# Correlation and Path Coefficient Analysis of Selected Semi-Dwarf Tef Recombinant Inbred Lines for Yield and Yield Component Traits

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*Abstract:* **A total of fourty nine recombinant inbred lines were evaluated for 16 traits using simple lattice design at Holeta and Debre Zeit in 2017 cropping season. All the traits measured over the locations showed highly significant differences among the lines except fertile tiller per plant, while the lines x locations interaction effect was highly significant for most of the traits measured. Both the genotypic and phenotypic correlation coefficients showed positive association of grain yield with most traits. Lodging index showed negative phenotypic correlation with most lodging related traits and positive with grain yield as well as phenological traits. Path coefficient analysis revealed that above ground biomass exerted the highest positive genotypic and phenotypic direct effect on grain yield. This study revealed that four recombinant inbred lines had higher yield than local and standard checks. RIL# 14 showed the highest grain yield and low lodging index, longer panicle, higher number of spikelets per panicle, as well as the highest above ground biomass than all recombinant inbred lines, which could be the base for future tef breeding program.**

*Keywords:* **Direct effect, Genetic association, Indirect effect, Phenotypic association, Tef, Traits.**

## 1. INTRODUCTION

Tef [*Eragrostis tef* (Zucc.) Trotter] is the main cereal crop widely produced and consumed in Ethiopia and favored by millions of local smallholder farmers (Seyfu, 1997). In terms of area of cultivation, it is the leading cereal crop followed by maize and wheat. According to the Central Statistical Agency (CSA, 2018), the area covered by tef during the 2017/2018 cropping season was over 3.02 million hectares or 30% of the total area occupied by cereals in the country. Despite being a staple food for many people in Ethiopia for centuries, tef has gained prominence as a food crop in other parts of the world very recently. This interest is mainly associated with its gluten-free grains and its nutritive value that is generally comparable with other common cereals (Hailu *et al.,* 2001; Spaenij-Dekking *et al.,* 2005; USDA, 2015; Cheng, 2017*)*. However, it is also grown as a pasture crop in several countries (Kebebew *et al*., 2011*).* The straw from tef is a valuable source of livestock feed because it is more palatable and nutritious than that from wheat and barley (Alemu, 2013).

Tef is a highly versatile crop with respect to adaptation to different agro-ecologies being widely grown from sea level up to 2800 m.a.s.l. with reasonable resilience to both drought and water logging (Kebebew *et al*., 2010). The national average yield of tef is about 1.75 ton per hectare (CSA, 2018), but it has a potential of yielding four to five tons of grain per hectare if the lodging problem is resolved (Yifru and Hailu, 2005). The major yield limiting factors are lack of cultivars that

are tolerant to lodging and shortage of improved varieties (Kebebew *et al.,* 2015). Besides, the grains are also often lost in the harvesting and threshing process because of their minute size and traditional cultural practices (Tadesse, 1975). Tef possesses tall, weak stems that easily succumb to lodging due to wind or rain. In addition, lodging hinders the use of high input husbandry practices since the application of increased amounts of nitrogen fertilizer to boost the yield results in severe lodging (Kebebew *et al*., 2015).

So far, no cultivar with reasonable lodging resistance has been obtained to-date except a novel tef mutant named *kegne*, and GA-10-3 which have a semi-dwarf phenotype developed from an ethyl methane sulphonate-mutagenized population (Jöst *et al*., 2015*)*, resulting in increased lodging tolerance (Jöst *et al*., 2015). Some important works have also reported based on morphological, molecular and biochemical markers. Efforts made so far have enabled the development and release of over 49 improved varieties to the farming communities in Ethiopia (MoA,2019). However, development of high yielding and lodging tolerant tef varieties, adapting to the changing climate remains to be the primary focus of tef research (Solomon, 2009; Solomon *et al.*, 2013). Especially, semi-dwarf tef types did not studied much yet on measuring correlations among traits and path analysis of agronomic traits affecting grain yield using recombinant inbred lines and there is no lodging resistant tef (Habte *et al*., 2017). Therefore, the objective of the current study was to estimate correlations and path coefficients among selected semi-dwarf tef recombinant inbred lines with emphasis on lodging tolerance, yield and yield components.

## 2. MATERIALS AND METHODS

### DESCRIPTIONS OF EXPERIMENTAL LOCATIONS

The field experiment was carried out at two locations (Debre Zeit and Holetta) in the central parts of Ethiopia during the 2017 cropping season (July to December). Debre Zeit is located at 47 km to south east of Addis Ababa, while Holetta is located at 42 km to the west of Addis Ababa. DZARC found at ($8^{o}$ 44' N, $38^{o}$ 58' E and 1860 m.a.s.l) whereas, HARC found at ($9^{o}$ 03' N, $38^{o}$ 30' E and 2400 m.a.s.l) latitude, longitude and altitude, respectively. The two locations represent two different agro-ecologies of the country. Debre Zeit receives mean annual rainfall of 832 mm during the main growing season with maximum and minimum mean annual temperature of 24.3 $^{o}$C and 8.9 $^{o}$C, respectively. The experimental field at Debre Zeit characterized by heavy black soil (Vertisol) with a pH of 6.9 and described as very fine montmorillonitic typic pellustert with very high moisture retention capacity (Tamirat, 1992; Habte *et al*., 2015).

In contrast, Holeta often receives annual total rainfall 1100 mm with maximum and minimum mean annual temperature of 24.1 $^{o}$C and 6.6 $^{o}$C, respectively. The experimental field at this location characterize by light red soil (Andosol) with a pH of 6.3 and good moisture holding capacity. The weather conditions during the growing season were favorable and the experiment received sufficient amount of rainfall for normal growth of tef crop at each of the test locations.

### 2.1. PLANTING MATERIALS

These experimental plant materials comprised 49 semi-dwarf tef recombinant inbred lines including local and standard checks. These included 45 recombinant inbred lines (RIL) derived from the crosses of DZ-01-192 x GA-10-3, the two parents (pure lines), one standard and one local check (TABLE I). The RILs are descendants of the intra-specific cross through continuous maintenance of progenies up to the seventh filial generation (F7) through selfing using F2-derived single-seed-decent breeding method. The tef cultivar DZ-01-192 is late maturing, thick culmed, tall, has loose panicle and white seed color. GA-10-3 is a mutant line developed through mutation breeding by using Ethyl methane sulphonate (EMS) assisted by Targeted Induced Local Lesions IN Genomes (TILLING) method and introduced from university of Bern (Switzerland). It has lodging tolerance characters, early maturity, semi-dwarf structure and pale white seed color. The experimental materials obtained from Debre Zeit agricultural research center.

**TABLE I: List of experimental plant materials**

| No. | Recombinant Inbred Lines SD-Tef | No. | Recombinant Inbred Lines SD-Tef |
|---|---|---|---|
| 1 | DZ-01-192 x GA-10-3 (RIL # 1) | 26 | DZ-01-192 x GA-10-3 (RIL # 58) |
| 2 | DZ-01-192 x GA-10-3 (RIL # 2) | 27 | DZ-01-192 x GA-10-3 (RIL # 68) |
| 3 | DZ-01-192 x GA-10-3 (RIL # 4) | 28 | DZ-01-192 x GA-10-3 (RIL # 75) |
| 4 | DZ-01-192 x GA-10-3 (RIL # 5) | 29 | DZ-01-192 x GA-10-3 (RIL # 160) |
| 5 | DZ-01-192 x GA-10-3 (RIL # 6) | 30 | DZ-01-192 x GA-10-3 (RIL # 161) |
| 6 | DZ-01-192 x GA-10-3 (RIL # 8) | 31 | DZ-01-192 x GA-10-3 (RIL # 162) |
| 7 | DZ-01-192 x GA-10-3 (RIL # 12) | 32 | DZ-01-192 x GA-10-3 (RIL # 166) |
| 8 | DZ-01-192 x GA-10-3 (RIL # 14) | 33 | DZ-01-192 x GA-10-3 (RIL # 169) |
| 9 | DZ-01-192 x GA-10-3 (RIL # 15) | 34 | DZ-01-192 x GA-10-3 (RIL # 171) |
| 10 | DZ-01-192 x GA-10-3 (RIL # 16) | 35 | DZ-01-192 x GA-10-3 (RIL # 172) |
| 11 | DZ-01-192 x GA-10-3 (RIL # 19) | 36 | DZ-01-192 x GA-10-3 (RIL # 174) |
| 12 | DZ-01-192 x GA-10-3 (RIL # 20) | 37 | DZ-01-192 x GA-10-3 (RIL # 175) |
| 13 | DZ-01-192 x GA-10-3 (RIL # 21) | 38 | DZ-01-192 x GA-10-3 (RIL # 178) |
| 14 | DZ-01-192 x GA-10-3 (RIL # 22) | 39 | DZ-01-192 x GA-10-3 (RIL # 179) |
| 15 | DZ-01-192 x GA-10-3 (RIL # 24) | 40 | DZ-01-192 x GA-10-3 (RIL # 180) |
| 16 | DZ-01-192 x GA-10-3 (RIL # 25) | 41 | DZ-01-192 x GA-10-3 (RIL # 182) |
| 17 | DZ-01-192 x GA-10-3 (RIL # 27) | 42 | DZ-01-192 x GA-10-3 (RIL # 185) |
| 18 | DZ-01-192 x GA-10-3 (RIL # 28) | 43 | DZ-01-192 x GA-10-3 (RIL # 195) |
| 19 | DZ-01-192 x GA-10-3 (RIL # 33) | 44 | DZ-01-192 x GA-10-3 (RIL # 203) |
| 20 | DZ-01-192 x GA-10-3 (RIL # 41) | 45 | DZ-01-192 x GA-10-3 (RIL # 262) |
| 21 | DZ-01-192 x GA-10-3 (RIL # 44) | 46 | Boset (standard check) |
| 22 | DZ-01-192 x GA-10-3 (RIL # 45) | 47 | DZ-01-192 (parental check) |
| 23 | DZ-01-192 x GA-10-3 (RIL # 48) | 48 | GA-10-3 (parental check) |
| 24 | DZ-01-192 x GA-10-3 (RIL # 52) | 49 | Local Check |
| 25 | DZ-01-192 x GA-10-3 (RIL # 57) | | |

Where; SD: - Semi-dwarf tef; DZ-01: -Debre Zeit tef cultivar released through selection; GA-10-3: - -Mutant elite tef line.

## 2.2. EXPERIMENTAL DESIGN, LAYOUT AND MANAGEMENT

The field experiments conducted using 7x7 simple lattice designs with two replications at both locations. Each plot (1 m x 1 m) consisted of five rows of 1 m length with an inter-row spacing of 0.2 m. The distances are 1 m, both between plots and incomplete blocks and 1.5 m between replications. The tef recombinant inbred lines allotted to plots at random within each replication. Sowing were done on 13 August, 25 July 2017 at Debre Zeit and Holetta, respectively. As per the research recommendations, 15 kg/ha seed rate was used for both locations.

The fertilizer rate used for each location recommended depending on the type of soil. The fertilizers used for Holetta (light red soil) were 40kg N, 60kg $P_2O_5$, and 11kg S per hectare, as well as 60kg N, 60kg $P_2O_5$ and 11 kg S per hectare for Debre Zeit (Vertisol). All NPS were applied at planting with a rate of 158 kg/ha and the remaining urea applied at the rate of 22 kg/ha for HARC and 65 kg /ha for DZARC. Half of the urea applied at sowing, while the remaining half applied at tillering. Hand weeding and other management practices were performed as required for both locations.

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### 2.3. DATA COLLECTED

Data collected from sixteen quantitative traits including seven traits taken on plot basis and nine traits assessed on randomly taken five plants of tef from the central rows of each plot. For individual plant trait sampled, averages of data from the five random samples of plants per plot used for statistical analyses.

**The following data have been taken from plot basis:**

**Days to heading/ panicle emergence** (DH): Number of days from seedling emergence to the appearance of the tips (about 5 cm) of the main shoot panicle on 50% of the plants in a plot. Note that tef panicle appears without showing the booting stage, which is unlike the other small cereals like wheat and barley, but similar to that in rice.

**Days to maturity** (DM): Number of days from seedling emergence to physiological maturity as judged by the change to straw color of the vegetative parts on 75% of the plants in the plot.

**Grain filling period** (GFP): This computed as the difference between the days to panicle emergence and that to maturity.

**Above ground biomass yield** (ABM): The total dry weight in kilogram of the above ground biomass per plot before threshing

**Grain yield** (GY): The entire plot of grains weight in kilogram after threshing and sun drying.

**Harvest index** (HI): The ratio of grain yield to the total biomass in percent.

**Lodging index** (LI): lodging assessment was performed as suggested by Caldicott and Nuttall (1979) as follows:

$$LI = \frac{\textbf{Sum (lodging scores} * \textbf{ percentage of area lodged)}}{\textbf{5}}$$

Lodging score was recorded on a 0-5 scale as the degree of leaning from the upright position and whereby zero=completely upright non-lodged plants and five=completely flat on the ground. The severity of lodging for each degree assessed as the proportion in percent of plants in a plot manifesting each degree of lodging. Finally, the lodging index for each plot was computed as the average of the product sum of each degree of lodging and the corresponding severity as indicated in the formula above.

The following observations have been recorded based on measurements made on five randomly taken and pre-tagged plants from the three central rows of each plots.

**Plant height** (PH): - The length of the plant in centimeter from ground level to the tip of the panicle.

**Panicle length** (PL): - The length in centimeter from the node where the first panicle branch starts to the tip of the panicle.

**Culm length** (CL): - The length in centimeter from ground level to the node where the first panicle branch starts.

**Peduncle length** (PDL): - The length in centimeter of the top most culm internode spanning from the last culm node until the start of the first panicle branch. It stretches from the node where the flag leaf starts to where the first panicle branch starts.

**Second basal culm internode length** (SCIL): - The length in centimeter of the second basal culm internode.

**Second basal culm diameter** (SCID): The diameter in millimeter of the second basal culm internode measured using caliper.

**Fertile tiller number per plant** (NFT): - Counts of the panicle-bearing tillers of pre tagged main plants that have produced a fertile panicle.

**Numbers of branches per main shoot panicle** (NBP): - Counts of the total number of branches per main panicle from bottom to top.

**Number of spikelets per panicle** (NSP): - It is the number of spikelets counted on the panicle.

## 2.4. STATISTICAL ANALYSES

Tests of homogeneity and normality of error variances were done mainly using relationships of predicted means and residuals for all traits. ANOVA were done for single location as well as for the combined over locations. For combined analysis of variance over locations, the homogeneity of error variance was tested using F-max test method of Hartley (1950), which requires independent random samples of the same size from normally distributed populations (Ott & Longnecker, 2015). It is based on the ratio of the larger mean square of error (MSE) from the separate analysis of variance to the smaller mean square of error given by the following formula:

$$Fmax = \frac{\text{Largest MSE}}{\text{Smallest MSE}}$$

If the calculated value of Fmax was less than three, it means that the ratio of the highest error mean square is not three-fold larger than the smallest error mean square, and this indicates that the variance was considered homogenous thereby making it to possible to proceed with the combined analysis of variance (Gomez and Gomez, 1984).

Estimates of coefficients of phenotypic and genotypic variances, heritability and genetic advance done from mean square value and grand mean for each trait. For multivariate analysis such as cluster, distance and principal component analysis mean records on all traits are pre-standardized to mean zero and variance unity to avoid bias due to the differences in measurement scales (Manly, 1986).

### 2.4.1. Analysis of Variance

All measured traits using simple lattice design were subjected to analysis of variance (ANOVA) of SAS software version 9.3 (SAS institute, 2011). Total variability present among the recombinant inbred lines for each of the traits were partitioned into known (treatment) and unknown (residual) effects following the standard procedures of ANOVA using the following model according to Gomez and Gomez (1984) indicated. After two error terms (Mean square error of block ($E_b$) and Mean square of Experimental error ($E_e$)) calculated from combined ANOVA analysis (TABLE II).

Comparing $E_b$ with $E_e$; If $E_b > E_e$ an adjustment of the treatments was carried out, otherwise if $E_b < E_e$ no need of an adjustment of the treatments and the block effect is negligible then the data can be analyzed by RCBD, using replication as block. The SAS program for analyzing lattice design consists of two parts. In the first, PROC GLM was used to calculate unadjusted block SS (TYPE I SS–Sequential SS), adjusted block SS (TYPE III SS), unadjusted treatment SS, and intra-block error. To calculate the unadjusted block SS from TYPE I SS, the order in which variables were entered into the model statement is important. The block was entered before the treatment in the model statement. These estimates were used in the second part of the program to calculate the adjusted treatment SS, adjusted means, and the average effective error, respectively (Gomez and Gomez ,1984).

The comparison of mean performance of genotypes was done following the significance of mean squares using Duncan's Multiple Range Test (DMRT). Genotypic, environmental and phenotypic variances were estimated according to Falconer (1981) as follows:

Genotypic variance for single location $\sigma^2 g = \frac{\text{MSg} - \text{MSe}}{r}$ ;

Interaction variance $\sigma^2 I = \frac{\text{MSI} - \text{Mse}}{r}$

Over locations genotypic variance $\sigma^2 g = \frac{\text{MSg} - \text{MSI}}{rl}$ ;

Environmental variance $\sigma^2 e = \frac{\text{Mse}}{r}$

Phenotypic variance $\sigma^2 p = \sigma^2 g + \sigma^2 e$ Where, $\sigma^2 g$ - Genotypic variance; MSg - Mean square of genotype; MSe - Mean square of error; $\sigma^2 I$ - Interaction variance; MSI – Mean square of interaction variance; $\sigma^2 p$ – phenotypic variance; $\sigma^2 e$ – Error variance; r - Number of replication and l - Number of locations.

### Model of the experiment:

For combined analysis of variance over locations, the total variations among the inbred lines measured using the following model:

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$$P_{ijkz} = \mu + G_i + B_{k(j)(z)} + R_{j(z)} + L_z + (GL)_{iz} + E_{ijkz}$$

Where, $P_{ijkz}$ = phenotypic value of $i^{th}$ genotype under $j^{th}$ replication at $z^{th}$ location and $k^{th}$ incomplete block within replication j and location z; $\mu$ = grand mean; Gi = the effect of ith genotype; Bk(j)(z) = the effect of incomplete block k within replication j and location z; $R_{j(z)}$ = the effect of replication j within location z; $L_z$ = the effect of location z; (GL)$_{iz}$ = the interaction effects between genotype and location; and Eijkz = the residual or effect of random error.

Comparing $E_b$ with $E_e$: - If $E_b \leq E_e$, Adjustment of treatment means will have no effect and analyze as if it were an RCBD using replications as blocks If $E_b > E_e$ then compute an adjustment factor A.

$A = (E_b − E_e)/(b(r − 1)Eb)$, used to compute adjusted treatment means

Relative Efficiency: - Estimate the error mean square of an RCBD

$E_{RCBD} = (SSB+SSE)/((g–1)(r–1))$, Then the relative efficiency of the lattice is RE = $E_{RCBD}/E_e$

From the analysis of variances of data from each locations efficiency of simple lattice design over RCBD was calculated depending on the above formula and simple lattice have 26.2% efficient than randomized complete block design (RCBD).

### 2.4.2. Estimation of correlation

Phenotypic and genotypic correlation coefficients were computed from the components of variance and covariance based on the method described by Singh and Chaudhary (1996), using the CANDISC procedure of SAS software (SAS, 2011).

### 2.4.3. Path coefficient analysis

Path coefficient analysis was carried out using the phenotypic correlation coefficients as well as genotypic correlation coefficients. This analysis computed as suggested by Dewey and Lu (1959) with the following formula.

$$rij \;=\; Pij \;+\; \sum rik\, Pkj$$

Where, $r_{ij}$ is the mutual association between independent trait (i) and dependent variable (j), Pij is component of direct effect of the independent (i) on the dependent (j) and ∑rikPkj is sum of components of indirect effect of a given independent trait (i) on the dependent variable (j) *via* all other independent traits (k).

The residual effect (U) calculated using the formula suggested by Dewey and Lu (1959). $U \;=\; \sqrt{1 − R^2}$ Where; $R^2 =$ ∑rikPkj, U = the residual; unexplained variation of the dependent variable.

## 3.  RESULTS AND DISCUSSIONS

### 3.1 ANALYSIS OF VARIENCE

The combined analysis of variance over the two locations of the 49 semi-dwarf tef recombinant inbred lines showed highly significant (p<0.01) genotype effects for all 16 traits, except for number of fertile tillers per plant (TABLE II).

**TABLE II: Analysis of variance for 16 traits of 49 semi-dwarf tef recombinant inbred lines over the two locations**

| Traits | Locations(L) (df=1) | Replications(r) (df=1) | Intra Block(b)(df=12) | Inbred lines(I)(df=48) | I x L (df=48) | Error(e) (df=85) | CV (%) | R² |
|---|---|---|---|---|---|---|---|---|
| | 8294.01** | 1.47ns | 9.22* | 42.09** | 11.83** | 4.69 | 4.00 | 96.57 |
| DM | 36235.84** | 780.01** | 59.95** | 54.80** | 38.75** | 19.96 | 4.20 | 96.20 |
| GFP | 9857.65** | 713.65** | 63.37** | 56.21** | 39.14** | 20.07 | 8.59 | 90.71 |
| PH | 8320.05** | 51.22ns | 63.36** | 267.03** | 50.21** | 26.64 | 5.36 | 91.95 |
| PL | 2996.78** | 38.80** | 7.44ns | 44.67** | 8.92* | 6.04 | 6.83 | 91.96 |
| CL | 1330.17** | 0.86ns | 44.40ns | 134.06** | 46.59** | 26.93 | 8.61 | 83.40 |
| PDL | 17.34* | 32.15** | 5.79ns | 13.12** | 5.79ns | 4.25 | 8.92 | 76.48 |
| SCIL | 631.52** | 1.57ns | 4.49** | 3.99** | 2.18ns | 1.77 | 12.79 | 86.85 |
| SCID | 0.17** | 0.04ns | 0.04* | 0.06** | 0.02ns | 0.02 | 8.31 | 68.44 |
| NFT | 231.04** | 2.21ns | 1.24ns | 0.77ns | 0.69ns | 0.87 | 21.33 | 81.09 |
| NBP | 1.90 ns | 11.22 ns | 11.90* | 10.60** | 10.50** | 5.51 | 9.10 | 72.36 |
| NSP | 19872.94** | 6372.6 ns | 4382.45 ns | 13649.28** | 12226.54** | 2501.54 | 11.28 | 86.54 |
| ABM | 197799029** | 3082888.8** | 1531599.9** | 6604503.8** | 3131395.8** | 491640.4 | 10.41 | 94.79 |
| GY | 182640.23* | 435881.02** | 159891.98** | 358714.8** | 322262.61** | 49196.92 | 14.17 | 91.21 |
| HI | 3330.69** | 22.65 ns | 6.88 ns | 26.19** | 34.37** | 9.44 | 12.82 | 85.95 |
| LI | 1098.45** | 19.61 ns | 42.03 ns | 130.43** | 94.53** | 23.88 | 7.96 | 87.05 |

Where; *, ** Significant at p ≤ 0.05 and p ≤ 0.01 respectively, while ns- non-significant, DH= days to heading, DM = days to maturity, GFP= grain filling period, PH= plant height, PL= panicle length, CL= culm length, PDL= peduncle length , SCIL=second culm internode length , SCID= second basal culm internode diameter, NFT= no. of fertile tillers per plant, NBP= no. of branches per panicle, NSP= no. of spikelets per panicle, ABM = above ground biomass yield(kg/ha), GY= grain yield(Kg/ha), HI= harvest index, LI=lodging index, df=degree of freedom and CV=coefficient of variation (%).

## 3.2 ASSOCIATION OF TRAITS

The phenotypic and genotypic correlations of the different traits combined over the locations were presented Table III.

**TABLE III: Genotypic (below) and phenotypic (above) diagonal correlation coefficients**

| Traits | DH | DM | GFP | PH | PL | CL | PDL | SCIL | SCID | NBP | NSP | ABM | GY | HI | LI |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DH | 1 | 0.83** | 0.50** | -0.38** | -0.46** | -0.23** | -0.03 | -0.60** | 0.03 | 0.07 | -0.03 ns | -0.33** | 0.08 | 0.48** | 0.16 * |
| DM | 0.40** | 1 | 0.90** | -0.36** | -0.52** | -0.17* | 0.07 | -0.62** | -0.07 | -0.01 ns | -0.09 ns | -0.29** | 0.23** | 0.62** | 0.25** |
| GFP | -0.41** | 0.67** | 1 | -0.27** | -0.44** | -0.08 | 0.13 | -0.49** | -0.12 | -0.07 ns | -0.11 ns | -0.19** | 0.30** | 0.59** | 0.25** |
| PH | 0.33** | 0.53** | 0.26** | 1 | 0.77** | 0.90** | 0.23** | 0.68** | 0.35** | 0.12 | 0.11 | 0.63** | 0.26** | -0.47** | -0.18** |
| PL | 0.41** | 0.48** | 0.15* | 0.80** | 1 | 0.43** | 0.05 | 0.66** | 0.45** | 0.17** | 0.19** | 0.56** | 0.14* | -0.53** | -0.22** |
| CL | 0.23 | 0.47** | 0.28* | 0.94** | 0.56** | 1 | 0.29** | 0.53** | 0.19** | 0.06 | 0.02 | 0.52** | 0.27** | -0.31** | -0.10 |
| PDL | -0.27 | -0.03 | 0.19 | 0.44** | 0.16 | 0.53** | 1 | 0.09 | -0.03 | 0.19** | -0.09 ns | 0.03 | 0.10 | 0.08 | -0.02 |
| SCIL | 0.16 | 0.22 | 0.09 | 0.61** | 0.49** | 0.58** | 0.30* | 1 | 0.24** | 0.17** | 0.21** | 0.52** | 0.12 | -0.52** | -0.19** |
| SCID | 0.52** | 0.44** | 0.01 | 0.48** | 0.50** | 0.39** | 0.01 | 0.34** | 1 | 0.11 | 0.29** | 0.20** | 0.04 | -0.22** | -0.08 |
| NBP | 0.09 | -0.13 | -0.20 | 0.23 | 0.30* | 0.16 | 0.08 | 0.41** | 0.15 | 1 | 0.19** | -0.07 ns | -0.01 ns | 0.04 | 0.04 |
| NSP | 0.17 | 0.04 | -0.10 | 0.01 | 0.05 | -0.02 | -0.13 | 0.20 | 0.27 | 0.08 | 1 | 0.08 | 0.007 ns | -0.13 ns | 0.11 |
| ABM | 0.36** | 0.59** | 0.30* | 0.62** | 0.45** | 0.61** | 0.16 | 0.43** | 0.24 | -0.04 ns | 0.07 | 1 | 0.66** | -0.41** | -0.04 |
| GY | 0.26 | 0.57** | 0.36** | 0.47** | 0.40** | 0.43** | 0.10 | 0.43** | 0.19 | 0.01 | 0.07 | 0.87** | 1 | 0.39** | 0.20** |
| HI | -0.23 | -0.03 | 0.15 | -0.28* | -0.10 | -0.33** | -0.07 | 0.01 | -0.10 | 0.08 | -0.05 ns | -0.16 ns | 0.31* | 1 | 0.29** |
| LI | -0.27* | -0.13 | 0.09 | -0.17 | -0.14 | -0.16 | -0.06 | 0.09 | -0.13 | 0.05 | 0.23 | 0.13 | 0.23 | 0.30* | 1 |

Where, *, ** Significant at p ≤ 0.05, and p ≤ 0.01, respectively and non-signed replies non-significant among the traits, DH= days to heading, DM= days to maturity, GFP= grain filling period, PH= plant height, PL= panicle length, CL= culm length, PDL=peduncle length, SCIL= second culm internode length, SCID= second culm internode diameter, NBP= no of branches per panicle, NSP= no of spikelets per panicle, ABM= above ground biomass (kg/ha), GY=grain yield(kg/ha), HI=harvest index(%), LI=lodging index.

### 3.2.1 Grain yield association with other traits

At genotypic level, grain yield showed highly significant (p ≤ 0.01) positive correlation with above ground biomass (r=0.87), days to maturity (0.57), plant height (0.47), culm length (0.43), second culm internode length (0.43), panicle length (0.40) and grain filling period (0.36). It also showed significant (p ≤ 0.05) positive correlation with harvest index (0.31). These indicate that all the traits governed by additive gene action and these findings in line with (Habte et al., 2017). Similarly, Solomon (2009) reported positive genotypic correlation of grain yield with the majority of the traits tested, while no negative correlations where been recorded for grain yield with all traits tested. The positive correlation could be due to linkage or pleiotropic genetic effects causing the traits to change in the same direction (Falconer and Mackay, 1996).

However, lodging index and other traits such as days to heading, peduncle length, second culm internode diameter, number of branches per panicle and number of spikelets per panicle were haven't correlated with grain yield statically in this study. The breeding implications of positive significant association provide that improvement for one trait could improve the others because they governed by one gene.

At phenotypic level, grain yield (0.25) positively correlated with above ground biomass (0.66), harvest index (0.39), grain filling period (0.30) culm length (0.27), plant height (0.26), days to maturity (0.23), panicle length (0.14) and lodging index (0.20) corresponding to (Habte *et al.*,2017). The remained traits have no correlation with grain yield.

### 3.2.2 Lodging index association with other traits

Lodging index had positive phenotypic coefficient of correlation with days to heading, days to maturity, grain filling period, plant height, grain yield, and harvest index and negatively correlated with panicle length, and second culm internode length. However, it did not show significant correlation with the rest of the traits. The negatively correlated traits indicate

that the pleiotropic effects of one gene on the other. This improved by selecting other secondary traits to improve that trait indirectly. Phenotypic positive association of lodging index with phenological traits depicted in the current result revealed that the shorter time to heading, maturity and grain filling might help to reduce lodging of tef as well as the longer the time to give higher grain may causes higher lodging in line with the results of (Hailu *et al*.,2001; Habte *et al*.,2015 and Nigus *et al*., 2016).

Dagnachew and Girma (2014) also reported that there was a positive phenotypic association of harvest index with grain yield but a negative association with biomass yield in tef landraces collected from different zones of Ethiopia. The current study results contradict with the previous findings of Nigus *et al*. (2016), who reported that high harvest index have high grain yield and high grain yield in turn correlated negatively with high lodging index. However, the present result showed lodging correlated positively with harvest index as well as grain yield. This indicated that the high yielders are likely vulnerable to lodging and *vice versa*.

### 3.3 PHENOLOGICAL TRAITS ASSOCIATION WITH OTHER TRAITS

In the case of phenological traits association with others, days to heading showed significant positive genotypic association with days to maturity, plant height, panicle, second culm internode diameter and aboveground biomass. On the other hand, days to heading showed significant negative genotypic association with grain filling period and lodging index, while no significant with the rest traits including grain yield, similar to (Habte *et al*., 2017). Days to maturity also exhibited positive genotypic correlation with grain yield, days to heading, aboveground biomass, plant height, panicle length, culm length and second culm internode diameters, while not correlated with the remaining traits.

### 3.4 MORPHOLOGICAL TRAITS ASSOCIATION WITH OTHER TRAITS

Most of the morphological traits such as showed positive phenotypic associations with grain yield, above ground biomass but negative correlations with harvest and lodging index as well as phenological traits, while not correlated with some of the traits. This finding corresponding to previous study of (Habte *et al.*2017). At genotypic level plant height, panicle length, culm length, second basal culm internode length and diameter showed positive correlation coefficients with grain yield, above ground biomass and phenological traits, while not correlated with other traits such as harvest index and lodging index (Ayalneh *et al.,*2012*)*. Similar to present findings Fufa *et al.*(2000) reported positive correlation of shoot biomass with plant height, panicle length; while Solomon *et al*.(2010) also reported that above ground plant biomass was strongly correlated with grain yield, plant height and panicle length.

For traits with highly significant and negative association, the improvement of one trait would result in the reduction of another trait. Interestingly, this may enhance low above ground biomass and reduce lodging, which had reported as important traits of semi-dwarf varieties of small cereals such as tef, wheat, barley and rice (Wondewosen *et al*., 2012). Relatively tall tef varieties are desire by farmers because of tef is highly valued for its straw yield as a major source of animal feed (Yami, 2013). However, tall tef varieties have relatively thin stems and shallow root system that are sensitive to lodging (Van Delden *et al*., 2010). Late maturing and tall tef varieties possess deeper root systems than early maturing genotypes that have shorter plant heights (Ayele *et al*., 1999).

Therefore, breeding tef varieties with a good stem thickness and improved root depth could offer high adoption rate of tef varieties by farmers than breeding dwarf varieties to reduce lodging. However, tef genotypes with long days to maturity have tall plant height and longer panicle, consequently, more photosynthetic products is not used for the seed setting. As a result, development of considerably semi-dwarf tef varieties have been the goal of tef breeding to enhance grain yield and reduce effect of lodging without affecting multipurpose income of tef producers (Esfeld and Tadele, 2010; Kebebew *et al.*, 2011).

Generally, correlation may arise from different factors of gene action (additive or non-additive) and the other factors such as pleiotropy expresses the extent to which two traits are influenced by the same gene, but the correlation resulting from pleiotropy is the overall effect of all segregating genes that affect both traits some genes may increase both traits, while others increase one and reduce the other; the former tend to cause a positive correlation while, the later a negative correlation (Welsh, 2008)

**3.5 PATH COEFFICIENT ANALYSIS**

Path coefficient analysis measures the direct influence of one variable upon the other, and permits separation of correlation coefficients into components of direct and indirect effects. Path analysis allows identification of direct and indirect effects association and measure the relative importance of each trait. Combined over locations, the phenotypic and genotypic correlations were partitioned into direct and indirect effects using grain yield as a dependent variable as shown in TABLE IV and V, respectively for genotypic and phenotypic path coefficient correlations. Only those traits having significant correlations with grain yield were included in the path coefficient analyses at each of the genotypic and phenotypic level.

**3.5.1 Phenotypic path coefficient analysis**

At phenotypic level, aboveground biomass (0.965) had highest positive direct effect on grain yield followed by harvest index (0.777) and days to maturity (0.096) (TABLE IV). This showed that the strong correlations of above ground biomass yield and harvest index with grain yield were largely due to the additive gene effect of the traits. Therefore, direct selection of the high performing genotypes for these traits will improve the mean grain yield of the selected genotypes. Aboveground biomass as well as harvest index and days to maturity can be considered as good contributor to grain yield and suggesting important traits for selection in a breeding program for higher grain yield of tef. However, traits with negative indirect effect through above ground biomass yield need to be managed during selection because the selection of traits might have reducing effect on yield, this finding also agree with (Nigus *et al.*, 2016).

Similarly, Abel *et al.* (2012) as well as Dagnachew and Girma (2014) found highest direct effect on grain yield of harvest index and above ground biomass. Habtamu *et al.* (2011) findings also showed that biomass had the higher direct effect on grain yield. The residual factor for phenotypic level was 0.192 thus indicating that the traits included in the analysis explained 80.8% of the total variation in the grain yield per hectare whereas; the remaining 19.2% was out of the path. The maximum value of residual factor in phenotypic path analysis indicates that higher environmental factor influences on grain yield at phenotypic level rather at genotypic level.

**TABLE IV: Estimates of direct (bold/diagonal) and indirect (off diagonal) effects at phenotypic level**

| Traits | DM | GFP | PH | PL | SCIL | ABM | HI | LI | $GYp_r$ |
|--------|------|------|------|------|------|------|------|------|------|
| DM | **0.096** | -0.024 | 0.005 | -0.009 | -0.042 | -0.280 | 0.482 | 0.003 | 0.23** |
| GFP | 0.086 | **-0.027** | 0.003 | -0.007 | -0.034 | -0.183 | 0.459 | 0.003 | 0.3** |
| PH | -0.034 | 0.007 | **-0.013** | 0.013 | 0.047 | 0.608 | -0.365 | -0.002 | 0.26** |
| PL | -0.050 | 0.012 | -0.010 | **0.017** | 0.045 | 0.540 | -0.412 | -0.002 | 0.14* |
| SCIL | -0.059 | 0.013 | -0.009 | 0.011 | **0.068** | 0.502 | -0.404 | -0.002 | 0.12ns |
| ABM | -0.028 | 0.005 | -0.008 | 0.009 | 0.036 | **0.965** | -0.319 | 0.000 | 0.66** |
| HI | 0.059 | -0.016 | 0.006 | -0.009 | -0.036 | -0.396 | **0.777** | 0.003 | 0.39** |
| LI | 0.024 | -0.007 | 0.002 | -0.004 | -0.013 | -0.039 | 0.225 | **0.010** | 0.2** |

Residual effect = 0.192 for dependent variable.

Where, **-represents highly significance genotypic correlation coefficient of grain yield with all traits at (P ≤ 0.01) except two traits. DM-Days to Maturity (days); GFP- Grain Filling Period (days);PH- Plant Height(cm);PL-Panicle Length(cm); SCL-Second culm internode length(cm); ABM-Above ground biomass kg per hectare and HI- Harvest Index(%), Lodging index(%) and GYp$_r$ – Grain yield of phenotypic correlation coefficient.

**3.5.2 Genotypic path coefficient analysis**

Under genotypic path coefficient, above ground biomass yield had the highest positive direct effect on grain yield followed by harvest index, 0.908 and 0.455 (TABLE V). The residual factor for tef at genotypic level was 0.183 implying that the characters included in the path analysis explained 81.7% of the total variation in grain yield; while, the remaining 18.3% was contributed by other factors not included in the path analysis. Therefore, selection for these characters would

give good responses to yield improvement. Corresponding to current results, Habtamu *et al.* (2011) reported biomass yield and harvest index for their highest direct effect and their correlation with grain yield of tef landraces. The authors suggested that selecting for these traits indirectly selects for grain yield. Similarly, Abel *et al.* (2012) and Ayalneh *et al.* (2012) also reported that harvest index and biomass yield had a strong direct effect and positive correlation with grain yield in tef.

However, plant height (0.112, days to maturity (0.059) and second culm internode length (0.031) had weak positive direct effect on the grain yield (TABLE V). Conversely, grain filling period, culm length and panicle length showed weak negative direct effects of (-0.019, -0.038 and -0.098) on grain yield trait of tef. This indicates that late maturity tends to decrease grain yield performance by increasing only the above ground biomass or vegetative parts. Similarly, Sintayehu and Getachew (2011) found better grain yield performance of early maturing recombinant inbred lines than late maturing types in a moisture stressed environment.

In addition to its direct effect, days to maturity showed relatively strong negative indirect effects via grain filling period, plant height, panicle length, number of productive tillers per plant. Generally, the genotypic path analysis indicated that selection for high above ground biomass yield, harvest index and long maturity could provide increased grain yield as the result of this study revealed. While in moisture stressed environments, yield improvement can achieve through selection for reduced days to maturity, high biomass yield and harvest index as reported by (Nigus *et al.*, 2016).

**TABLE V: Estimates of direct (bold/diagonal) and indirect (off diagonal) effects at genotypic level**

| Traits | DM | GFP | PH | PL | CL | SCIL | ABM | HI | GYg$_r$ |
|--------|------|------|------|------|------|------|------|------|------|
| DM | **0.059** | -0.013 | 0.059 | -0.018 | -0.046 | 0.007 | 0.536 | -0.014 | 0.57** |
| GFP | 0.040 | **-0.019** | 0.029 | -0.006 | -0.027 | 0.003 | 0.272 | 0.068 | 0.36** |
| PH | 0.031 | -0.005 | **0.112** | -0.030 | -0.092 | 0.019 | 0.563 | -0.127 | 0.47** |
| PL | 0.028 | -0.003 | 0.090 | **-0.038** | -0.055 | 0.015 | 0.409 | -0.046 | 0.40** |
| CL | 0.028 | -0.005 | 0.105 | -0.021 | **-0.098** | 0.018 | 0.554 | -0.150 | 0.43** |
| SCL | 0.013 | -0.002 | 0.068 | -0.019 | -0.057 | **0.031** | 0.390 | 0.005 | 0.43** |
| ABM | 0.035 | -0.006 | 0.069 | -0.017 | -0.060 | 0.013 | **0.908** | -0.073 | 0.87** |
| HI | -0.002 | -0.003 | -0.031 | 0.004 | 0.032 | 0.001 | -0.145 | **0.455** | 0.31** |

Residual effect = 0.183 for dependent variable.

Where, **= highly significant genotypic correlation coefficient of grain yield with all traits at (P≤ 0.01). DM-days to maturity, GFP- grain filling period, PH- plant height, PL- panicle Length CL- culm length, SCL- second culm internode length, ABM- above ground biomass kg per hectare and HI- harvest index and GYg$_r$ – Grain yield of genotypic correlation coefficient.

## 4. CONCLUSIONS

The current experiment carried out on 49 semi-dwarf tef recombinant inbred lines that selected from GA-10-3 X DZ-01-192 crosses of F$_7$ single seed descent developed inbred lines at DZARC. The results of analysis of variance allow carrying out further genetic analyses for all traits, except number of fertile tillers per plant, which was not significant. Both genotypic and phenotypic correlation coefficient analyses showed positive association of grain yield with most traits. Lodging index showed positive phenotypic correlation with phenological and agronomical traits except above ground biomass, while not statistically correlated with most morphological traits except plant height, panicle length and second culm internode length, which negatively correlated with lodging.

However, path analysis revealed that effect of above ground biomass on grain yield had high and positive genotypic and phenotypic path coefficient correlation. The rest of the traits showed consistently low positive or negative effect. This indicated that attention should be given for those traits, which have which have positive correlation with grain yield in the process of selection, as these traits are helpful for indirect selection. Trait association among yield components and grain yield with its component in this particular study indicated various magnitude of association, which can be carefully looked into while exploiting in selection to improve traits of interest in tef breeding.

However, the level of genetic variations for many traits including grain yield might be not sufficient to expect progress in selection and showed moderate to low genetic coefficient of variation that made improvement through selection a difficult task. Aboveground biomass showed maximum genetic advance as percent of mean, as well as positive direct effect correlation compared to other traits. Hence, it will be a useful trait for indirect selection to increase grain yield, even though negatively correlated with harvest index. Plant height and panicle length showed high heritability, relatively better genetic advance as percent of mean and positive correlation coefficient and direct effect on grain yield. This implies that these characters may be included as a component of indirect selection. Recombinant inbred lines like RIL-14 have significantly low lodging index, longer panicle, higher number of spikelets per panicle, as well as the highest above ground biomass and grain yield. Genotypes identified with better grain yield related traits and reasonable lodging tolerance require further evaluation and eventual release to the farming communities in tef growing environments in Ethiopia.

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