

## Genetic Divergence, Trait Association and Path Analysis of TEF (*Eragrostis tef* (Zucc.) Trotter) Lines

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**Abstract:** The study was conducted with the objective to determine genetic divergence, association among various economic traits and their direct and indirect effects in tef (*eragrostis tef* (zucc.) trotter) lines. Forty nine tef lines were evaluated for 16 traits in simple lattice design of 7 X 7 with two replications at two locations. Estimating genetic similarity and dissimilarity between lines is an essential point for clustering and analyzing inter and intra population diversity. Based on the D<sup>2</sup>-value lines were grouped into five clusters indicating that the tested lines were divergent. Distribution of the lines showed that twenty one lines in cluster I (42.86%), six lines in cluster II (12.25%), four lines in cluster III (8.16%), sixteen lines in cluster IV (32.65%) and two lines in cluster V (4.08%). Combined over locations, genotypic and phenotypic correlations were partitioned into direct and indirect effects using grain yield as a dependent variable. Grain yield showed positive and significant phenotypic correlation with number of productive tillers, grain yield per main panicle, shoot biomass, harvest index, thousand kernel weight and grain yield per plant at phenotypic level at both locations. Genotypic path coefficient analysis combined over the two locations revealed that thousand kernel weight and grain yield per plant had the highest direct effects (0.393 and 0.307, respectively) and positive significant correlation coefficient with grain yield.

**Key words:** Genetic divergence • Trait association • Path analysis • Tef

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### INTRODUCTION

Tef (*Eragrostis tef* (Zucc.) Trotter) is a C4 and annual cereal crop cultivated widely in Ethiopia [1] and it has a great adaptive potential in different agro-ecologies especially in areas where rain fall distribution difficult to predict and reliability in question in some places of Ethiopia where tef frequently cultivated by farmers [2].

In Ethiopia, tef can be grown from low to high altitude, indicating that the crop has great flexibility and plasticity in growing over a wide range of agronomic and edaphic conditions and under various rainfalls, temperature and soil regimes. This cereal crop takes 25-81 days to emerge the panicle tip, 60-140 days to mature and 29-76 days for the reproductive phase or grain filling period from panicle emergence to maturity [3].

With regard to the potentiality of the crop, it is now getting increasing importance in face of producers as high source of income comparably with other cereal crop for producers. Interests for the product of tef are getting higher around the world for many reasons. For instance, it contains little or no gluten which is found in wheat and thus individuals with severe allergies to wheat gluten are among those buying it these days. Tef is easy to include in porridge, pancakes, biscuits, cookies, cakes, soups, stews and puddings [4].

Breeding for improved tef is a continuous process and requires exhausting efforts by breeders. Availability of genetic variability is fundamental for any breeding program, which provides an opportunity for selection of desirable lines. The main purpose of this study was to determine genetic divergence, association among various

economic traits and their direct and indirect effects which provide the base information for selection and creating variability.

**MATERIALS AND METHODS**

The study was conducted at two locations, Sinana and Adaba, south east of Ethiopia. Simple Lattice Design of 7x7 with two replications and spacing of 1 m between plots, 1.5 m between blocks were used. The seeds were sown on 2 m x 2 m plot area in accordance with the recommended seeding rate of 30 kg/ha and fertilizer rate of 60 kg/ha N and P<sub>2</sub>O<sub>5</sub>, respectively. Agronomic data were collected on plant and plot basis for sixteen agronomic traits. The mean data of both locations combined were subjected to correlation and cluster analysis using statistical software packages of SAS and SPSS.

Clustering lines for genetic divergence analysis among the lines were estimated by equation of Mahalanobis [5]. The analysis was based on all yield contributing characters influencing yield. The generalized distance between any two set of population is defined as  $D^2 = (\text{means } X_i - \text{means } X_j) S^{-1} (X_i - X_j)$ . Phenotypic correlation which includes both genotypic and environmental effects and genotypic correlation were estimated using the standard procedure suggested by Miller *et al* [6],

$$rp_{xy} = \frac{COVP_{xy}}{\sqrt{\sigma^2 p_x \sigma^2 p_y}}$$

Path coefficient analysis was carried out using phenotypic and genotypic correlation coefficients to know the direct and indirect contribution of all the characters on seed yield [7],

$$r_{ij} = p_{ij} + \sum r_{ik} p_{kj}$$

To determine P<sub>ij</sub> values, square matrices of the correlation coefficients between independent characters in all possible pairs inverted and then multiplied by the correlation coefficient between the independent and dependent characters using statistical program (SAS).

**RESULTS AND DISCUSSIONS**

**Cluster Analysis:** The number of clusters indicates that tested lines were divergent. Distribution of the genotypes showed that twenty genotypes in cluster I (42.86%), six genotypes in cluster II (12.25%), four genotypes in cluster III (8.16%), sixteen genotypes in cluster IV (32.65%) and two genotypes in cluster V (4.08%) as shown in Table 1.

Highest intra-cluster distance was observed in cluster V (7.78) followed by cluster III (5.59) (Table 2). Maximum inter cluster distance was observed between cluster III and IV (138.78) followed by IV and V (117.02), III and V (100.68). The lowest inter cluster distance was observed between cluster I and II (25.82). The genetic improvement through hybridization and selection depends on the extent of genetic diversity between parents. Crossing for desirable traits can be successful between clusters with the highest and the lowest divergent cluster.

Highest panicle length (30.46 cm), culm length (41.34 cm), plant height (71.80 cm), productive tiller (7.00), harvest index (21.33%), grain yield per main panicle (1.06 g), above ground shoot biomass (1.55 kg), thousand kernel weight (0.38 g), grain yield per plant (9.39 g), grain yield per hectare (2145.84 kg) were in cluster V while the lowest panicle length (24.91 cm), plant height (64.58cm),

Table 1: distribution of genotypes into five clusters for 49 tef lines tested at Sinana and Adaba, 2008

Genotypes											
Cluster	G1	G11	G12	G17	G18	G21	G25	G26	G27	G28	G30
I	G32	G34	G35	G36	G41	G44	G46	G47	G48	G49	
II	G2	G5	G6	G14	G37	G40					
III	G3	G4	G9	G10							
IV	G13	G15	G16	G19	G20	G22	G23	G24	G29		
	G31	G33	G38	G39	G42	G43	G45				
V	G7	G8									

G = genotype

Table 2: Generalized squared distance within (bold face) and to clusters of 49 genotypes into five clusters

Clusters	I	II	III	IV	V
I	0.67	25.82ns	35.58**	58.36**	51.45**
II		3.89	30.47*	81.21**	95.04**
III			5.59	138.78**	100.68**
IV				5.59	117.02**
V					7.78

Where, ns = non significant, \* = significant, \*\* = highly significant

Table 3: Combined over location phenotypic (rp) below and genotypic (rg) above diagonal correlation coefficient of the sixteen traits in 49 tef lines, 2008

Traits	DPE	DM	PL	CL	PH	NN	PTLN	HI	GPA	LOD	SBM	GP	NPB	TKW	Gypl	Gyha
DPE		0.36**	-0.04	-0.049	-0.05	0.2	-0.33**	-0.34**	-0.35*	0.006	-0.13*	-0.72**	0.02	-0.37**	-0.31	-0.29
DM	0.66**		-0.1	0.11	0.04	0.07	0.04	-0.33*	-0.08	-0.31*	0.008	-0.72	0.13	-0.09	0.03	-0.01
PL	0.54**	0.69**		-0.1	0.70**	0.35*	-0.07	0.04	-0.02	0.01	0.49**	0.07	0.43**	0.12	-0.02	0.02
CL	-0.56**	-0.65**	-0.57**		0.89**	0.08	0.04	-0.15	0.03	-0.06	0.54**	0.23	0.22	0.11	0.02	-0.03
PH	-0.26**	-0.26**	0.07	0.77**		0.22	-0.002	-0.09	0.01	-0.04	0.63**	0.14	0.37**	0.14	0.005	-0.01
NN	.41**	0.45**	0.54**	-0.37**	-0.03		-0.03	-0.23	-0.06	-0.01	0.2	-0.05	0.09	0.008	-0.05	-0.02
PTLN	0.01	0.13	0.08	-0.08	-0.03	0.03		0.61**	0.87**	-0.01	0.28*	-0.01	-0.17	0.89**	0.96**	0.92**
HI	-0.1	-0.66**	-0.52**	0.47**	0.18	-0.44**	0.29**		0.64**	0.19	0.11	-0.08	-0.17	0.71**	0.64**	0.7
GPa	-0.58**	0.29**	0.27**	-0.27**	-0.11	0.15	0.78**	0.28*		0.01	0.31*	-0.02	-0.19	0.89**	0.89**	0.86**
LOD	0.03	0.01	0.09	-0.09	-0.04	0.05	0.01	0.01	0.06		0.17	0.04	-0.08	0.07	-0.03	-0.03
SBM	0.04	-0.63**	-0.42**	0.76**	0.59**	-0.36**	0.06	0.57**	-0.17	0.07		0.19	0.22	0.38**	0.31*	0.29*
GP	-0.53**	0.03	0.09	0.1	0.19	0.004	-0.005	-0.03	0.037	0.05	0.06		0.15	0.008	-0.04	-0.12
NPB	-0.52**	-0.32	-0.11	0.47**	0.49	-0.18	-0.1	0.27**	-0.28**	-0.13	0.49	0.12		-0.12	-0.15	-0.21
TKW	-0.29**	0.05	0.17	-0.03	0.08	0.08	0.78**	0.07	0.72**	0.09	0.13	0.006	-0.11		0.91**	0.93**
GYpl	0.14	0.4	0.35**	-0.35**	-0.15	0.24	0.88**	0.37*	0.84**	-0.01	-0.20*	-0.01	-0.27**	0.78**		0.94**
Gyph	-0.23	-0.11	-0.05	0.09	0.06	-0.04	0.83**	0.54**	0.69**	-0.04	0.26**	-0.09	-0.05	0.85**	0.74**	

Where, \*\* = highly significant, \* = significant, DPE = days to panicle emergence, DM = days to maturity, PL = panicle length (cm), CL = culm length (cm), PH = plant height (cm), NN = number of node, PTLN = productive tiller number, HI = harvest index, GPA = grain yield per main panicle (g), LOD = lodging percentage, SBM = shoot biomass (kg), GP = grain filling period, NPB = number of panicle main branch, TKW = thousand kernel weight (g), GYpl = grain yield per plant (g), Gyph = grain yield per hectare (kg).

productive tiller (2.62), harvest index (14.33%), grain yield per main panicle (0.58 g), above ground shoot biomass (1.23 kg), thousand kernel weight (0.23 g), grain yield per plant (3.95 g), grain yield per hectare (1025.86 kg) and culm length (38.41 cm), were in cluster I and II, respectively.

**Correlation among Other Traits:** Combined over location, both at genotypic and phenotypic levels, highly significant ( $P < 0.01$ ) positive correlation were observed among yield components such as thousand kernel weight with grain yield per plant, productive tiller number and harvest index (Table 3). Highly significant ( $P < 0.01$ ) positive correlation also observed harvest index with culm length, grain yield per main panicle with days to maturity, panicle length and productive tiller are some of yield related traits that observed over location at phenotypic level. Above ground shoot biomass also showed highly positive significant correlation with plant height and culm length. Similar to present findings Fufa *et al.* [8] reported positive correlation of shoot biomass with plant height, panicle length and panicle weight per plant; while, Solomon [9] reported that above ground plant biomass was strongly ( $p < 0.01$ ) correlated with traits of plant seed weight, panicle seed weight, panicle weight, panicle length and plant height.

**Phenotypic and Genotypic Correlation Coefficients:**

Combined over location, grain yield was positively and highly significantly correlated with productive tiller, harvest index, grain yield per main panicle and grain yield per plant, thousand kernel weight and shoot biomass at both phenotypic and genotypic level (Table 3). Correlation at the genetic level may arise from different factors. Correlation arising from pleiotropy expresses the extent to which two characters are influenced by the same gene, but the correlation resulting from pleiotropy is the overall or net effect of all segregating genes that affect both characters, some genes may increase both characters, while others increase one and reduce the other; the former tend to cause a positive correlation, the later a negative one [10].

**Path Coefficient Analysis:** Combined over location genotypic and phenotypic correlations were partitioned into direct and indirect effects using grain yield as a dependent was shown in Tables 4 and 5). According to Ariyo *et al.* [11]

path analysis allows identification of direct and indirect effects of association and measures the relative importance of each character.

Table 4: Combined over location phenotypic path coefficient direct (bold face) and indirect effects of five traits on grain yield at Sinana and Adaba, 2008

Traits	PTLN	GPa	HI	TKW	GYPL	r <sub>p</sub>
PTLN	-0.179	0.014	0.082	0.342	0.240	0.499
GPa	-0.140	0.018	0.079	0.316	0.229	0.502
HI	-0.111	0.005	0.286	0.162	0.101	0.443
TKW	-0.139	0.013	0.077	0.439	0.213	0.603
GYpl	-0.157	0.015	0.106	0.342	0.273	0.579

Where, PTLN = productive tiller, HI = harvest index (%), GPa = grain yield per main panicle, TKW = thousand kernel weight, GYpl = grain yield per plant, rp = phenotypic correlation.

Table 5: Estimates of direct (bold diagonal) and indirect effect (off diagonal) at genotypic level of five traits on grain yield in tef lines combined over the two locations at Sinana and Adaba, 2008

Traits	PTLN	GPa	SBM	TKW	Gypl	r <sub>g</sub>
PTLN	-0.070	0.150	0.034	0.361	0.295	0.770
GPa	-0.061	0.173	0.037	0.356	0.273	0.778
SBM	-0.200	0.054	0.122	0.149	0.095	0.220
TKW	-0.050	0.154	0.046	0.393	0.279	0.683
GYpl	-0.067	0.152	0.038	0.358	0.307	0.788

Where, PTLN = productive tiller number, SBM = shoot biomass (kg), GPa = grain yield per main panicle (g), TKW = thousand kernel weight (gm), GYpl = grain yield per plant (g), rg = genotypic correlation.

Phenotypic path coefficient analysis combined over the two locations revealed that thousand kernel weight, grain yield per plant and harvest index (%) which had positive and highly significant phenotypic correlation coefficient ( $r = 0.85$ ), ( $r = 0.74$ ) and ( $r = 0.54$ ) were high direct path coefficient (0.439), (0.273) and (0.286) combined over location respectively. Number of productive tillers showed positive correlation coefficient with grain yield (0.83) and had negative direct phenotypic path coefficient (-0.179). The rest of the traits have found to be positive direct phenotypic path coefficient. Genotypic path coefficient analysis combined over the two locations revealed that thousand kernel weight was highest direct effect (0.393) and positive and significant correlation coefficient with grain yield followed by grain yield per plant (0.307).

### CONCLUSION

Genetic improvement through hybridization and selection depends upon the extent of genetic diversity between parents. Crossing for desirable traits can be successful between divergent clusters since they are genetically distant.

Genotypic path coefficient analysis combined over the two locations showed that thousand kernel weights showed the highest direct effect (0.393) and was positively and significantly correlated with grain yield and

followed by grain yield per plant (0.307). This indicated that attention should be given for these traits 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.

### ACKNOWLEDGMENTS

The authors would like to acknowledge Oromia Agricultural Research Institute for financial support and Cereal Case team for their technical support of field management and data collection.

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