

## Genetic Analyses of Agronomic Traits of Tef (*Eragrostis tef*) Genotypes

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**Abstract:** Genetic variation, associations, and heritability for grain yield and component traits (days to heading, shoot biomass, 100 seed weight, individual plant above ground biomass, plant seed weight, panicle seed weight, plant height, panicle length and lodging index) were studied in a trial using 18 tef genotypes at two locations in Ethiopia. Highly significant differences were observed among genotypes for most of the traits examined. When correlations between yield component characters were taken into account, most of the values between various character pairs were significant and positive. Lodging index was negatively correlated with harvest index, shoot biomass, above ground plant biomass, plant height and panicle length. Plant seed weight and shoot biomass appeared to contribute substantially to grain yield at the genotypic level. The values for genotypic and phenotypic correlations between the traits were in the same direction indicating that most of the phenotypic correlations were due to genotypic causes. High heritability estimates were observed for days to heading, plant height, and panicle length and intermediate heritability for days to maturity, lodging index, grain yield, panicle seed weight and shoot biomass. Moderately high values for genotypic coefficients of variability, heritability, and genetic advance estimated for grain yield, panicle seed weight and above ground plant biomass may suggest the predominance of additive gene action, and that direct selection based on these traits would be effective for improvement of tef.

**Key words:** association, *Eragrostis tef*, genetic variation, grain yield, tef

### INTRODUCTION

Tef (*Eragrostis tef*) is a crop with great adaptative potential in different agro-ecologies in Ethiopia. It is a very important crop in the country, especially in areas of unpredictable and unreliable rainfall. In areas which have only a brief rainy season with erratic distribution and drought spells, growers can obtain a harvest mainly because this crop has advantages in aspects such as drought tolerance, poor or degraded soils, frost tolerance in the early period of development, etc<sup>[9]</sup>. The average yield of tef is about 900 kg/ha but it varies from 500 to 2700 kg/ha. Despite considerable genetic progress made for agronomic traits in tef, a variety resistant to lodging has not been developed so far.

It is important that breeders understand the amount of variation, correlation and inheritance of important agronomic traits. Grain yield is a highly complex trait. It can be divided into component characters, like the number of fertile tillers, size and form of panicles, number of florets per panicle, and seed weight. Studies in tef have shown that the number of tillers per plant, panicle weight, and shoot biomass are an important determinant of yield<sup>[11, 4, 5]</sup>. In addition, grain yield is influenced directly or indirectly by a number of agronomic characters, such as plant height, leaf area,

dry-matter yield, heading date, lodging resistance and proneness to shattering<sup>[7]</sup>. Therefore, it is imperative in the improvement of grain yield traits of tef to have a clear understanding of the relationships between grain yield and other agronomic characters.

The objective of present investigation was to provide information for the improvement of grain yield and related traits in tef by obtaining estimates of the amount of genetic variation, simple correlation coefficients among traits and heritability for grain yield and other agronomically important traits. To accomplish the objective, 18 tef genotypes were grown and evaluated at Debre Zeit and Melkassa Research Centers, Ethiopia.

### MATERIALS AND METHODS

**Plant Material:** The materials used comprised of 18 genotypes of which some are varieties, germplasm lines and accessions, and some farmer's cultivars.

**Field Trials:** The 18 genotypes were evaluated in the field at Debre Zeit (8° 44' N, 38° 58' E, ca. 1860 m.a.s.l.) and Melkassa (8° 33' N, 39° 17' E, ca. 1620 m.a.s.l.) Agricultural Research Centers of the Ethiopian Institute of Agricultural Research (EIAR), Ethiopia, in

2003 and 2004. The experimental design was a randomized complete block with four replications. Plots were spaced 50 cm apart and consisted four rows of 2 m long each with 20 cm of row spacing. Seeding rate was 1.2 g row<sup>-1</sup>. At the early tillering stage stands were thinned to 5 cm intra-row spacing. All other stand establishment and cultural management operations were in accordance with the recommendations for each particular test site.

The following traits were evaluated. (1) Days to heading: number of days from planting until 50% of the plants in the plots headed. (2) Days to maturity: number of days from planting to the day when 50% of the plants in the plot reached physiological maturity. (3) Shoot biomass: total above ground biomass for the entire plot. (4) Grain yield: the weight of the seed harvested from each plot. (5) 100 seed weight: the weight of 100 seeds. (6) Individual plant above ground biomass: the average weight of above ground biomass of ten pre-tagged plants in each plot. (7) Plant seed weight: the average weight of the seeds from ten pre-tagged plants. (8) Panicle seed weight: the average weight of the seeds harvested from the primary panicle of ten pre-tagged plants. (9) Plant height: the average height of ten pre-tagged plants. (10) Panicle length: the average length from the base of the panicle to the tip. (11) Lodging index: assessed as per the procedure of<sup>[3]</sup>.

**Data Analysis:** Kurtosis analysis and means were calculated for all traits. Variance analyses were performed using GenStat software<sup>[14]</sup>. After testing the homogeneity of the error variance of the individual locations, combined analysis of variance over the two locations and years was performed as per the formula given by<sup>[6]</sup>. Correlations were calculated based on the means across locations and years. Genotypic and phenotypic correlations between pairs of traits were calculated using the method of<sup>[10]</sup>.

**Results:** The mean square values from the combined analysis of variance are given in Table 1. Highly significant ( $P \leq 0.01$ ) and significant ( $p \leq 0.05$ ) differences among the genotypes were observed for all traits except 100 seed weight. Location effects were also significant for all traits except panicle seed weight and panicle length. However, for genotype x location interaction, significant differences were observed for days to heading, days to maturity, shoot biomass, grain yield, above ground plant biomass, lodging index, harvest index and plant seed weight.

Mean values, coefficients of variability and heritability (%) are presented in Table 2. Panicle seed weight showed the maximum GCV followed by above ground plant biomass and plant seed weight. Grain yield and harvest index showed intermediate GCV values. Whereas, GCV values of lodging index, panicle

length, plant height, days to heading and days to maturity were smaller. However, there was no genotypic variability for 100 seed weight.

GCV (Table 2) was higher than PCV for shoot biomass, harvest index, above ground plant biomass, and panicle seed weight. The differences between GCV and PCV for all traits, except above ground plant biomass and panicle seed weight was small. Relatively, a wide range of GCV was observed for plant weight and panicle seed weight.

Across the traits studied, the PCV ranged from 10.52% for days to maturity to 50.99% for plant seed weight. The PCV values were relatively high (> 25%) for grain yield and panicle seed weight. In contrast, shoot biomass, above ground plant biomass, lodging index, panicle length, harvest index, plant height, days to heading and maturity showed comparatively low PCV values.

Broad sense heritability value was highest (78.3%) for days to heading followed by plant height (72.4%) and panicle length (71.7%). Days to maturity, shoot biomass, grain yield, panicle seed weight and lodging index showed moderate H values. The expected GA, expressed as a percentage of the mean, ranged from 4.8% for days to maturity to 47.85% for panicle seed weight (Table 2). The phenological traits, days to heading and days to maturity and the developmental characters, plant height and panicle length had relatively low GA values. The highest expected GA was observed for panicle seed weight (47.85%), above ground plant biomass (33.85%) and grain yield (31.26%). The remaining six traits (*i.e.*, plant seed weight, shoot biomass, harvest index, lodging index and panicle length) showed genetic advance values between 15 and 26%.

The phenotypic and genotypic coefficients of correlation are summarized in Tables 3 and 4, respectively. At the phenotypic level, grain yield showed a relatively strong positive correlation with harvest index ( $r = 0.606$ ) and plant seed weight ( $r = 0.596$ ). In addition, shoot biomass, days to maturity, plant height, above ground plant biomass, 100 seed weight and panicle length showed positive correlations with grain yield. Lodging index was the only trait which showed a negative but non-significant correlation with yield.

At the genotypic level, grain yield was positively and significantly correlated with plant seed weight, shoot biomass, 100 seed weight, panicle length, harvest index, plant height, panicle seed weight and above ground plant biomass. Lodging index had a negative and significant correlation with grain yield.

Correlations among other traits: Among grain yield component traits, strong positive phenotypic correlations were observed between above ground plant

**Table 1:** Mean square values from combined analysis of variance of 18 genotypes of tef grown at two locations

Trait	Location df <sup>1</sup> =1	Genotypes df <sup>1</sup> =17	Genotype x Location df <sup>1</sup> =17	Location x Year x Genotype df <sup>1</sup> =34	Error df <sup>1</sup> =203
Days to heading	381.28**	322.22**	32.69**	39.85**	5.44
Days to maturity	5656.06**	713.18**	441.58**	67.62**	12.19
Shoot biomass	2759431.5*	496367.0*	141103.0*	86752.0*	44109.0
Grain yield	879157.0*	43010.0*	17646.0*	10984.0*	2919.0
100 Seed weight	0.019*	0.0001ns	0.0007ns	0.0001ns	0.0001
Above ground plant biomass	7333.6**	26.21**	18.64*	8.44ns	8.55
Plant seed weight	37.31*	2.49*	1.58*	-	0.52
Panicle seed weight	0.44ns	0.52**	0.11ns	0.16*	0.09
Plant height	786.06*	2376.34**	65.05ns	96.82ns	54.58
Panicle length	115.39ns	587.71**	19.91ns	22.83*	14.24
Lodging index	6431.67**	901.94**	96.79*	110.87*	47.18
Harvest index	0.12*	0.01**	0.006*	0.005*	0.003

<sup>1</sup>df = degree of freedom; \*, \*\* = significant at  $p \leq 0.05$  and  $0.01$ , respectively.

**Table 2:** Mean values, coefficients of variation and heritability for grain yield and yield components in the 18 tef genotypes

Traits	Mean $\pm$ se	PCV (%)	GCV (%)	$h^2$ (%)	GA (% of mean)
Days to heading	38.38 $\pm$ 1.2	13.22	6.1	78.3	9.75
Days to maturity	83.71 $\pm$ 2.6	10.52	4.17	56.3	4.80
Shoot biomass	882.78 $\pm$ 95.9	22.56	23.79	45.4	22.02
Grain yield	181.16 $\pm$ 22.7	36.76	29.82	50.5	31.26
100 Seed weight	0.04 $\pm$ 0.01	-	-	-	-
Above ground plant biomass	6.92 $\pm$ 0.4	18.95	42.25	39.3	33.88
Plant seed weight	1.99 $\pm$ 0.08	50.99	34.81	34.5	25.33
Panicle seed weight	0.58 $\pm$ 0.1	29.86	54.52	45.2	47.85
Plant height	81.12 $\pm$ 6.7	15.15	9.11	72.4	13.56
Panicle length	36.23 $\pm$ 3.1	16.85	10.42	71.7	15.35
Lodging index	44.75 $\pm$ 3.9	17.94	15.35	55.2	17.36
Harvest index	0.212 $\pm$ 0.02	16.34	25.83	37.3	19.65

biomass and plant height, above ground plant biomass and panicle length, and above ground plant biomass and plant seed weight. Whereas, at the genotypic level, strong and positive correlations were observed between panicle length and plant height ( $r = 0.952$ ), above ground plant biomass and panicle length ( $r = 0.934$ ), shoot biomass and plant seed weight ( $r = 0.917$ ), above ground plant biomass and panicle seed weight ( $r = 0.924$ ), above ground plant biomass and plant height ( $r = 0.917$ ), plant height and shoot biomass ( $r = 0.913$ ), and 100 seed weight and panicle seed weight ( $r = 0.901$ ). The correlation between shoot biomass and 100 seed weight, shoot biomass and above ground plant

biomass, shoot biomass and panicle length, panicle seed weight and plant height, panicle length and panicle seed weight, and harvest index and panicle seed weight were also positive and significant (Table 4). In addition, days to heading and maturity had also positive and significant correlations with all traits except plant seed weight. However, lodging index showed a negative significant correlation with all traits except harvest index and plant seed weight.

**Discussion:** Highly significant differences were observed among genotypes for most of the traits examined. Coefficients of phenotypic and genotypic

**Table 3:** Estimates of phenotypic correlation coefficients among different traits of 18 tef genotypes.

	Dm	Sb	Gy	Sw	Pb	Psw	Pnsw	Ph	Pnl	Li	Hi
Dh	0.597**	-0.359*	0.092ns	0.337*	0.347*	-0.105ns	0.151*	0.443**	0.496**	-0.478**	0.077ns
Dm	-	0.209*	0.229*	0.325*	0.175*	0.025ns	0.169*	0.323*	0.238*	-0.272*	0.038ns
Sb		-	0.467**	0.354*	0.402**	0.465**	-0.068ns	0.468**	0.295*	-0.209*	-0.195*
Gy			-	0.307*	0.302*	0.596**	0.015ns	0.390*	0.185*	0.111ns	0.606**
Sw				-	0.512**	0.311*	0.293*	0.526**	0.379*	-0.214*	0.107ns
Pb					-	0.710*	0.302*	0.888**	0.745**	-0.442**	-0.014ns
Psw						-	0.368*	0.057ns	0.141ns	-0.004ns	0.560**
Pnsw							-	0.123ns	0.205*	-0.094ns	0.121*
Ph								-	0.742**	-0.464**	-0.021ns
Pnl									-	-0.581**	-0.054ns
Li										-	0.066ns
Hi											-

\*, \*\* significantly different at 5% and 1% probability levels, respectively. Dh: days to heading; Dm: days to maturity; Sb: shoot biomass; Gy: grain yield; Sw: 100 seed weight; Pb: individual plant above ground biomass; Psw: plant seed weight; Pnsw: panicle seed weight; Ph: plant height; Pnl: panicle length; Li: lodging index; Hi: harvest index.

**Table 4:** Estimates of genotypic correlation coefficients among different traits of 18 tef genotypes

	Dm	Sb	Gy	Sw	Pb	Psw	Pnsw	Ph	Pnl	Li	Hi
Dh	0.739**	0.721**	0.117ns	0.504*	0.632*	-0.113ns	0.744**	0.706**	0.875**	-0.724**	0.168*
Dm	-	0.563*	0.284*	0.765**	0.724**	0.014ns	0.867**	0.824**	0.822**	-0.721**	0.120ns
Sb		-	0.866**	0.841**	0.843**	0.917**	0.531*	0.915**	0.861**	-0.662**	-0.123ns
Gy			-	0.774**	0.388*	0.939**	0.422*	0.475*	0.662**	-0.615*	0.580*
Sw				-	0.750**	0.099ns	0.901**	0.823**	0.678**	-0.431*	0.348*
Pb					-	0.466*	0.924**	0.913**	0.934**	-0.850**	-0.514*
Psw						-	0.246*	0.0114ns	0.116ns	-0.051ns	0.915**
Pnsw							-	0.814**	0.844**	-0.786**	0.788**
Ph								-	0.952**	-0.790**	-0.499*
Pnl									-	-0.774**	0.155ns
Li										-	0.108ns
Hi											-

\*, \*\* significantly different at 5% and 1% probability level, respectively. Dh: days to heading; Dm: days to maturity; Sb: shoot biomass; Gy: grain yield; Sw: 100 seed weight; Pb: individual plant above ground biomass; Psw: plant seed weight; Pnsw: panicle seed weight; Ph: plant height; Pnl: panicle length; Li: lodging index; Hi: harvest index.

variation suggest that there is a good scope for yield improvement through selection for above ground plant biomass and panicle seed weight.

When correlations between yield component characters were taken into account, most of the values between various character pairs were significant and positive. However, lodging index was negatively correlated with harvest index, shoot biomass, above ground plant biomass, plant height and panicle length. Plant seed weight and shoot biomass appeared to

contribute substantially to grain yield at the genotypic level, as the strongest correlation of grain yield was with these traits. The strong correlation of plant seed weight and shoot biomass with grain yield has previously been reported in tef<sup>[8,13]</sup>.

The values for genotypic and phenotypic correlations between the traits were in the same direction. The level of significance for these two types was also similar. This indicates that most of the phenotypic correlations were due to genotypic causes.

However, genotypic correlations were comparable to the respective phenotypic correlations in this study using tef germplasms unlike the RIL populations where phenotypic correlations showed higher values than genotypic<sup>[5]</sup>. This could be because of linkage disequilibrium. This is in congruence with previous study of<sup>[2]</sup>.

The high H estimates observed in this study for days to heading, plant height, and panicle length and intermediate H for days to maturity, lodging index, grain yield, panicle seed weight and shoot biomass suggest the possibility of improving tef genotypes through selection. Relatively high H estimates for heading date and panicle length have also been reported in tef<sup>[1, 12]</sup>. In general, the moderately high values for GCV, H, and GA% estimated for grain yield, panicle seed weight and above ground plant biomass may suggest the predominance of additive gene action, and that direct selection based on these traits would be effective for improvement of tef.

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