



International Journal of
**Plant Breeding
and Genetics**

ISSN 1819-3595



Academic
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Genetic Variability, Heritability and Genetic Advance in Tef (*Eragrostis tef* (Zucc.) Trotter) Lines at Sinana and Adaba

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ABSTRACT

Assessing variability is fundamental to identify the most important traits in tef improvement program. The objective of the present study was to estimate variability, heritability and genetic advance on sixteen morphological characters in tef (*Eragrostis tef* (Zucc.) Trotter). Forty-nine genotypes were evaluated at two locations of Bale in south east of Ethiopia in 2008 cropping season. Simple lattice design of 7×7 with two replication was used to test the treatments. Pooled ANOVA of the two locations showed highly significant ($p < 0.01$) for days to panicle emergence, lodging percentage, thousands kernel weight, grain yield per plant and grain yield per hectare. Significant differences ($p < 0.05$) were noted for panicle length, shoot biomass and number of branch per main panicle. Genotype by location interaction was none significant for all traits which indicated that performance of the genotypes were consistent for these traits across the test locations. High phenotypic coefficient variation were observed for thousand kernel weight (78.82), productive tiller (46.45) and grain yield per plant (34.15) while high genotypic coefficient of variation were noted for traits, thousand kernel weight (40.34), productive tiller (32.46) and grain yield per plant (21.18). Maximum heritability estimate were observed for days to panicle emergence (75.50%) and grain filling period (66.79). High genetic gain was observed for lodging (10.90%) and days to panicle emergence (8.05%). The study showed that there are variation in extent of variability, heritability and genetic advance in traits under study which can facilitate selection for further improvement of important traits in tef.

Key words: Genetic advance, genetic variability, heritability, traits, lines, tef

INTRODUCTION

Tef (*Eragrostis tef* (Zucc.) Trotter) is an allotetraploid species with a base chromosome number of 10 ($2n = 4x = 40$) and belongs to the family Poaceae, sub-family Eragrostidae and genus *Eragrostis*, coupled with disomic inheritance patterns (Berhe *et al.*, 2001). There are a number of close relatives of tef but the molecular-based studies suggested that *Eragrostis pilosa* is an allotetraploid species of tef closest relative and possibly the immediate wild progenitor of tef (Ingram and Doyle, 2003).

Tef is preferred for the production of basic staple food and relatively higher market price than most of other cereal crops in Ethiopia (Woyessa and Assefa, 2011). It has better storage keeping qualities under local conditions than more familiar cereal grains and therefore be stored for longer period than other cereals with fewer losses, making it a very important cash crop for most farmers (FAO, 2010).

Tef production that was restricted to Ethiopia and Eritrea, nowadays started spreading to some countries like USA, Netherlands and Israel. Tef is also gaining popularity as health food (Spaenij-Dekking *et al.*, 2005). According to CSA (2008), it is one of the most important cereal grown in Ethiopia and accounts for about 28% of the total acreage and 19% of the gross grain production of the major cereals cultivated in Ethiopia. In Ethiopia, major tef producing areas are found within Oromiya and Amhara Regional States. It is widely grown in both high-potential and marginal production areas. These areas include most parts of the vertisols that suffer from water logging and other non-vertisol parts of the country that suffer from low-moisture stress (Ketema, 1993). According to Ketema (1997), tef performs very well at an altitude of 1800-2100 m, annual rainfall of 750-850 mm, growing season rainfall of 450-550 mm and a temperature range of 10-27°C.

Breeding information on the nature and the magnitude of variability present in the genetic material is very essential for a breeder to start any valuable selection program. Genotypic and phenotypic coefficients of variation along with heritability plus genetic advance are very essential to improve traits of interest (Denton and Nwangburuka, 2011).

There are a number of problems in tef production; Low yielding, easily susceptibility to lodging which is the major bottleneck for tef mechanization and limitation of variation in landraces are among the existing constraints in tef improvement programme. Breeding information on the nature and the magnitude of variability present in the genetic material is very essential for a breeder to start any effective selection program. Therefore, the present study was, conducted to know the nature and extent of genetic variability, heritability and genetic advance in some important traits of tef.

MATERIALS AND METHODS

Forty-nine Tef lines (Table 1) including one local and two standard checks were brought from Debreziet Agricultural Research Center and tested in 2008 main season. The field experiment was conducted at locations, Sinana and Adaba. Sinana station is located at 2400 m.a.s.l and 463 km south east of Addis Ababa in Bale zone and 33 km east of Robe town. The total annual rain fall for the year 2008 was 1475.90 mm. The mean minimum and maximum annual temperature of the same year was 9.56 and 20.19°C, respectively. The soil type of Sinana is dark-brown (pellic Vertisol) with slightly acidic reaction (Geremew *et al.*, 1998). Adaba station is located 347 km from Addis Ababa on the way to Bale Robe. Total rain fall of the test location during growing season was 1172.2 mm with the average temperature maximum of 20.36°C and minimum of 10.66°C, respectively (source: Herero State Farm Meteorology Station). The soil type of Adaba station is clay soil (source: SARC).

Simple Lattice Design of 7×7 with two replications and spacing of 1 m between plots, 1.5 m between blocks were used. The treatments were sown on 2×2 m plot area in accordance with the recommended seeding rate of 30 kg ha⁻¹ and fertilizer rate of 60 kg ha⁻¹ N and P₂O₅, respectively.

Table 1: Lists of lines used in an experiment and their origin

No.	Genotypes	Origin	No.	Genotypes	Origin
1	DZ-cr-387 (Quncho)	DZARC	26	(354x2788)-HT ⁰³ -408 (sel383b)	DZARC
2	DZ-cr-1285 (Koye)	DZARC	27	(354x2788)-HT ⁰³ -408 (sel383c)	DZARC
3	Local check (tafi dima)	DZARC	28	(354x2788)-HT ⁰³ -408 (sel161c)	DZARC
4	DZ-01-3373	DZARC	29	(354x2788)-HT ⁰³ -408 (sel189c)	DZARC
5	DZ-01-3146	DZARC	30	(354x2788)-HT ⁰³ -408 (sel193e)	DZARC
6	DZ-01-3149	DZARC	31	(354x2788)-HT ⁰³ -408 (sel280a)	DZARC
7	Ho-TFS-920	HARC	32	(354x2788)-HT ⁰³ -408 (sel293b)	DZARC
8	Ho-TFS-1393	HARC	33	(354x2788)-HT ⁰³ -408 (sel30b)	DZARC
9	Ho-cr-415	HARC	34	(354x2788)-HT ⁰³ -408 (sel85e)	DZARC
10	DZ-01-3372	DZARC	35	(354x2788) HT ⁰³ -408 (sel206b)	DZARC
11	DZ-01-3046	DZARC	36	(974x196)-HT ⁰⁰ -387 (RIL417)	DZARC
12	DZ-01-3121	DZARC	37	(354x2788) HT ⁰³ -408 (sel392b)	DZARC
13	DZ-01-3126	DZARC	38	(974x2786) HT ⁰¹ -398 (sel63)	DZARC
14	(974x196)-HT ⁰⁰ -387 (RIL446)	DZARC	39	(974x2786) HT ⁰¹ -398 (sel80b)	DZARC
15	(974x196)-HT ⁰⁰ -387 (RIL43)	DZARC	40	(974x2786) HT ⁰¹ -398 (sel82)	DZARC
16	(974x196)-HT ⁰⁰ -387 (RIL481)	DZARC	41	(974x2786) HT ⁰¹ -398 (sel86a)	DZARC
17	(974x196)-HT ⁰⁰ -387 (RIL351)	DZARC	42	(974x2786) HT ⁰¹ -398 (sel116)	DZARC
18	(974x196)-HT ⁰⁰ -387 (RIL60)	DZARC	43	(974x2786) HT ⁰¹ -398 (sel117)	DZARC
19	(974x196)-HT ⁰⁰ -387 (RIL176)	DZARC	44	(974x2786) HT ⁰¹ -398 (sel121)	DZARC
20	(974x196)-HT ⁰⁰ -387 (RIL157)	DZARC	45	(Alba x Kaye Murri) HT ⁰¹ -407 (sel171)	DZARC
21	(974x196)-HT ⁰⁰ -387 (RIL147)	DZARC	46	(974 x Cr-37) HT ⁰¹ -402 (sel40)	DZARC
22	(974x196)-HT ⁰⁰ -387 (sel661)	DZARC	47	(974 x 2787) HT ⁰¹ -399 (sel51e)	DZARC
23	(974x196)-HT ⁰⁰ -387 (sel924)	DZARC	48	(974 x 2787) HT ⁰¹ -399 (sel180)	DZARC
24	(354x2788)-HT ⁰³ -408 (sel296c)	DZARC	49	(974 x 2788) HT ⁰¹ -401 (sel27a)	DZARC
25	(354x2788)-HT ⁰³ -408 (sel328c)	DZARC			

Data were collected on plant and plot basis for 16 agronomic traits. Data per plant were collected after thinning to 5 cm between plants on plot size of 0.60 m×2 m from 2×2 m experimental unit so that to record data per plant precisely and all data per plot were taken from a plot size of 1 m² using a quadrant.

Statistical analysis: Pooled Analysis of variance for locations were done using the mean values of ten sampled plants for all data taken on plant basis as well as for those taken on plot base. The data of the two locations were tested for normal distribution and homogeneous variance and analyzed by using simple lattice design (Gomez and Gomez, 1998). Least Significant Difference (LSD) were used to separate the means both at 1 and 5% probability levels using SAS statistical software. Genotypic (σ^2_g) and phenotypic (σ^2_P) components of variances were estimated as suggested by Burton and De Vane (1953), Heritability (h^2) for all characters was computed as suggested by Falconer and Mackay (1996).

$$h^2 = \frac{\sigma^2_g}{\sigma^2_P} \times 100$$

and Expected Genetic Advance (GA) for each character at 5% selection intensity were computed using the methodology described by Johnson *et al.* (1955).

$$GA = K \times \sigma^2 \times h^2$$

RESULTS AND DISCUSSION

Combined analysis for traits showed that highly significant ($p < 0.01$) differences for days to panicle emergence, lodging percentage, thousands kernel weight, grain yield per plant and grain yield per hectare. Similar result was also reported by Asfaw and Danno (2011) in case of days to panicle emergence (days to head). Significant differences ($p < 0.05$) were observed for panicle length, shoot biomass and number of branch per main panicle (Table 2). Non significant ($p < 0.05$) variations in genotypes were observed for days to maturity, culm length, plant height, number of node, productive tiller number, grain yield per panicle and grain filling period. Non significant variation ($p < 0.05$) in location was observed only for traits harvest index, lodging percentage, grain filling period and thousand kernel weight; but the rest of the traits were significant ($p < 0.05$). Coefficient of variations ranges from 2.34-23.71%. Highest coefficient of variation (23.71%) was observed for productive tiller number and the lowest coefficient of variation (2.34%) was observed for days to maturity.

Genotype by location interaction were non significant for all traits which indicated performance of the genotypes were consistent for these traits across locations. Balcha *et al.* (2003) reported that the presence of substantial genetic variability for grain yield and component traits was observed among tef genotypes comprising land races and improved cultivars.

Genotypic coefficients of variation, phenotypic coefficients of variation, Heritability and Genetic advance: High phenotypic coefficient of variation was observed for thousand kernel weight (78.82), productive tiller (46.45) and grain yield per plant (34.15). Greater genotypic coefficient of variation were also observed for traits, thousand kernel weight (40.34), productive tiller (32.46) and grain yield per plant (21.18) (Table 3). All phenotypic coefficient of variation result is greater than genotypic coefficient of variation in this study which is congruent with the

Table 2: Combined analysis of variance for 16 traits of 49 Tef genotypes planted at Sinana and Adaba in 2008

Traits	Loc (L)	BMS	Geno (G)	G x L	EMS	CV (%)
DPE	3064.41**	84.30**	47.93**	29.55	21.77	6.70
DM	3557.27**	10.98 ^{ns}	12.94 ^{ns}	13.23	10.50	2.34
PL	1635.04**	3.21 ^{ns}	11.51*	8.36	6.90	9.93
CL	4287.44**	95.57*	27.11 ^{ns}	17.84	31.30	14.11
PH	626.07*	107.22*	50.22 ^{ns}	27.79	44.32	10.07
NN	7.07**	0.10 ^{ns}	0.13 ^{ns}	0.10	0.15	11.48
PTLN	7.36**	7.58**	6.55 ^{ns}	1.07	0.77	23.71
HI	7690.78	17.33**	14.94**	16.30	11.68	21.35
GPa	0.77**	0.12**	0.06 ^{ns}	0.01	0.02	19.30
LOD	371.93	447.44	450.59**	229.23	109.79	26.30
SBM	19.92**	0.08	0.16*	0.12	0.05	17.14
GP	1.14	22.06	28.36 ^{ns}	18.39	21.29	10.77
NPB	212.32**	2.07	9.27**	6.72	4.79	9.49
TKW	0.006	0.007**	0.006**	0.001	0.00	16.34
Gyha	337071.40*	702307.20*	370203.80**	28105.90	74328.30	20.60

*: Significant ($p < 0.05$), **: Highly significant ($p < 0.01$), ns: Not significant, BMS: Block mean square, TrtMS: Treatment mean square, CV: Coefficient of variation, DPE: Days to panicle emergence, DM: Days to maturity, PL: Panicle length (cm), CL: Culm length (cm), PH: Plant height (cm), NN: No. 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: No. of panicle main branch, TKW: Thousand kernel weight (g), GYpl: Grain yield per plant (g), GYha: Grain yield per hectare (kg)

Table 3: Components of variances, coefficients of variation, heritability, genetic advance for sixteen characters in Tef genotypes grown at Sinana and Adaba in 2008

Traits	σ^2_p	σ^2_g	σ^2_e	σ^2_{gl}	PCV (%)	GCV (%)	h^2 (%)	GA (%)	GAM (%)
DPE	26.90	20.31	6.23	0.36	7.45	6.47	75.50	8.05	11.56
DM	11.46	4.97	4.85	1.64	2.44	1.61	43.37	3.02	2.18
PL	5.08	2.64	1.94	0.50	8.52	6.14	51.97	2.41	9.10
CL	66.50	8.56	44.33	13.61	20.57	7.38	12.87	2.16	5.44
PH	75.42	19.31	37.20	18.91	13.14	6.65	25.60	4.57	6.92
NN	0.07	0.03	0.03	0.01	7.97	5.22	42.86	0.23	7.02
PTLN	2.97	1.45	0.92	0.60	46.45	32.46	48.82	1.73	46.63
HI	0.035	0.02	0.009	0.006	1.17	0.88	57.14	0.22	1.37
GPa	0.051	0.01	0.04	0.001	33.71	14.93	19.61	0.09	13.59
LOD	180.27	71.20	96.56	12.51	33.70	21.18	39.50	10.90	27.37
SBM	0.137	0.027	0.07	0.04	28.69	12.74	19.71	0.15	11.63
GP	13.67	9.13	3.52	1.02	8.63	7.05	66.79	5.08	11.85
NPB	5.33	2.77	1.78	0.78	10.01	7.21	51.97	2.47	10.69
TKW	0.042	0.011	0.03	0.001	78.82	40.34	26.19	0.11	42.44
GYpl	3.275	1.045	1.12	1.11	34.15	19.29	31.91	1.19	22.40
Gyha	115973.00	54719.00	44243.00	17011.00	25.72	17.67	47.18	330.36	24.95

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: No. of panicle main branch, TKW: Thousand kernel weight (g), GYpl: Grain yield per plant (g), GYha: Grain yield per hectare (kg)

present study of Kotal *et al.* (2010), Mohammed *et al.* (2011), Yadav *et al.* (2011) and Jalata *et al.* (2011). Previous study reported that high phenotypic coefficient of variation for productive tillers (21%) and grain yield per panicle (22%) in tef (Kebebew *et al.*, 2001). Wide difference of Phenotypic coefficient of variability (78.82%) and genotypic coefficient of variability in 40.34% in thousand kernel weight, contradict with the reports of Riaz and Chowdhry (2003). High genotypic variability facilitates selection for improvement and widens the chance of heritability of traits from parent to offspring.

Maximum heritability estimate were observed for days to panicle emergence (75.50%) and grain filling period (66.79) (Table 3). Heritability estimates along with expected genetic gain is more useful than the heritability value alone in predicting the resultant effect for selecting the best genotypes (Johnson *et al.*, 1955). High genetic gain was observed for lodging (10.90%) and days to panicle emergence (8.05%).

CONCLUSION

Most of traits under study were showed significant variations, from low to high magnitude of heritability and genetic advance. These can facilitate selecting and utilizing the most preferred traits of interest and also hint the potential of tef for further improvement. High phenotypic and genotypic coefficient of variation especially for traits like thousand kernel weight, productive tiller and grain yield per plant are detrimental which make possible tef improvement breeding program. Broad sense heritability estimates together with genotypic coefficient of variation is important to exploit selection in germplasm improvement, since it bases all genetic effects.

ACKNOWLEDGMENT

The authors would like to acknowledge Tesfaye Letta, Tilahun Bayisa, Deme Nuguse, Tesfaye Tadess, Habtamu Legese, Gezahegn Tadess for their technical support and Oromia Agricultural Research Institute for financing this study.

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