

## Genetic Variability, Heritability and Trait Relationships in Recombinant Inbred Lines of Tef [*Eragrostis Tef* (Zucc.) Trotter]

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**Abstract:** Characterization of genetic variability in a population is pertinent as genetic diversity within population and within species determines the extent of improvement achieved through crop improvement methods. One hundred ninety six F<sub>8</sub> recombinant inbred lines (RILs) of tef, developed by single-seed descent method from a cross between two tef varieties DZ-01-196 and DZ-01-2356, were evaluated to assess genetic variation, broad sense heritability, genetic advance and trait relationships for grain yield and yield related traits. The RIL population was evaluated for 11 traits at two locations, Melkassa and Debre Zeit, Ethiopia, during 2003 and 2004. Highly significant and significant variations were obtained among the RILs except for seed weight. The highest values for phenotypic coefficient of variation (PCV) was observed for above ground plant biomass, grain yield, shoot biomass, and harvest index. The genotypic coefficient of variation (GCV) estimates was higher for grain yield, above ground plant biomass and panicle seed weight. Days to heading, panicle length, above ground plant biomass and panicle seed weight showed a relatively high broad-sense heritability values. High expected genetic advance were observed for above ground plant biomass, panicle seed weight and grain yield. Strong positive associations were observed between panicle length and plant height, shoot biomass and above ground plant biomass and days to maturity and panicle length. The present study showed the presence of genetic variability for important agronomic traits suggesting the possibility of improving tef through direct selection for the primary grain yield related traits. These observations have implications in tef improvement.

**Key words:** *eragrostis tef*, genetic variability, heritability, tef, trait relationship

### INTRODUCTION

The genus *Eragrostis* consists of about 350 species <sup>[12]</sup> of which *Eragrostis tef* is the only cereal crop grown in Ethiopia where it is ground into flour, fermented and then made into *injera*. Tef is an allotetraploid ( $2n = 4x = 40$ ) C<sub>4</sub> cereal plant <sup>[18]</sup>. Effective selection to develop better varieties is dependent on the existence of genetic variability. The characterization of this variability in a population is pertinent since genetic diversity within population and within species determines the rates of adaptive evolution and the extent of response in crop improvement. Dissimilarity will always exist among individuals in a population and assessing the origin and magnitude of variability is the key to success in a crop improvement program <sup>[23,32]</sup>. Genetic variability studies, conducted to investigate diversity for various traits in tef showed the existence of wide trait diversity <sup>[22,11,20,30,21,1,2]</sup> among the tef germplasm lines. This is

indicative of the potential existing for the genetic improvement of the crop through selection <sup>[30]</sup>. Attempts have also been made to measure diversity in tef using amplified fragment length polymorphism (AFLP) <sup>[4,5]</sup> and random amplified polymorphic DNA (RAPD) <sup>[6]</sup>.

In tef, several studies have estimated heritabilities in both the broad sense and narrow sense levels <sup>[30,29,27,15,2,26]</sup>. The large broad sense heritability values for important traits in tef indicates the relative ease with which selection can be made based on phenotype, but their practical value in breeding is further enhanced if accompanied by high genetic advance estimates <sup>[17]</sup>. However, all these above stated studies have been conducted using tef cultivars or germplasm. There is limited report yet using recombinant inbred lines (RILs) of tef. The present study is therefore, aimed at assessing genetic variation, broad sense heritability, expected genetic advance and trait relationships for grain yield and yield related traits in the RILs of tef.

## MATERIALS AND METHODS

**Plant material:** The materials used in the present study comprised of 196  $F_8$  RIL populations of an intra-specific cross of two released varieties, namely, DZ-01-196 x DZ-01-2356. Both parental varieties have been developed through selection from germplasm accessions. DZ-01-196 was developed by mass selection from a landrace cultivar called *Magna*. It has very white seed color, large kernels, fairly loose type of panicle with branches arranged multilaterally, deep red anthers and lemmas are variegated (yellowish white with red tips and margins). On the other hand, DZ-01-2356 has yellowish white lemma color, very loose panicle type and white seed color. The cross was made at Debre Zeit Agricultural Research Center and  $F_2$  plants were selfed and subsequent generations were advanced by single-seed descent method.

**Field experiment and data analysis:** The RILs and their parents were evaluated in field experiments 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) in Ethiopia during the 2003 and 2004 main cropping seasons. The experimental design was a simple lattice with two replications. Each experimental unit was a plot of 2 m length and 0.5 m width, having two rows of 2 m length with row spacing of 20 cm. Based on the recommended seeding rate of 30 kg/ha 1.2 g of seeds was broadcasted along the surface of each row. At the early tillering stage, stands were thinned to 5 cm intra-row spacing. All other stand establishment and cultural management operations were done as per recommended package of practices for each particular test site.

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

index as the ratio of grain yield to shoot biomass sampled from the entire plot.

For all traits, kurtosis analysis and means were calculated. Variance analyses were performed using GenStat software<sup>[31]</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<sup>[13]</sup>. Correlations between traits were calculated using variances and covariances<sup>[25]</sup>. Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were calculated following Burton's<sup>[8]</sup> method. Broad-sense heritability ( $h^2$ ) was calculated as the ratio of the genotypic variance to the phenotypic variance<sup>[24]</sup>. Genetic advance as percentage of the mean was also estimated.

## RESULTS AND DISCUSSION

Combined analysis of variance showed significant differences among genotypes for all traits studied except seed weight and panicle seed weight (Table 1), suggesting that these traits could be genetically manipulated in order to improve the yield of tef. These results are in congruence with previous studies<sup>[14,29]</sup>. However, location effects were not significant for seed weight, above ground plant biomass and plant height. Significant genotype by environment interactions was observed for days to heading, days to maturity, grain yield and above ground plant biomass. Similar results were also reported by earlier investigators<sup>[1,28,29]</sup>. However, plant height and panicle length did not show significant interaction. Genotype by environment interaction has also been reported for grain yield and shoot biomass per plant in tef germplasm lines<sup>[3]</sup>. Significant genotype by environment interaction indicates that lines did not perform consistently, relative to each other, over the environments, thus indicating the importance of testing the RILs in time and space.

The PCV and GCV values for the combined analysis for two locations are presented in Table 2. The PCV and GCV are useful for comparing the relative amount of phenotypic and genotypic variation among different traits. The PCV showed large variations for most of the traits studied. This is in agreement with the findings reported in earlier studies in tef<sup>[30, 21, 1, 19]</sup>. The GCV in all experiments was not close to the PCV, indicating high environmental effects in estimating these traits. However, grain yield, shoot biomass and above ground plant biomass showed a relatively high GCV and moderate genetic advance indicating their amenability for improvement. Earlier studies<sup>[30, 1, 3]</sup> also reported a relatively high GCV for grain yield. On the other hand, plant height, days to maturity and harvest

**Table 1:** Mean square values from combined analysis of variance of 196 RILs of the cross DZ-01-196 x DZ-01-2356

Trait	Location df <sup>1</sup> = 1	RIL df <sup>1</sup> = 195	RIL x Locations df <sup>1</sup> = 195	Location x Year df <sup>1</sup> = 1	Location x Year x RILdf <sup>1</sup> =195	Error df <sup>1</sup> =780
Days to heading	13659.62**	38.55**	13.54**	24849.32**	11.31**	8.45
Days to maturity	482828.59**	51.76**	52.46**	53686.11**	27.24**	16.82
Shoot biomass (g)	12294538**	55374**	31908**	3322949ns	25077ns	22194
Grain yield (g)	1624679*	3713**	2768**	686546*	2056**	1579
Seed weight (mg)	0.09ns	0.001ns	0.002ns	0.072ns	0.0001ns	0.0001
Individual plant above ground biomass (g)	65090.25*	16.84**	14.67**	299.01ns	7.71ns	7.67
Panicle seed weight (g)	7.08*	0.078**	0.015ns	7.51*	0.019ns	0.017
Plant height (cm)	765.66ns	140.15**	43.01ns	27070.95*	46.55ns	45.06
Panicle length (cm)	2762.10*	48.64**	10.84ns	2577.23*	11.95ns	11.41
Lodging index	62850.60*	212.55**	126.72**	165918.56**	116.47**	84.65
Harvest index	3.22**	0.004**	0.004**	0.32*	0.003*	0.002

<sup>1</sup>df = degree of freedom; \*, \*\* = significant at  $p \leq 0.05$  and  $0.01$ , respectively; ns = not significant.

**Table 2:** Mean values, estimates of PCV and GCV, h<sup>2</sup> and GA (% of mean) for grain yield and yield related traits in 196 RILs from a combined data analysis

Traits	Mean $\pm$ se	PCV (%)	GCV (%)	h <sup>2</sup> (%)	GA (% of mean)
Days to heading	33.84 $\pm$ 1.67	10.804	6.515	35.3	4.4
Days to maturity	78.91 $\pm$ 3.37	6.735	4.295	24.9	1.89
Shoot biomass (g)	618.8 $\pm$ 137.67	27.174	12.604	17.8	6.24
Grain yield (g)	120.6 $\pm$ 25.59	38.123	19.169	23.2	11.13
Seed weight (mg)	0.035 $\pm$ 0.003	-	-	-	-
Individual plant above ground biomass (g)	8.027 $\pm$ 2.47	38.806	17.745	32.4	16.32
Panicle seed weight (g)	0.507 $\pm$ 0.10	31.186	17.641	30.5	11.83
Plant height (cm)	73.72 $\pm$ 5.74	10.246	4.819	23.4	3.11
Panicle length (cm)	32.534 $\pm$ 3.11	12.343	7.033	33.2	5.01
Lodging index	54.58 $\pm$ 7.77	19.555	9.919	19.2	3.16
Harvest index	0.212 $\pm$ 0.02	25.836	6.671	21.2	4.72

**Table 3:** Estimates of phenotypic (above diagonal) and genotypic (below diagonal) correlation coefficients among 11 traits of 196 RILs of tef grown at two locations

Traits <sup>a</sup>	Dh	Dm	Sb	Gy	Sw	Pb	Pnsw	Ph	Pnl	Li	Hi
Dh	-	0.163*	0.226*	0.316*	-0.014ns	0.189*	0.225*	0.177*	0.159*	-0.319*	0.064ns
Dm	-0.159*	-	-0.068ns	-0.134*	0.025ns	-0.098ns	0.042ns	-0.043ns	-0.044ns	0.078ns	-0.131*
Sb	-0.129ns	0.681**	-	0.658**	-0.078ns	0.469*	0.184*	0.255*	0.268*	-0.329*	0.025ns
Gy	0.137*	0.003ns	0.526**	-	-0.107ns	0.629**	0.394*	0.250*	0.214*	-0.161ns	0.724**
Sw	0.011ns	0.051ns	0.018ns	0.016ns	-	-0.054ns	0.045ns	-0.011ns	-0.062ns	0.032ns	-0.060ns
Pb	-0.187*	0.813**	0.844**	0.285*	0.051ns	-	0.446*	0.233*	0.329*	-0.158*	0.323*
Pnsw	0.280*	0.603**	-0.329*	0.182*	-0.012ns	0.423*	-	0.239*	0.359*	-0.144*	0.204*

Table 3: Continue

Ph	0.145*	-0.486**	-0.147*	0.227*	-0.003ns	-0.285*	0.640**	-	0.839**	-0.028ns	0.098ns
Pnl	0.168*	-0.419*	-0.151*	0.207*	0.019ns	-0.258*	0.616**	0.844**	-	0.018ns	0.111ns
Li	-0.355*	0.588**	0.476**	0.178*	0.069ns	0.574**	-0.471**	-0.358*	-0.303*	-	-0.013ns
Hi	0.226*	-0.772**	-0.582**	0.307*	-0.020ns	-0.664**	0.527**	0.362	0.334*	-0.451**	-

\*, \*\* significantly different at  $P \leq 0.05$  and  $0.01$ , respectively; ns = not significant. <sup>a</sup>Dh: days to heading; Dm: days to maturity; Sb: shoot biomass; Gy: grain yield; Sw: 100 seed weight; Pb: individual plant above ground biomass; Pnsw: panicle seed weight; Ph: plant height; Pnl: panicle length; Li: lodging index; Hi: harvest index.

index showed low GCV suggesting the difficulty of manipulating these traits through selection. Seed weight consistently had GCV estimates of zero across all environments (data not shown). Hence, the study showed that it was not worthwhile to consider seed weight as a trait for indirect selection in tef.

In the present study days to heading, panicle length, above ground plant biomass and panicle seed weight exhibited relatively higher broad sense heritability values (Table 2). The estimate of expected genetic advance, which evaluates the expected rate of genetic gain under selection, was inconsistent among traits and in some cases it was zero or close to zero, suggesting the lack of additive genetic variance. However, high expected genetic advance estimates were obtained for above ground plant biomass, panicle seed weight and grain yield. The low heritability and genetic advance estimates for lodging index suggested that breeding for lodging resistance in tef would be a demanding task. Previous studies have reported low heritability estimates for traits such as culm diameter of the first and second internodes<sup>[28]</sup> and lodging index<sup>[26]</sup>. However, high genetic advance and heritability have been reported for shoot biomass, grain yield per plant<sup>[7]</sup>, panicle length and plant height<sup>[28,29]</sup>.

The intermediate to high estimates of heritability with less fluctuation across environments and relatively high estimates of genetic advance (as percent of mean) observed in the present study for grain yield and yield related traits suggested the possibility of improving tef through direct selection for the primary grain yield related traits. However, among the primary components of grain yield, panicle length showed relatively lower estimates for genetic coefficient of variation. This would indicate that improvement of the trait through selection may not be effective in this population, due to non-genetic sources of variation. Heritability values for days to maturity and culm length fluctuated across environments (data not shown) suggesting that the use of these traits should depend on environmental conditions at the selection site.

The phenotypic correlations, estimated from the combined analysis, showed strong positive association of grain yield with harvest index ( $r = 0.724$ ), shoot biomass ( $r = 0.658$ ) and above ground plant biomass ( $r$

$= 0.629$ ). Among the yield component traits, correlation between plant height and panicle length was the strongest (Table 3). The correlation coefficients between seed weight and all other traits studied were very weak or absent. At the genotypic level grain yield had appreciable positive correlations with shoot biomass, harvest index and above ground plant biomass. In this study, both at the phenotypic and genetic levels, grain yield was positively correlated with shoot biomass, above ground plant biomass, plant height, and panicle length, suggesting that vigorous and tall plants were high yielding and could serve as indicator of high yielding ability. Moreover, the correlations between most of the grain yield related traits were also positive indicating a common genetic/physiological basis in these traits. In addition, grain yield showed strong positive correlation with harvest index which is obviously due to importance of harvest index in determining yield. However, seed weight did not show any appreciable correlation with any of the traits studied indicating that this trait should not be considered as a selection criterion in this population and related germplasm of tef.

The positive correlation of lodging index with grain yield, though not strong, indicated that high yielding plants tend to lodge because of failure to bear the heavy panicles. Previous studies<sup>[22, 16, 28, 29]</sup> also reported positive association between grain yield and lodging index. However, negligible negative association between lodging index and grain yield has been observed in RIL population derived from the interspecific cross between *E. tef* (DZ-01-2785) and *E. pilosa* (Acc. 30-5)<sup>[10]</sup>.

The positive correlations observed between shoot biomass and above ground plant biomass, and plant height and panicle length, were plausibly due to the fact that the increasing level of one trait increases the other corresponding traits. This suggests a common physiological basis among these traits. Hence, simultaneous improvement of these characters would be possible. On the other hand, positive association of days to heading with shoot and above ground plant biomass revealed that long duration plants were more vigorous. In conclusion, the present study showed the presence of genetic variability and high estimates of

broad sense heritability and genetic advance for important agronomic traits suggesting the possibility of improving tef through direct selection for the primary grain yield related traits.

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