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Genetic Variation, Heritability and Genetic Advance Among Semi-Dwarf Tef [Eragrostis tef (Zucc.) Trotter] Recombinant Inbred Lines

Getahun Bekana*
Ethiopian Institute of Agricultural Research; Holeta Agricultural Research Center,
P.O Box 31 , Holeta, Ethiopia

Kebebew Assefa
Ethiopian Institute of Agricultural Research; Debre Zeit Agricultural Research Center,
P.O Box 32 , Debre Zeit, Ethiopia

Abstract
A total of forty-nine recombinant inbred lines were evaluated for 16 traits using simple lattice design. All the traits measured over the locations showed highly significant differences among the lines except fertile tiller per plant, while the inbred lines x location interaction effect was highly significant for most of the traits measured. Grain yield showed the highest phenotypic coefficients of variation (PCV) (26.36%) followed by above ground biomass (23.16%), while the remaining traits showed low (<10%) to moderate (10-20%). Moderate (10-20%) genotypic coefficient of variation was recorded for above ground biomass. Plant height and panicle length showed high heritability(H^2) (>60%), whereas half of the remained traits showed low (<30%) and moderate (30% to 60%) heritability. Genetic advance as percent of the mean (GAM) was the highest for above ground biomass (>17.02%) and least for number of branches per panicle (0.09%). From all the traits evaluated in this study, plant height, panicle length showed high $H^2$and aboveground biomass performs relatively high values of GCV, PCV and GAM. Therefore, these traits are important for selection and further improvements. This study revealed that four recombinant inbred lines had higher yield than local and standard checks. Recombinant Inbred Line (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.
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1. Introduction

Tef [Eragrostis tef (Zucc.) Trotter] belongs to the family Poaceae, subfamily Chloridoideae, genus Eragrostis with binomial nomenclature of Eragrostis tef (Zucc.) Trotter. It is an allotetraploid (2n=4X=40), self-pollinated with bisexual florets of chasmogamous pollination behavior, and C_4 plant (Stallknecht et al., 1993; Yu et al., 2006). Its center of origin and diversity is in Ethiopia (Vavilov, 1951). Fifty-four of the 350 Eragrostis species, including the 14 endemic species were found in Ethiopia where they believed to been domesticated by pre–Semitic inhabitants between 4000 and 1000 BC (Seyfu, 1997; Habtamu et al., 2011; Alganesh, 2013).

Tef 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, 2020), the area covered by tef during the 2019/2020 cropping season was over 3.1 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 growing 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 1.85 ton per hectare (CSA, 2020), 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).

Lodging greatly reduces both yields and quality of the grain as well as the straw. It is reported to decrease tef grain yield by approximately 15 to 45% (Zhu et al., 2012) depending on the weather condition and inherent nature of the variety used; it also hampers both manual and mechanical harvesting (Kebebew et al., 2015). Using lower seed rates and late sowing dates relatively decreases the problem of lodging. Although, various attempts have been made by the research community to develop lodging-resistant tef cultivars (Kebebew et al., 2011; Kebebew and Zarihun, 2012), 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, resulting in increased lodging tolerance (Jöst et al., 2015).

The tef germplasm accessions showed wide genetic variability in phonological, morphological and agronomical traits (Hailu et al., 2001; Solomon, 2007 and Kebebew et al., 2001, 2011). In spite of this, there has been lack of sufficient variability in the tef germplasm for some valuable traits such as lodging and shattering resistance. Since recent past, a chemical mutagen, ethyl methane sulphonate (EMS), has been successfully utilized to induce semi-dwarf tef variants with lodging resistance as well as tolerance to aluminum toxicity and other acidity-related soil fertility problems (Mesfin, 2007; Esfeld et al., 2009 and Ermias et al., 2017). The first semi-dwarf lodging-tolerant tef line, called kegne developed from an ethyl methane sulphonate-mutagenized population (Jöst et al., 2015).

Some important works have also reported based on morphological, molecular and biochemical markers. According to Tareke et al. (2011), many efforts made in the past to implement different techniques and tools in order to improve tef. Some of them are such as inter-specific crossing that made between tef (Eragrostis tef) and Eragrostis curvula in an attempt to transfer the lodging tolerant trait of Eragrostis curvula to tef. However, so far, no viable hybrid obtained from the crosses. In attempts to develop double haploids using gynogenesis technique, some promising tef lines were obtain (Likyelesh, 2006). The variations noted in panicle length (14-65 cm), culm length (11-82 cm), plant height (31-155 cm), culm thickness (1.2-4.5 mm) all indicate the potential for developing lodging-resistant genotypes through gene re-combination as suggested by Seyfu (1993).

Efforts made so far have enabled the development and release of over 51 improved varieties to the farming communities in Ethiopia (MoARD, 2020). 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 and there is no lodging resistant tef (Habte et al., 2017). Therefore, the current study conducted with the following objectives.

Objective

- To estimate the extent of genetic variability among selected semi-dwarf tef recombinant inbred lines with emphasis on lodging tolerance, yield and yield components, and thereby generate information as well as identify superior inbred lines.

2. Materials and Methods

2.1 *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 (8º 44’ N, 38º 58’ E and 1860 m.a.s.l) whereas, HARC found at (9º 03’ N, 38º 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 ºC and 8.9 ºC, 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 ºC and 6.6 ºC, 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. The mean monthly rainfall and maximum as well as minimum mean monthly temperatures during the crop-growing season in relation to the two locations (Appendix I).

2.2 *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 2). 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 materials kindly supplied by Debre Zeit agricultural research center, in Ethiopia. I have duly acknowledged DZARC for their kindness.

Table 1 Experimental 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)		

*SD: - Semi-dwarf tef; DZ-01:-Debre Zeit tef cultivar released through selection; GA-10-3: - -Mutant elite tef line. Source of all material were from cross of (DZ-01-192 x GA-10-3) and F_7 progeny of 2016-year gained from Debre Zeit center.

2.3 *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 was done on 13 August, 25 July 2017 at Debre Zeit and Holetta research center, 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.

2.4 *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 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:

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

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 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.

2.5 *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 were 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:

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

If the calculated value of Fmax was less than three, it means that the ratio of the highest error mean square is not threefold 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 (Manly, 1986).

2.5.1 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.

Comparing E_b with E_e; If $E_b > E_e$ an adjustment of the treatments were 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 $\sigma^2 g = \frac{MSg - MSe}{r}$; Interaction variance $\sigma^2 I = \frac{MSI - Mse}{r}$

Over locations genotypic variance $\sigma^2 g = \frac{MSg - MSI}{rl}$; Environmental variance $\sigma^2 e = \frac{Mse}{r}$

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 location.

Model of the experiment:

The ANOVA for individual location followed the following model:

$_{ijk} = \mu + g_i + b_{k(j)} + r_j + e_{ijk}$

Where, P_{ijk} = phenotypic value of i^{th} genotype under j^{th} replication and k^{th} incomplete block within replication j; μ=grand mean; G_i= the effect of i^{th} genotype; $B_{k(j)}$ =the effect of incomplete block k within replication j; R_j=the effect of replication j; and E_{ijk}= the residual or effect of random error. For combined analysis of variance over locations, the total variations among the inbred lines measured using the following model:

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

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; μ=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.

Table 2 Anova skeleton for individual locations (HARC and DZARC) in simple lattice design

Source of variation	Degree of freedom	Sum of Squares(SS)	Mean Squares(MS)
Replications(r)	r-1	SSr	
Genotypes(g un djusted)	g-1	SSg	
Block in rep(adjusted)	r(b-1)	SSB	E_b
Intra block error	(b-1)(rb-b-1)	SSE	E_e
Total(T)	rb-1	SST	

* g = Number of genotypes, b = Number of plots in a block or block size / intra block

*E_b – Error for block = SSB/r (b-1) and E_e – Experimental error = SSE/ ((b-1) (rb-b-1))

Table 3 Analysis of variances for combined over locations in simple lattice design

Source of variation	Degree of freedom	Mean square (MS)	Expected mean square (EMS)
Location (L)	L-1	MSL	$\sigma^2e+ r\sigma^2gi+ g\sigma^2L$
Replication with in location(r)	L(r-1)	MSr	$\sigma^2 e + g \sigma^2rL$
Blocks within replication(b)	r(b-1)	MSb	$\sigma^2e + r\sigma^2gi + r\sigma^2 g$
Genotypes (g)	g-1	MSg	$\sigma^2 e + r\sigma^2gi + rL\sigma^2g$
g x L interaction (i)	(g-1) (L-1)	MSi	$\sigma^2 e + r\sigma^2gi$
Error (e)	Lg(r-1)-(rb-1)	MSe	$\sigma^2 e$

Where, b- represent intra blocks; σ^2g= genotypic variance, σ^2e = environmental variance, σ^2L =location variance, σ^2r = replication variance, and σ^2gi = genotype x location interaction variance, L = number of locations, g = number of genotypes and r = number of replications.

Appropriate mean separation will be done if there is significance.

- 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).

2.5.2 Estimation of variance components

Phenotypic (PCV) and genotypic (GCV) coefficients of variation were calculated according to the method suggested by Burton (1953) as:

Phenotypic Coefficient of Variation:-

$PCV = \left[\frac{\sqrt{\delta^2 p}}{\mu}\right] x\ 100$, Where; PCV= phenotypic coefficient of variation; μ=Population mean

Genetic coefficient of Variation:-

$GCV = \left[\frac{\sqrt{\delta^2 g}}{\mu}\right] x\ 100$,Where; GCV= phenotypic coefficient of variation; μ= Population mean PCV and GCV values > 20% is regarded as high, 10 - 20% is considered as medium and < 10% is considered as low (Kherdade et al., 1985).

2.5.3 Estimates of broad sense heritability

Heritability in broad sense (H^2) was calculated according to Allard (1960) as – $H^2 = \frac{\sigma^2 g}{\sigma^2 p}$ x 100% Where, σ^2g and σ^2p are genetic and phenotypic variance, respectively.

According to Robinson et al.(1949), broad sense heritability in cultivated plants can be categorize into low for values of 0-30%, medium for estimates of 30-60%, and high for values above 60%.

2.5.4 Estimates of genetic advance

Genetic Advance (GA) was estimated using the formula of Johnson et al. (1955) as follows. $GA = H^2k*\sigma p$ Where, GA = Genetic advance, H^2 is broad sense heritability, k (= 2.056) was the selection differential expressed in phenotypic standard deviation depending on the selection intensity of 5%, σp is the phenotypic standard deviation. Where Genetic advance as percent of mean (GAM) as follows according to Falconer and Mackay (1996):

$GAM = \frac{GA}{Mean} x100\%$ where 0-10% is low, 10-20% is moderate and 20% and above is high.

3. Results and Discussions

3.1 *Mean Performance*

Mean squares of the 16 traits from analysis of variance (ANOVA) at individual location and combined over the two locations are presented in Tables 5, 6 and 7. From the separate analysis, at Holetta highly significant differences among inbred lines ($p<0.01$) were observed for all traits except number of fertile tillers per plant. At Debre Zeit, significant differences among lines ($p<0.01$) were observed for all traits except peduncle length, second culm internode length, Second culm internode diameter, number of branches per panicle and fertile tillers per plant.

For some traits like grain yield, harvest index, lodging index, days to heading and maturity lower mean values were recorded at Debre Zeit and higher values recorded at Holetta. In the case of remaining traits such as plant height, panicle length, culm length, second culm internode length, second culm internode diameter, number

of fertile tillers, number of branches and number of spikelets per panicle the highest value recorded at Debre Zeit whereas the lowest value at Holetta. This indicates that the locations had significant effects on the performance of semi-dwarf tef recombinant inbred lines (Table 5 and 6). This expected based on the distinct agro-climatic classification of the test locations (Kebebew et al., 2003b).

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 7). Locations revealed highly significant (P≤0.01) effects on 13 of the traits and significant (P≤0.05) effects on two traits (peduncle length and grain yield), while number of branches per main panicle was not significantly affected by locations. Genotype and locations interacted highly significantly on eleven of the traits, while one trait (panicle length) showed significant interaction and four traits (peduncle length, second culm internode length, second culm internode diameter and number of fertile tillers showed no statically significant interaction effects. This indicate that the two location environmental conditions highly different.

Comparisons of the mean performances of each traits of combined locations presented on (Appendix Table III). From grain yield traits RIL-14, RIL-45, RIL-28 and RIL-41 in this order had mean grain yields of 2.52, 2.29, 2.21and 2.19 t ha^{-1}, which were higher than that of the standard check Boset (1.83 t ha^{-1}) and the local check (2.14 t ha^{-1}). This indicates that grain yield potential of these semi-dwarf tef were different; thus, indicating that the opportunity for breeders to further improvement of tef yield through the existing breeding strategy. In line with the present findings, Yifru and Hailu (2005) also reported the grain yield potential in tef improvement.

In lodging index traits RIL-19(39.5%), RIL-75(44.5%), RIL-8(47.0%), RIL-169(50.5%), RIL-22(51.1%), RIL-14(54.0%) and DZ-01-192(53.0%) have the least lodging index than local and standard checks as well as the parent checks except RIL-14, which more than DZ-01-192 parental check by one percent. This indicate that there is high potential to increase grain yield by decreasing the loss exposed by lodging. From the main lodging related traits second basal culm internode diameter have the highest mean performance for the following recombinant inbred lines such as RIL- 169(2.13 mm), RIL- 14(2.08 mm), RIL-57(1.96), RIL-45(92 mm),RIL-175(1.91 mm) and parental check (DZ-01-192) which have 1.98mm, while the standard and local checks shown lower in diameter. As indicated above the highest in grain yield have highest culm diameter and lower lodging index, this finding in line with (Habte et al., 2017).

This indicate that as the second basal internode diameter increases the lodging become decrease and grain yield increase even if the other traits may averagely affect their association non –significant in this study. RIL-14(115.95 cm) also exhibited the longest plant height and length of the culm, panicle and second basal culm in addition to culm diameter, next to RIL-169, which have highest diameter. However, the parental line DZ-01-192 also had the longest better than the checks. Generally, all the recombinant inbred lines have shown clearly different mean performance in each traits comparing with each other and checks (Appendix Table III).

Table 4 Analysis of variance for the 16 traits of 49 semi-dwarf tef recombinant inbred lines evaluated at Holetta

Traits	Rep(df=1)	Intra blocks (df=12)	Inbred lines (df=48)	Error (df=36)	CV (%)	Mean	R^2
DH	16.33**	3.85ns	35.19**	2.29	2.49	60.69	96.04
DM	1489.02**	74.53**	68.55**	15.16	3.25	119.94	92.53
GFP	1193.51**	80.26**	58.46**	13.31	6.16	59.24	92.64
PH	18.17ns	125.85**	186.06**	9.98	3.52	89.76	96.73
PL	19.39*	7.34*	35.10**	3.22	5.59	32.09	94.23
CL	0.02ns	75.35**	87.20**	6.56	4.44	57.68	95.70
PDL	6.99ns	3.18ns	12.97**	2.32	6.50	23.41	90.00
SCIL	1.69ns	4.07**	4.09**	0.74	10.00	8.61	90.00
SCID	0.06ns	0.04ns	0.05**	0.02	8.32	1.78	76.26
NFT	0.06 ns	0.86 ns	0.62ns	0.73	25.91	3.29	61.81
NBP	12.93 ns	7.62 ns	11.77**	5.16	8.77	25.89	80.99
NSP	318.24 ns	3976.57 ns	8016.64**	2371.36	11.24	433.21	84.02
ABM	344680.1 ns	2295049.5**	2586895.7**	281746.60	9.26	5733.10	95.85
GY	251709.31**	317362.28**	158861.96**	40207.54	12.57	1595.56	93.58
HI	20.88 ns	16.20 ns	34.37**	12.86	12.77	28.09	81.91
LI	35.52 ns	9.53 ns	48.56**	12.46	5.54	63.72	88.93

*, ** 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 (%).

Table 5 Analysis of variance for the 16 traits of 49 tef recombinant inbred lines evaluated at Debre Zeit

Traits	Rep (df= 1)	Intra-blocks (df=12)	Inbred lines (df= 48)	Error (df = 36)	CV (%)	MEAN	R^2
DH	5.39 ns	9.03 ns	16.67**	6.99	5.55	92.74	79.71
DM	0.83 ns	9.19 *	16.56**	4.34	2.25	45.06	86.64
GFP	10.45 ns	10.74 ns	25.25**	11.24	7.44	102.79	79.66
PH	34.33 ns	24.84 ns	127.72**	23.79	4.74	39.91	90.30
PL	19.39 ns	4.48 ns	18.54*	9.57	7.75	62.89	74.75
CL	2.12 ns	36.84 ns	88.09**	34.40	9.33	22.81	82.21
PDL	28.88*	7.06 ns	5.66 ns	6.14	10.86	12.2	67.74
SCIL	9.43*	4.62**	2.08 ns	1.78	10.93	1.83	74.01
SCID	0.06 ns	0.02 ns	0.03 ns	0.03	8.74	6.93	64.16
NFT	5.49*	1.40 ns	0.74 ns	0.90	17.35	25.69	65.10
NBP	1.30 ns	7.44 ns	7.97 ns	6.71	10.08	453.35	66.20
NSP	9035.52*	4254.33*	16735.10 **	2169.42	10.27	4.32	92.38
ABM	3594830.4**	661930 ns	6456901.7**	380149.40	7.96	1534.61	96.20
GY	186602.9**	25269.68 ns	446728.35**	14970.99	7.97	19.85	97.83
HI	4.67 ns	5.44 ns	21.12**	4.43	10.61	3403.12	88.37
LI	0.09 ns	64.83*	158.46**	32.70	9.70	47.68	88.81

*, ** Significant at $p \leq 0.05$ and $p \leq 0.01$ 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 (%).

Table 6 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 (%)	R^2
DH	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

*, ** Significant at $p \leq 0.05$ and $p \leq 0.01$ 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 (%).

Relative efficiency of the simple lattice design compare to that of a randomized complete block design where done as follows:-

- First by computing MSE for the RCBD as: E_{RCBD} = (SSB+SSE) /(k^2 - 1)(r -1).
- Then % relative efficiency = (E_{RCBD} / E_e')100 while, Ee' = (1+(rkA)/(k+1))Ee and
- A = (E_b – E_e)/(k(r – 1)E_b). where E'_e- effective error mean square, A- adjusted treatment, k^2- number of treatments ,k- number of plot in block, r- number of replications, E_e = pooled error and E_b- block error
- Therefore, there is a 26.2% gain in efficiency from using the lattice as this study.

3.2 *Genotypic and Phenotypic Coefficients of Variation*

The value of genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV) were grouped to High>20%, intermediate 10-20% and low <10% (Kherdade et al., 1985). Depending on this for the current study, the GCV ranged from 0.61% for number of branches per panicle to 13.83 % for above ground biomass. All traits grouped in the low GCV value except above ground biomass, which grouped under the intermediate GCV value (Table 8). Similarly, Solomon et al. (2009) reported that plant height, days to maturity and harvest index had low GCV values. Correspondingly, Habtamu et al. (2011) and Habte et al. (2015) also reported that days to maturity and days to grain filling had low GCV values, respectively. This might be attributing to high influence of the environment on the inbred lines. Low values of GCV suggest less scope of improvement for these traits by selection. The magnitude of genetic variation better assessed from genotypic coefficients of variation (Solomon et al., 2013). Therefore, selecting the tef recombinant inbred lines having higher harvest index and lower lodging index could help enhancing the productivity of tef.

PCV values ranged from 4.55% for days to maturity to 26.36% for grain yield (Table 8). The grain yield and above ground biomass were categorized into high PCV (>20%). However, panicle length, culm length, second basal culm internode length, number of spikelets per main panicle, harvest index and lodging index were grouped into intermediate PCV values (10-20%). The third group of PCV had a low (0-10%) value, which computed for days to heading days to maturity, grain filling period, plant height, peduncle length and second basal culm internode diameter and number of branches per main panicle. PCV is usually the reflection of the effects of inbred lines and environment. If the PCV is greater than GCV it means the environment contributes more than the genes' effect for phenotypic expression of the trait. Previous findings by different researchers were also similar to the present study results (Kebebew et al., 2001b; Habtamu et al., 2011 and Habte et al., 2015).

3.3 *Heritability*

The broad sense heritability(H^2) ranged from 68.35% for plant height to 0.47% for number of branches per main panicle (Table 8). In addition to plant height, panicle length (66.71%) also had high heritability values >60% (Robinson et al., 1949). This indicates less influence of environment as compared to the genetic factors in controlling the traits and it suggested that the progenies would have a higher chance to perform the same as the parent. Days to heading, culm length, peduncle length, second basal culm internode length, second basal culm internode diameter, above ground biomass had estimates categorized under moderate heritability (30<60%).

Whereas days to maturity, grain filling period, number of branches per main panicle, number of spikelets per main panicle, grain yield, harvest index and lodging index categorized into low heritability values (<30%). Low heritability indicates the non- predictable of the phenotype range of environments. This showed that these traits are highly influenced by environment. This suggestion is supported with the findings of several authors who conducted studies on tef (Kebebew et al., 2000, 2001; Solomon et al., 2009; Habtamu et al.,2011; Abel et al., 2012; Habte et al., 2015).

3.4 *Expected Genetic Advance*

The expected genetic advance (GA), expressed as a percentage of the mean, ranged from 0.09% for number of branches to 17.02% for above ground biomass (Table 8). Similarly, moderate expected GA observed for plant height (13.02%) and panicle length (13.97%) and culm length (11.12%). All the rest of the traits showed low genetic advance values as a percentage of mean between 0.09% and 8.05%. Similar findings with this also study reported by (Abel et al., 2012; Kebebew et al., 2001 and Solomon et al., 2009).

Low heritability and genetic advance estimated for the traits suggest that breeding for those traits would be a difficult task. Johnson et al. (1955) in soybean suggested that heritability estimate with genetic gain are more useful for effective improvement. In addition to high heritability along with high genetic advance as percentage of mean implies the role of additive genes for the expression of the characters, and thus it could be very effective in improvement upon selection. In general, high GCV, heritability and genetic advances for traits could be an excellent tool for improving through selection of high performing genotypes. In the current study even if no high GCV recorded, high heritability (plant height and panicle length) and high above ground biomass genetic advance were displayed as also as reported by (Nigus et al., 2016).

Table 7 Phenotypic and Genotypic coefficients of variation, Heritability, Genetic advance and Genetic advance as percent of means for 15 traits in 49 recombinant inbred lines of semi-dwarf tef at Holetta and Debre Zeit.

Traits	σ^2g	σ^2e	σ^2gl	σ^2p	GCV	PCV	H^2	GA	GAM
DH	7.57	2.34	3.57	13.48	5.08	6.78	56.12	4.24	7.83
DM	4.01	9.98	9.40	23.39	1.88	4.55	17.16	1.71	1.61
GFP	4.27	10.04	9.54	23.84	3.96	9.36	17.90	1.80	3.45
PH	54.21	13.32	11.79	79.31	7.65	9.25	68.35	12.54	13.02
PL	8.94	3.02	1.44	13.40	8.30	10.17	66.71	5.03	13.97
CL	21.87	13.47	9.83	45.16	7.76	11.15	48.42	6.70	11.12
PDL	1.83	2.13	0.77	4.73	5.86	9.41	38.76	1.74	7.51
SCIL	0.45	0.89	0.20	1.54	6.47	11.94	29.34	0.75	7.22
SCID	0.01	0.01	0.001	0.02	5.52	7.81	50.00	0.15	8.05
NBP	0.02	2.75	2.50	5.28	0.61	8.88	0.47	0.02	0.09
NSP	355.69	1250.77	4862.50	6468.96	4.25	18.14	5.50	9.11	2.06
ABM	868277.00	245820.20	1319877.70	2433974.90	13.83	23.16	35.67	1146.48	17.02
GY	9113.06	24598.46	136532.85	170244.36	6.10	26.36	5.35	45.50	2.91
HI	2.05	4.72	12.46	19.23	5.97	18.29	10.63	0.96	4.01
LI	8.98	11.94	35.33	56.24	4.88	12.22	15.96	2.47	4.02

σ^2g- genotypic variance, σ^2e- environmental variance, σ^2gl- Genotypic by location interaction variance, σ^2p- phenotypic variance(, GCV- genotypic coefficients of variation(%), PCV- phenotypic coefficients of variation (%), H^2- Broad sense heritability (%), GA – genetic advance and GAM- Genetic advances as percent of means(%). 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.

4. Conclusion and Recommendation

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 Debre Zeit center. The results of this study indicate that highly significant difference among the recombinant inbred lines for all traits evaluated except for number of fertile tillers per plant. Genotypes by locations interactions were highly significant for 10 traits.

Grain yield showed the maximum phenotypic coefficient of variation (26.36%) followed by above ground biomass (23.16%), while moderate phenotypic coefficient of variation (20> 10%) estimates were recorded for number of spikelets per main panicle, harvest index, lodging index, second culm internode length, culm length and panicle length. The remaining traits showed low phenotypic coefficient of variation values. Moderate genotypic coefficient of variation (10-20%) was recorded for above ground biomass while, genotypic coefficient of variation was low for the rest of the traits.

Two of the traits (i.e. plant height and panicle length) showed high heritability (> 60%), while days to heading, culm length, peduncle length, second culm internode diameter, second culm internode length and above ground biomass showed intermediate heritability estimates. The remaining traits showed low heritability (<30%). Genetic advance as percentage of mean were maximum for above ground biomass (>17.02%) and lower for number of branches per panicle (0.09%).

Generally, genetic variation has supreme importance to the breeders, as it is prerequisite for any improvement in crop plants and identification of superior recombinant inbred lines. This study also revealed that four recombinant inbred lines from the studied recombinant inbred lines had higher yield than local and standard checks. There were differences in the performance of the recombinant inbred lines as there were statistically significant differences among recombinant inbred lines for most of the traits studied over the locations.

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. Hence, it will be a useful trait for indirect selection to increase grain yield. Plant height and panicle length showed high heritability, relatively better genetic advance as percent of mean. This implies that these characters may be included as a component of indirect selection.

To this end, the results revealed the existence of considerable variations for most traits of the test inbred lines, thus indicating the possibility of exploiting the variability in further tef breeding. Thus, 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.

Finally, since it is one season experiment, the research needs additional two or more years across wide range of environments to arrive at concrete recommendations for maximization of tef yields. Molecular marker assisted selection in combination with field evaluation of this semi-dwarf tef inbred recombinant inbred lines traits based on conventional breeding under different environmental conditions also comprehensively recommended.

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6. Appendices

Appendix Table I. Mean monthly rainfall and temperature during cropping season at both locations of the experiments

Locations	**Weather parameters**		**Months of the cropping season**						
			July	Aug	Sept	Oct	Nov	Dec	Means
Holeta	Rain Fall (mm)		172.8	311.4	244	29	0	0	126.2
	Temp.^{o}C	max	22.1	21.7	22.6	24.2	24	23.1	23.1
		Min	8.8	10.4	8.3	7.8	2.8	6.5	6.5
Debre Zeit	Rain Fall (mm)		262.3	200.2	115.2	19	0	0	99.5
	Temp.^{o}C	max	23.9	21.8	24.5	26.5	26.2	24.9	24.9
		Min	14.6	14.3	14	11.1	8.3	11.6	11.6

Source: DZARC and HARC (2017)

Appendix Table II. Clustering of 49 semi-dwarf tef recombinant inbred lines into four cluster using mean of 15 traits

Clusters	**No RILs**	**RILs exist under each clusters**	**Source**
C1	19	RILs NO- 1, 4, 6, 15, 16, 19,27, 44, 52, 58, 68, 160, 162, 166, 172, 174, 179, 180,and 182	F_7 of DZ-01-192 x GA-10-3
C2	15	RILs NO-2,8,12,20,21,22,24,33,57,75,161,171,178,262 and GA-10-3	F_7 of DZ-01-192 x GA-10-3
C3	13	RILs NO-5,25,28,41,48,169,175,185,195, 203 and Local check,DZ-Cr-192,Boset	F_7 of DZ-01-192 x GA-10-3 and Checks
C4	2	RILs NO-14 and 45	F_7 of DZ-01-192 x GA-10-3

C-represent cluster numbers, RILs-recombinant inbred lines, DZ-Cr-192 and Ga-10-3-parental lines, Boset is Standard check and Local check is the farmer cultivar for respective locations. All materials were taken from DZARC.

Appendix Table III. Mean performance of fifteen traits of 49 semi-dwarf tef recombinant inbred lines evaluated over two locations.

RILs	DH	DM	GFP	PH	PL	CML	PDL	SCL	SCD	BP	SP	SBM	GY	HI	Li
RIL # 1	44.0n	105.5a-m	61.5a	93.7i-o	35.9a-n	57.8e-l	23.4a-h	11.5a-e	1.7f-h	24.3e-i	408.6h-o	7165.9e-i	1888.8c-k	27.1a-d	67.5a-c
RIL # 2	52.0g-m	104.8f-m	52.8c-k	75.0s	29.5p	45.5m	17.9l	8.5f-h	1.8b-g	25.4b-i	493.7a-h	4742.0op	1059.3t-v	23.2d-j	66.0a-d
RIL # 4	49.3m	102.8j-m	53.5b-k	93.8i-o	33.9g-o	59.9c-k	23.4a-h	11.1a-e	1.6gh	25.4b-i	450.8c-l	7154.0e-i	1806.2e-m	26.4a-f	61.3a-g
RIL # 5	52.0g-m	104.5f-m	52.5c-k	89.2n-q	34.0g-o	55.2j-l	21.8e-k	10.5a-g	1.7f-h	24.1f-i	518.2a-d	7436.1d-h	1521.8k-r	20.9g-k	67.5a-c
RIL # 6	51.8h-m	105.8e-m	54.0a-k	100.6c-k	37.4d-i	63.3a-j	23.2b-h	11.1a-e	1.9b-g	29.2ab	475.2a-k	6790.5f-k	1557.8i-o	24.6a-i	68.8a
RIL # 8	57.5cd	106.8c-m	49.3g-m	110.6ab	41.6bc	69.1ab	22.5c-i	11.1a-e	1.9a-f	28.2a-f	403.7i-p	5434.4m-p	1309.4l-r	24.5a-i	47.0jk
RIL # 12	55.8c-g	102.0lm	46.3k-m	78.1rs	31.5op	46.6m	19.3i-l	7.7h	1.8c-g	24.7c-i	377.6l-q	4332.0pq	1138.2r-v	27.0a-e	58.8d-h
RIL # 14	62.5a	115.5a	53.0c-k	116.0a	46.5a	69.5a	24.0a-h	11.1a-e	2.1ab	24.5a-i	438.3d-l	9671.4a	2523.7a	26.1a-g	54.0f-j
RIL # 15	50.5k-m	101.8lm	51.3e-m	98.3d-n	34.7f-o	63.6a-i	23.7a-h	11.0a-e	1.9b-g	27.2a-g	475.4a-k	6091.9i-n	1335.5o-u	21.5f-k	60.0b-g
RIL # 16	53.5e-k	103.5h-m	50.0f-m	96.4g-o	34.1g-o	62.3a-j	24.9a-k	9.2a-h	1.8b-g	24.2f-i	343.0m-q	6914.4e-j	1446.1m-s	22.3d-k	63.0a-e
RIL # 19	52.3f-m	109.5a-l	57.3a-f	99.3d-l	32.9j-p	66.4a-f	23.7a-h	10.1a-g	1.7c-g	22.5i	331.8o-q	6160.6i-n	1067.6s-v	17.9k	39.5l
RIL # 20	54.5d-j	103.3i-m	48.8i-m	92.9j-o	35.6e-o	57.3j-l	24.9a-f	10.7a-f	1.9b-g	26.0a-i	488.8a-i	5166.0n-p	1212.6q-u	25.3a-h	60.5a-g
RIL # 21	55.8c-g	104.0g-m	48.3i-m	82.2q-s	32.5n-p	49.7lm	20.6h-l	7.7h	1.7d-h	23.0hi	450.7c-l	5409.8m-p	1146.8r-v	21.5f-k	62.0a-f
RIL # 22	52.8f-m	105.8a-m	53.0c-k	93.6i-o	35.3e-o	58.3d-l	23.9a-h	9.4e-h	1.7f-h	25.4b-i	489.3a-i	5733.0j-o	1371.4n-u	23.9b-j	51.5h-k
RIL # 24	56.8c-e	106.0d-m	49.3g-m	97.4g-o	38.6b-f	58.8d-k	20.4h-l	11.8a-d	1.8c-g	28.7a-d	485.7a-j	5537.0l-o	1309.9o-u	23.7c-j	60.8a-g
RIL # 25	58.8bc	103.3i-m	44.5lm	101.6e-j	39.5b-e	62.1a-j	20.4h-l	11.0a-e	1.9b-g	26.6a-i	433.7d-l	7653.2d-g	1491.5l-r	19.7i-k	65.5a-d
RIL # 27	52.8f-m	108.0a-m	55.3a-i	93.4i-o	33.1e-p	60.3b-k	24.3a-g	9.2e-h	1.7e-h	26.1a-i	378.8l-q	6159.8i-n	1431.3m-t	26.1a-g	60.3a-g
RIL # 28	61.5ab	113.5a-d	52.0c-l	106.6b-f	42.0bc	64.6a-i	20.8g-l	11.0a-e	1.9b-g	28.8a-c	394.3k-p	9039.3ab	2208.1a-c	24.4a-i	62.3a-f
RIL # 33	51.0i-m	102.0lm	51.0a-m	97.6g-o	37.0d-k	60.7a-j	22.9b-h	9.4d-h	1.8c-g	26.5a-i	338.5n-q	5264.7m-p	1138.8r-v	23.5c-j	61.8a-f
RIL # 41	54.3d-k	104.0g-m	49.8f-m	98.8d-l	38.8b-f	60.0b-k	22.8b-i	12.2a	1.8b-g	29.6a	398.8j-p	7917.3b-f	2191.9a-d	28.8a-c	64.3a-e
RIL # 44	53.5e-k	103.3i-m	49.8f-m	106.9b-d	40.8b-d	66.1a-g	25.5a-d	10.8a-e	1.8c-g	25.2b-i	503.5a-g	7090.0e-i	1629.6h-p	24.0a-j	61.8a-f
RIL # 45	54.5d-j	111.3a-h	56.8a-h	102.2b-i	35.8e-o	66.4a-f	23.5a-h	10.6a-f	1.9a-f	24.9c-i	418.1g-n	9669.0a	2289.7ab	23.6c-j	63.8a-e
RIL # 48	54.5d-j	106.0d-m	51.5d-m	103.8b-h	37.2d-i	66.7a-e	24.5a-f	10.1a-g	1.7c-h	25.1b-i	534.5a-c	8044.5b-e	1726.7f-n	21.6e-k	56.8e-i
RIL # 52	55.5c-h	108.0a-m	52.5c-k	105.0b-g	36.8d-l	68.2a-c	24.8a-f	10.1a-g	1.9b-g	25.7a-i	462.5a-l	6418.3h-m	1353.0n-u	21.1f-k	68.8a
RIL # 57	55.8c-g	102.8j-m	47.0j-m	95.5h-o	37.9c-h	57.7e-l	25.0a-f	11.2a-e	2.0a-d	26.1a-i	504.8a-g	5167.7n-p	1281.1p-u	25.1a-i	62.8a-e

Appendix Table III. (Continued)

RIL$_s$	DH	DM	GFP	PH	PL	CML	PDL	SCL	SCD	BP	SP	SBM	GY	HI	Li
RIL # 58	50.8j-m	110.0a-k	59.3a-d	97.8f-o	37.1d-j	60.8a-j	24.3a-g	11.1a-e	1.9b-g	27.5a-f	471.5a-k	6690.2g-l	1641.1g-p	24.9a-i	65.5a-d
RIL # 68	51.5i-m	103.3i-m	51.8c-l	98.0e-n	37.3d-i	60.7a-j	26.2ab	9.9a-h	1.7d-h	26.5a-i	494.3a-h	6914.7a-g	1670.1g-o	24.0b-j	64.8a-e
RIL # 75	54.0d-k	102.3k-m	48.3i-m	89.4m-q	32.6l-p	56.8h-l	25.0a-f	10.2a-g	1.8c-g	28.5a-e	428.4a-m	4786.2op	1004.8uv	20.8g-k	44.5kl
RIL # 160	54.8d-i	101.3m	46.5j-m	95.3h-o	32.2n-p	63.1a-j	22.1e-k	10.7a-f	1.7d-h	27.6a-f	548.8a	6992.2e-i	1621.8h-p	22.6d-k	66.3a-d
RIL # 161	49.5lm	103.0j-m	53.5b-k	99.0d-l	37.2d-i	61.8a-j	23.9a-h	10.5a-g	1.8b-g	25.1b-i	377.0l-q	3665.9q	896.4v	24.4a-i	62.3a-f
RIL # 162	52.8f-m	101.8lm	49.0h-m	91.5l-f	35.9e-n	55.7i-l	23.5a-h	9.7b-h	1.8c-g	25.6a-i	420.8f-n	7027.7e-i	1456.9l-r	22.0d-k	63.5a-e
RIL # 166	53.5e-k	101.8lm	48.3i-m	91.1l-k	32.9j-p	58.3d-l	25.7a-c	11.3a-e	1.7d-h	28.4a-e	393.9k-p	6161.1i-n	1468.4l-r	26.2a-g	63.5a-e
RIL # 169	62.5a	114.5ab	52.0c-l	108.9a-c	41.5bc	67.4a-d	21.7e-k	10.9a-e	2.1a	24.8c-i	520.9a-d	8542.7b-d	1548.6j-k	19.0jk	50.5i-k
RIL # 171	52.5f-m	112.0a-f	59.5a-c	98.9d-l	38.1c-g	60.8a-j	23.9a-h	10.5a-g	1.8b-g	26.4a-i	399.9j-p	5664.1k-o	1406.5n-t	25.7a-h	61.3a-g
RIL # 171	52.5f-m	112.0a-f	59.5a-c	98.9d-l	38.1c-g	60.8a-j	23.9a-h	10.5a-g	1.8b-g	26.4a-i	399.9j-p	5664.1k-o	1406.5n-t	25.7a-h	61.3a-g
RIL # 172	51.0i-m	102.8j-m	51.8c-l	88.9o-q	31.8n-p	57.2g-l	21.6f-k	9.5c-h	1.8b-g	25.0c-i	449.5c-l	6667.0g-l	1551.4i-k	26.4a-f	67.8a-c
RIL # 174	54.8d-i	104.3f-m	49.5f-m	97.0g-n	34.6f-o	62.4a-j	25.4a-e	12.0ab	1.9b-g	23.2g-i	466.6a-k	6990.1a-i	1637.5g-p	24.0b-j	65.8a-d
RIL # 175	55.5c-h	112.8a-e	57.3a-f	106.8b-a	42.5b	64.4a-i	22.8b-i	11.9a-c	1.9a-f	27.1a-h	501.0a-g	7790.7c-g	1460.7l-r	18.8jk	67.5a-c
RIL # 178	58.8bc	102.5j-m	43.8m	78.1rs	33.6h-p	44.5m	18.8kl	10.3a-g	1.8c-g	25.1b-i	513.1a-e	4669.9o-q	1274.6p-u	27.1a-d	58.5d-h
RIL # 179	52.0g-m	110.3a-j	58.3a-e	99.6d-l	34.8f-o	64.9a-h	25.5a-d	11.5a-e	1.9b-g	25.4b-i	427.1e-m	7092.5e-i	1954.0b-h	29.4a	66.0a-d
RIL # 180	53.0e-l	101.8lm	48.8i-m	92.2k-o	32.5m-p	59.7c-k	27.0a	9.7b-h	1.7d-h	24.5e-i	302.9q	6446.3h-m	1186.8q-v	20.6h-k	59.3c-h
RIL # 182	53.3e-k	103.3i-m	50.0f-m	92.3k-o	33.9g-o	58.4d-l	24.9a-f	10.2a-g	1.7c-g	27.6a-f	461.7b-l	6413.0h-m	1566.0i-q	26.2a-g	68.0ab
RIL # 185	57.5dc	114.3a-c	56.8a-h	97.8f-o	32.7k-p	65.1a-h	21.9d-k	10.9a-e	1.9a-f	24.2f-i	446.3d-l	8062.1b-e	2069.4b-f	25.4a-h	61.0a-g
RIL # 195	53.0e-l	113.8a-c	60.8ab	102.3b-i	36.8d-m	65.6a-h	23.5a-h	10.2a-g	1.9a-f	24.2f-i	545.0ab	7720.4d-g	1924.6b-j	25.9a-h	66.3a-d
RIL # 203	59.0bc	107.3b-m	48.3i-m	96.2g-o	34.1g-o	62.1a-j	23.0b-h	11.3a-e	1.9a-e	25.0c-i	506.5a-f	8422.5b-d	2006.0b-g	24.0a-j	62.3a-f
RIL # 262	51.3i-m	109.5a-k	58.3a-e	79.7rs	35.1f-o	44.6m	21.5f-k	8.2g-h	1.8c-g	24.6d-i	452.8c-l	5223.1n-p	1536.5k-q	29.2ab	61.0a-g
Boset	57.5dc	111.5a-g	54.0a-k	98.8d-l	33.4i-p	65.5a-h	23.1b-h	10.8a-f	1.8c-g	25.8a-i	473.0a-k	8502.2b-d	1830.7d-l	21.7d-k	64.8a-e
DZ-01-192	56.0c-f	110.3a-j	54.3a-j	108.8a-c	41.5bc	67.3a-d	24.4a-g	11.0a-e	2.0a-c	28.1a-f	389.2k-p	8919.1a-c	1927.1b-i	21.9d-k	53.0g-j

Appendix Table III. (Continued)

RILs	DH	DM	GFP	PH	PL	CML	PDL	SCL	SCD	BP	SP	SBM	GY	HI	Li
GA-10-3	54.3d-k	102.8j-m	48.5i-m	83.5p-r	32.0n-p	51.5k-m	18.9j-l	9.8b-h	1.8c-g	24.4a-i	410.5h-o	5572.8l-o	1465.1l-r	26.4a-f	63.5a-e
Local	54.0d-k	111.0a-i	57.0a-g	98.3d-m	38.2c-g	60.2b-k	22.3c-j	9.9a-h	1.5h	23.3g-i	322.7pq	9047.4ab	2145.0b-e	24.7a-i	64.3a-e
Mean	54.2	106.3	52.2	96.3	36.0	60.3	23.1	10.4	1.8	25.8	443.3	6737.7	1565.0	24.0	61.4
CV	4.0	4.2	8.6	5.4	6.8	8.6	8.9	12.8	8.3	9.1	11.3	10.4	14.2	12.8	8.0
Duncan	0.6	1.3	1.3	1.5	0.7	1.5	0.6	0.4	0.0	0.7	14.2	199.2	63.0	0.9	1.4

*Means with the same letter are not significantly different, 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, CV = coefficient of variation (%) and RIL$_s$= Recombinant inbred lines.