155,509.75** | 22,447 | 7.05    | 0.88 | 100.18 |
| AGBY    | 14837        | 102,614 | 1,017,136** | 124,847 | 4.3     | 0.89 | 94.4   |
| HI      | 0.596        | 6.89    | 19.28** | 3.68             | 7.6     | 0.85 | 109.07 |
| TSW     | 0.0006       | 0.004   | 0.008** | 0.0058          | 18.98   | 0.58 | 88.84  |

* and ** significant $(p \leq 0.05)$ and highly significant $(p \leq 0.01)$, respectively, $ns = non-significant, \ DF = degrees of freedom, CV = coefficient of variation, R^2 = coefficient of determination, RE = relative efficiency, DH = days to heading, DM = days to physiological maturity, GFP = grain filling period, PH = Plant height, MSPL = main shoot panicle length, PDL = peduncle length, NPPBMS = number of branches per main shoot panicle, TLN = total tiller number, FTN = fertile tiller number, MSPNW = main shoot panicle weight, MSPGY = main shoot panicle grain yield, LI = lodging index, GY = grain yield, AGBY = above ground biomass yield, HI = harvest index and TSW = thousand-seed weight.
per main shoot panicle (18.9–31.2) with a mean of 25.43, lodging index (31.2–62.7%) with mean of 45%, above ground biomass yield (7005–10,212.5 kKg ha$^{-1}$) with mean of 8189.6 kKg ha$^{-1}$.

From the present study 51%, 44.9%, 53.06%, 48.97%, and 36.73% of the tested genotypes provided mean values higher than the grand mean for plant height, total tiller number, fertile tiller number, number of primary branches per main shoot panicle and above ground biomass yield respectively. Similarly for lodging index, 57.14% of the tested genotypes showed below their mean value. Thus, there is plenty of variability among the genotypes for selection designed for improvement of these traits. These results are in close similarity with Haftamu (2018) and Worku (2018) for those traits.

### 3.2.3. Yield and yield related traits

Main shoot panicle length ranged from 26.4 to 51.3 cm with mean of 39.6 cm, main shoot panicle weight (1.58–3.97 g) with mean of 2.33 g, main shoot panicle grain yield (1.32–2.7 g) with mean of 1.81 g, grain yield (1596.7–2862.5 kg ha$^{-1}$) with mean of 2212 kg ha$^{-1}$ and harvest index (20.5–33.9%) with mean of 27.75% showed wide ranges of variations. From this result, 48.98%, 44.9%, 38.78%, 42.86% and 42.86% of the tested genotypes provided greater mean values than the grand mean for main shoot panicle length, main shoot panicle weight, main shoot panicle grain yield, grain yield and harvest index respectively.

More specifically, grain yield showed genotypic performances between the local check and the RILs, i.e. 1596.7 kg ha$^{-1}$ (local check) to 2862.5 kg ha$^{-1}$ RIL69 and harvest index provided a maximum mean value of 33.9% for DZ-01-96xHo-TF-1486 (RIL162). Therefore, those genotypes can be considered for improvement of these traits. Consequently, progress of this trait can be more effective when those genotypes are considered and used in the improvement program. This result is in line with Worku (2018) and Tsion et al. (2018).

| Trait | Min. Value | Genotype | Max. Value | Genotype | Mean | SEM (±) |
|-------|------------|----------|------------|----------|------|---------|
| DH    | 27.50      | RIL-58   | 60         | Local    | 36.96| 0.643   |
| DM    | 67.5       | Ebba     | 89.5       | Local    | 79.2 | 0.528   |
| GFP   | 24         | RIL-69   | 53.5       | RIL105   | 42.3 | 0.724   |
| PH (cm)| 58.6      | RIL-174  | 110.5      | RIL-69   | 82.5 | 1.305   |
| MSPL (cm)| 26.4     | RIL-127  | 51.3       | RIL32    | 39.6 | 0.689   |
| PDL (cm)| 14.4     | RIL-26   | 24.45      | RIL-90   | 17.97| 0.345   |
| TNL   | 81         | RIL-105  | 143        | RIL-90   | 111.58| 1.530 |
| FNTN  | 37.5       | RIL-170  | 106        | RIL52    | 69.8 | 1.623   |
| NPBMS  | 18.9      | RIL-174  | 31.2       | RIL32    | 25.43 | 0.368 |
| MSPNW (g)| 1.58    | Ho-TF-1486 | 3.97    | RIL55    | 2.33  | 0.064   |
| MSPGY (g)| 1.32    | RIL-163  | 2.7        | RIL108  | 1.81  | 0.044   |
| LI (%)| 31.2       | Negus    | 62.7       | RIL123   | 45.1 | 0.842   |
| GY (kg ha$^{-1}$)| 1596.7 | Local    | 2862.5     | RIL69    | 2212 | 30.825  |
| AGBY (kg ha$^{-1}$)| 7005 | Local    | 10,212.5   | RIL280   | 8189.6| 75.947 |
| HI (%)| 20.5       | RIL280   | 33.9       | RIL162   | 27.75 | 0.360   |
| TSW (mg)| 0.296   | RIL-285  | 0.58       | RIL-313  | 0.404 | 0.0084  |

**DH** = days to heading, **DM** = days to physiological maturity, **GFP** = grain-filling period, **PH** = Plant height, **MSPL** = main shoot panicle length, **PDL** = peduncle length, **TLN** = total tiller number, **FTN** = fertile tiller number, **NPBMS** = number of primary branches per main shoot panicle, **MSPNW** = main shoot panicle weight, **MSPGY** = main shoot panicle grain yield, **LI** = lodging index, **GY** = grain yield, **AGBY** = above ground biomass yield, **HI** = harvest index and **SEM** = standard error of mean.
3.3. Estimates of variance components

3.3.1. Phenotypic and genotypic coefficients of variation

The estimates of phenotypic ($\sigma^2_p$) and genotypic ($\sigma^2_g$) variances, phenotypic and genotypic coefficients of variation (PCV and GCV), broad sense heritability ($H^2$), genetic advance (GA) and genetic advance as percent of the mean (GAM) are shown in Table 4.

The phenotypic coefficient of variation (PCV) ranged from 6.55% for days to physiological maturity to 25.03% for main shoot panicle weight. While genotypic coefficient of variation (GCV) ranged from 5.79% for days to physiological maturity to 18.71% for main shoot panicle weight (Table 4). This range value is in agreement with Chekole et al. (2016). Woreda and Tefera (2020), in a study with tef interspecific RILs, also reported similar results for these traits. Likewise, Wondwosen and Abebe (2018) reported lower PCV and GCV values for days to physiological maturity in their study.

According to the category made by Sivasubramanian and Menon (1973) and Deshmukh et al. (1986), high PCV values were recorded for main shoot panicle weight (25.03%), main shoot panicle grain yield (24.08%) and fertile tiller number (22.69%). Furthermore, days to heading (16.56%), grain-filling period (16.16%), plant height (14.24%), main shoot panicle length (15.63%), peduncle length (17.74%), number of primary panicle branches per main shoot (13.45%), tiller number (13.52%), lodging index (17.68%), grain yield (13.49%) and harvest index (12.50%) had moderate PCV values, while days to heading (15.27%), grain-filling period (14.47%), main shoot panicle length (11.43%), total tiller number (11.68%), fertile-tiller number (18.03%), main shoot panicle weight (18.71%), main shoot panicle grain yield (18.24%), grain yield (11.66%) and harvest index (10.31%) had moderate GCV values. These results indicated presence of sizable genetic variability among the studied genotypes and the possibility of improving these traits through selection. Similarly, Habtamu et al. (2011) reported a medium GCV value for harvest index and medium PCV and GCV values for grain yield, lower PCV and GCV values for days to physiological maturity.

Lower GCV values were recorded for days to physiological maturity (5.79%), plant height (9.24%), above ground biomass yield (8.156%), peduncle length (9.05%), number of primary branches per main shoot panicle (7.86%) and lodging index (9.52%). This implies limited chance of improving the traits by directly selecting high performing genotypes due to a relatively lower variability. This was in line with the studies reported by Sintayehu and Getachew (2011) and Abel et al. (2012).

Magnitude of the difference between PCV and GCV in the present study was lower for days to heading, days to physiological maturity, grain-filling period, total tiller number and biomass yield. This is an indication of reduced environmental effects and genetic expression of these traits enables phenotypic based selection for better genetic improvement. Similar result was reported by Worku (2018). On the other hand, higher magnitude of differences of PCV and GCV was recorded for main shoot panicle weight, peduncle length and lodging index (Table 4). This is due to the influence of environmental effect on trait expression, since phenotypic variance contains environmental variance in addition to genotypic variance.

3.3.2. Broad sense heritability

The broad sense heritability ($H^2$) estimates for the studied traits ranged from 27.26% for peduncle length to 85.66% for days to heading. A very higher estimates of heritability values were detected for days to heading (85.66%), grain-filling period (80.28%) and total tiller number (80.13%) while; days to physiological maturity (78.25%), panicle length (61.33), fertile tiller number (64.22%), grain yield (74.77%) and above ground biomass yield (78.14%) provided a moderately higher value of breed sense heritability (Table 4); it shows that these traits provided heritable variation and can easily be selected based on phenotype and resulting in quick progress. Similar result was reported by Abel et al. (2012) for these traits. Haftamu (2018) and Habte et al. (Habte, et al., 2015a) also...
Table 4. Variance components, broad sense heritability ($H_b^2$), genetic advance (GA) and genetic advance as percent of mean (GAM) for 15 traits of 49 tef genotypes

| Traits        | $\sigma^2_g$ | $\sigma^2_p$ | GCV (%) | PCV (%) | $H_b^2$ (%) | GA  | GAM (%) |
|---------------|--------------|--------------|---------|---------|-------------|-----|---------|
| DH           | 31.96        | 37.31        | 15.29   | 16.53   | 85.66       | 10.78 | 29.16   |
| DM           | 21.085       | 26.945       | 5.79    | 6.55    | 78.25       | 8.37  | 10.56   |
| GFP          | 37.45        | 46.65        | 14.47   | 16.15   | 80.28       | 11.30 | 26.72   |
| PH (cm)      | 58.105       | 138.015      | 9.24    | 14.24   | 42.10       | 10.19 | 12.35   |
| PL (cm)      | 25.01        | 40.78        | 12.64   | 16.14   | 61.33       | 8.07  | 20.39   |
| PDL (cm)     | 2.74         | 10.05        | 9.22    | 17.65   | 27.26       | 1.78  | 9.91    |
| TLN          | 173.325      | 216.305      | 11.79   | 13.18   | 80.13       | 24.28 | 21.76   |
| FTN          | 160.025      | 249.165      | 18.13   | 22.62   | 64.22       | 20.88 | 29.92   |
| NPBMSF       | 4.085        | 11.555       | 7.95    | 13.37   | 35.35       | 2.48  | 9.73    |
| MSPNW (g)    | 0.19         | 0.34         | 18.71   | 25.03   | 55.88       | 0.67  | 28.81   |
| MSPGY (g)    | 0.11         | 0.19         | 18.24   | 24.08   | 57.37       | 0.52  | 28.46   |
| LI (%)       | 20.22        | 61.78        | 9.97    | 17.43   | 32.73       | 5.30  | 11.75   |
| GY (kg ha$^{-1}$) | 66,531.4  | 88,978.35   | 11.66   | 13.49   | 74.77       | 459.46 | 20.77   |
| AGBY (kg ha$^{-1}$) | 446,144.5    | 570,991.5   | 8.2     | 9.23    | 78.14       | 1216.26 | 14.85   |
| HI (%)       | 7.8          | 11.48        | 10.31   | 12.50   | 67.96       | 4.74  | 17.50   |

$DH =$ days to heading, $DM =$ days to physiological maturity, $GFP =$ grain filling period, $PH =$ Plant height, $MSPNW =$ main shoot panicle length, $PDL =$ peduncle length, $TLN =$ total tiller number, $FTN =$ fertile tiller number, $NPBMSF =$ number of primary branches per main shoot panicle, $MSPGY =$ main shoot panicle grain yield, $LI =$ lodging index, $GY =$ grain yield, $AGBY =$ above ground biomass yield, $HI =$ harvest index.

obtained higher broad sense heritability, which is in agreement with this study. Ayalneh et al. (2011) obtained higher broad sense heritability for grain-filling period. The result is in agreement with the one reported by Woreda and Tefera (2020) who document higher estimates of heritability for days to heading and panicle length in interspecific RILs of tef.

On the other hand, medium heritability estimates were noted for plant height (42.1%), number of primary branches per main shoot panicle (35.35%), main shoot panicle weight (55.88%), main shoot panicle grain yield (57.37%) and lodging index (32.73%). These medium broad sense heritability values suggested the possibility of advancing the tested tef genotypes through selection. Medium broad sense heritability values of RILs were reported by Worku (2018) and Demeket al. (2013) for those traits.

Low heritability values were recorded for peduncle length (27.26%) (Table 4). Such low values indicated the limited and impractical scope for improvement of this trait through direct selection due to higher masking effect by the environment. Worku (2018) showed lower broad sense heritability value for peduncle length which agrees with the present finding.
3.3.3. Genetic advance as percent of mean

Traits like days to heading (29.16%), grain-filling period (26.72%), main-shoot panicle length (20.39%), total tiller number (21.76%), fertile tiller number (29.92%), main-shoot panicle weight (28.81%), main-shoot panicle grain yield (28.46%) and grain yield (20.77%) provided higher value of genetic advance as percent of the mean. This implies that improvement of traits in genotypic values for the new population compared with the base population increases. This is in line with the work of Sintayehu and Getachew (2011) for grain yield; and Habte et al. (Habte, et al., 2015a) for days to heading, grain-filling period, panicle length and grain yield. Likewise, Tsion et al. (2018) found a higher GAM for tiller number, fertile-tiller number and main-shoot panicle weight. The finding also agrees with that of Worede and Tefera (2020) who reported higher estimate for kernel weight per main-shoot panicle.

Moderate genetic advance as percent of the mean was computed for days to physiological maturity (10.56%), plant height (12.35%), lodging index (11.75%), above ground biomass yield (14.85%) and harvest index (17.5%) (Table 4). Closely related results stating moderate GAM for plant height (13.8%) and biomass yield (19.67%) were found by Tsion et al. (2018) and by Habte et al. (Habte, et al., 2015a) for lodging index (19.67%).

The GAM values were lower (<10%) for peduncle length (9.91%) and number of primary branches per main shoot panicle (9.73%) as shown in Table 4. This implies that improvement of characters in genotypic values for the new population compared with the base population under one cycle of selection is less than 10% at 5% selection intensity. This have close agreement with Worku (2018) who found a lower genetic advance as percent of the mean for peduncle length, number of primary branches per main shoot panicle.

A wider range of genetic advance under selecting the top 5% of the genotypes provided a GAM value of 6.16–29.92%, which is higher than Hailu et al. (2003) with range of 1–15.8%. Therefore, this wider range helps in improvement of the genotypes as compared to the base population with a single cycle of selection at a given selection intensity (Singh, 2002).

In this study, high broad sense heritability coupled with high GAM was observed for days to heading and grain-filling period. These are implications for contribution of additive genes for trait expression and trait improvement through effective direct selection as stated by Johnson et al. (1955). Moreover, relatively high to moderate phenotypic and genotypic coefficients of variation along with high to moderate broad sense heritability and high genetic advance estimates were obtained for days to heading, fertile tiller number, main shoot panicle weight and main shoot panicle grain yield. Therefore, phenotypic based selection and improvement is possible for these traits. This is because there would be a close correspondence between the genotype and the phenotype due to the relative small contribution of the environment to the phenotype (Singh, 2002).

4. Conclusion and recommendations

This study indicated the presence of significant variation among the tested tef genotypes for most of the studied traits showing the presence of adequate genetic variability. Most of the lines had early maturity than the early maturing variety Boset. Moreover 53% and 24.5% of the genotypes have provided higher grain yield than the high yielder checks and these can be suggested for further evaluation and to be used as parental lines for the future tef breeding programs. High to moderate PCV and GCV values recorded for the studied traits indicated the possibility of selection for further improvement of these traits. Higher to moderate estimates of broad sense heritability and genetic advance as percent of the mean values detected for the studied traits implied possibility of phenotypic based selection improvement.

Therefore, focus will be given on the improvement of tef by selecting traits that directly increases grain yield and yield components. RILs that performed better in yield and yield related traits from
both crosses will be further evaluated for these and more traits. To have more representative information, further study should be carried out by including more seasons and locations with emphasis on marginal and stressed areas as that of West Belesa district.

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