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VARIABILITY, HERITABILITY AND GENETIC ADVANCE IN QUANTITATIVE TRAITS OF TEF [*ERAGROSTIS TEF* (ZUCC.) TROTTER]: IMPLICATION FOR GENETIC IMPROVEMENT STRATEGIES

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ABSTRACT: Seventy nine tef populations collected from ten administrative regions and seven altitude classes were planted with two improved varieties in simple lattice design at Gute and Bako during 2007 and 2008 cropping season, respectively, to assess variability, and estimate heritability and genetic advance of quantitative traits. The combined analysis of variance across locations showed significant location effects on all the quantitative traits considered. The genotype mean squares were also significant ($P \leq 0.01$) for all quantitative traits except number of spikelet per panicle, number of internodes and number of fertile floret per spikelet at the top of main panicle. Genotype *x* Environment interaction was significant (($P \leq 0.01$) for grain yield per plant, lodging index, harvest index, above ground weight and number of panicle branches. The phenotypic coefficient of variation was higher than the corresponding genotypic coefficient of variation for all quantitative characters considered in this study. This implies that; beside the genetic factors; environmental factors have high contribution for the variations observed. Genotype x Environment coefficient of variation was found to be less than the genotypic coefficient of variation for most of the quantitative characters. This indicates that variability observed in tef landraces was more due to the genotypic component than due to interaction between genotype and environment. Relatively, the higher heritability coupled with higher genetic advance noted for grain yield per plant, lodging index and biomass weight per plant in the study indicates the ease of phenotype-based selection for the improvement of these traits. However, low heritability range and genetic advance range were recorded for culm length, number of culm internodes per main shoot, days to maturity, number of fertile floret per spikelet at the top, middle and base of the panicle across the two locations. This implies that most of the variations for these traits were environmental rather than genetic.

Key words/phrases: *Eragrostis tef*, Genetic advance, Heritability, Landraces, Variation

INTRODUCTION

Tef [*Eragrostis tef* (Zucc.) Trotter] is an indigenous cereal to Ethiopia. As a

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cereal, it is obvious that it belongs to the grass family Poaceae. Tef originated in Ethiopia (Vavilov, 1951). Tef is an allotetraploid (2n=4x=40) plant with a basic chromosome number of x=10 for the genus *Eragrostis* (Tavassoli, 1986; Likyelesh Gugsa, 1993; Hailu Tefera and Seyfu Ketema, 2001). It is grown in almost all regions of the country, Ethiopia since it is the preferred grain for local consumption and fetches the highest market price compared to other cereals (Seyfu Ketema, 1997). Its special resistance to various biotic and abiotic stresses has made it a "low risk" crop for cultivation (Seyfu Ketema, 1993). The area devoted to tef cultivation has been increasing from year to year. In 2003/04, it occupied about 2 million hectares, which accounted for 29% of the total acreage of cereal crops grown in the country (CSA, 2004). But in 2004/05, 2005/06 and 2006/07 main cropping season, the total land allocated for tef production was 2.14, 2.25 and 2.41 million hectares, respectively (CSA, 2007).

When compared with other cereal crops grown in the country, tef is highly valued by farmers and consumers. Some of the specific merits of tef that make it more preferable by farmers compared to other cereals are the higher prices for its grain, more nutritious straw for feed and better adaptation under both low and high moisture stress, importance as a rescue crop planted after other cereals have failed because of moisture shortage, less susceptibility to disease and insect pests and low susceptibility to storage pest attacks (Seyfu Ketema, 1997; Hailu Tefera and Seyfu Ketema, 2001). Despite its food, feed and economic importance, the productivity of tef is relatively low primarily due to the low yielding ability of the local varieties, and various biotic and abiotic constraints.

Variations can always exist among individuals in a population and assessing the source of and magnitude of variation plays a vital role in crop improvement programs. The relative importance of source of variation is due to that source as a proportion of the total phenotypic variance (Falconer and Mackay, 1996). The variation within or among populations can be genotypic, phenotypic or the interaction of these two factors.

Heritability is of interest to plant breeders primarily as a measure of the value of selection for a particular character in various types of progenies and as an index of transmissibility. If the percentage is large, the character is heritable but if it is small, environment is correspondingly prominent in the character expression (Hayes *et al*., 1955). Allard (1960) indicated that the heritability values for quantitative traits are low mainly due to their sensitivity to environmental factors and genetic advance should be used

along with heritability estimates in predicting the efficiency of selection, and this high heritability value could be obtained with genotypes having small or large genetic variance but genetic progress would be larger with larger genotypic variance. According to Panes (1957), the association of high heritability with equally high genetic advance is chiefly due to the additive gene effect, but if heritability is mainly due to dominance and epitasis; the genetic gain would be low.

Overall, genetic variability, heritability and genetic advance are pre-requisites for breeding programs and provide opportunity to plant breeders for selecting high yielding genotypes or to combine or transfer genes having desirable traits (Khorgade *et al.*, 1985). Therefore, the present study aimed to assess the diversity extent and patterns, heritability and genetic advance of quantitative traits in tef germplasm collection for use as a clue for effective conservation and improvement strategies.

MATERIALS AND METHODS

A total of 79 landrace populations and two improved tef varieties were evaluated at Gute and Bako Agricultural Research Center during the 2007 and 2008 main cropping seasons (June – Dec.), respectively. These landraces were collected by the Institute of Biodiversity Conservation from the major tef producing areas of western, south western, south eastern and north and central parts of Ethiopia, particularly, Arsi, Bale, East Gojam, East Wellega, Horro Guduru Wellega, Illuababor, Jimma, South Wello, West Shewa and West Wellega (Table 1). The improved varieties DZ-Cr-255 (Gibe) released by Debre Zeit Agricultural Research Center in 1993 and well adapted for mid to high altitude (1500-2200 m a.s.l.), and DZ-01-1880 (Guduru) released by Bako Agricultural Research Center in 2005 and well adapted to mid to high altitude region (1800-2450 m a.s.l.) were also included for comparison.

Seven altitude classes were used to group tef populations with relative resemblance of agro-climatic origin using the formula: $K = 1+3.32\log_{10}n$ and W= (L-S)/K (Agrawal, 1996) where K= number of class intervals, W= width of class interval, L= the largest value, S= the smallest value and n= sample size (in this case the number of accessions)

The experiment was laid out in 9 x 9 simple lattices with two replications. The plot size was 0.5 m long rows with 0.1 m row width ($0.05m^2$). The spacing was 1 m between plots and 2 m between adjacent blocks. Based on the recommended seeding rate of 30 kg/ha, 0.15 g of seeds was hand-broadcasted along the 0.1 m breadth of the row surfaces. From each plot,

eight individual plants were selected randomly and, marked before panicle emergence, for use as samples for collection of some quantitative morphological data.

Data were recorded for days to panicle emergence, days to maturity, plant height (cm), panicle length (cm), culm length (cm), number of culm internodes per culm, number of panicle branches, number of spikelet per panicle of the main plant/culm, lodging index, first culm internode diameter (cm), second culm internode diameter (cm), number of fertile floret per spikelet at top, middle and base of the panicle, above ground weight per plant (g), biomass per plant (g), 100 kernel weights (g), grain yield per plant (g) and harvest index per plant (HI %)

Table 1 List of experimental materials with their region, soil type and altitude of collection.

No.	Acc.	Admin. Region	District	Altitude
1	229966	Arsi	Sherka	2550
2	229971	Arsi	Ziway Dugda	1730
3	231217	Arsi	Chole	1540
4	231219	Arsi	Jeju	1600
5	236952	Arsi	Dodotana Sire	2710
6	232245	Arsi	Sherka	2550
7	236942	Arsi	Gedeb	2350
8	236944	Arsi	Tiyo	2000
9	55014	Bale	Sinanana Dinisho	2565
10	55015	Bale	Agarfa	2500
11	55016	Bale	Goro	1710
12	237737	Bale	Adaba	2400
13	229981	Bale	Sinanana Dinisho	2560
14	229982	Bale	Mennana Herena Bulu	1440
15	55018	Bale	Ginir	1630
16	55019	Bale	Gaserana Gololcha	1980
17	55022	Bale	Gaserana Gololcha	2300
18	55045	East Gojam	Hulet Ej Enese	2260
19	55046	East Gojam	Hulet Ej Enese	1920
20	55047	East Gojam	Goncha Siso Enese	2670
21	222174	East Gojam	Dejen	1500
22	229754	East Gojam	Hulet Eju Enese	1790
23	55172	East Gojam	Machakel	2440
24	55267	East Gojam	Dejen	1570
25	55062	East Gojam	Enemay	2560
26	203010	East Wellega	Bila Seyo	1600
27	202991	East Wellega	Arjo	2420
28	237704	East Wellega	Sibu Sire	1760
29	237706	East Wellega	Guto Wayu	1620
30	237707	East Wellega	Gida Kiremu	1450
31	237700	East Wellega	Bila Seyo	2470
32	236364	East Wellega	Diga Leka	2420
33	236365	East Wellega	Jimma Arjo	2470
34	55261	East Wellega	Limu	2210
35	239391	East Wellega	Gatama	2260
36	236359	East Wellega	Guto Wayu	2100
37	239384	Horro Guduru	Jimma Horo	2500
38	203030	Horro Guduru	Jimma Horo	2210
39	236357	Horro Guduru	Guduru	2200

Continued from Table 1

No.	Acc.	Admin. Region	District	Altitude
40	239376	Horro Guduru	Guduru	2300
41	236326	Horro Guduru	Abay Chomen	2420
42	236336	Horro Guduru	Jimma Horo	2520
43	236328	Horro Guduru	Jimma Horo	2480
44	239379	Horro Guduru	Abay Chomen	2300
45	55253	Illubabor	Bedele	2000
46	55254	Illubabor	Bedele	1910
47	55248	Illubabor	Yayu	1750
48	202979	Illubabor	Gechi	2140
49	202972	Illubabor	Bedele	1710
50	202952	Jimma	Sokoru	1920
51	202966	Jimma	Kersa	1770
52	202950	Jimma	Sokoru	1390
53	239396	Jimma	Kersa	1790
54	239398	Jimma	-	1750
55	212597	South Wello	Legambo	2360
56	212599	South Wello	Legambo	2450
57	212608	South Wello	Kutaber	2400
58	212615	South Wello	Tehuledere	1690
59	212616	South Wello	Ambasel	1460
60	55101	South Wello	Dessie Zuria	2500
61	203034	West Shewa	Bako Tibe	1610
62	203036	West Shewa	Cheliya	1680
63	228666	West Shewa	Ambo	1500
64	55091	West Shewa	Jeldu	2470
65	239375	West Shewa	Cheliya	2410
66	236752	West Shewa	Dendi	2160
67	236756	West Shewa	Cheliya	2100
68	236757	West Shewa	Adda Berga	2600
69	236758	West Shewa	Wonchi	2280
70	236340	West Shewa	Bako Tibe	1710
71	236754	West Shewa	Ambo	2150
72	55131	West Wellega	Gimbi	1900
73	208753	West Wellega	Ayra Guliso	1800
74	202997	West Wellega	Jimma Gidami	2190
75	237712	West Wellega	Gimbi	1800
76	237713	West Wellega	Gimbi	1800
77	55156	West Wellega	Nejo	2750
78	55147	West Wellega	Jarso	2000
79	55154	West Wellega	Nejo	2000
80	DZ-01-1880	Released	-	-
81	DZ-Cr-255	Released	-	-

Key: NI= Not Identified

Data analysis

The relative efficiency of simple lattice over the RCBD was tested using MSTATC (Michigan State University, 1991) computer software and found to be less efficient for all quantitative traits except days to panicle emergence and second culm internod diameter. Analysis of variance for simple lattice was done using RCBD provided that the relative efficiency of simple lattice over the RCBD was less than 25% (Cochran and Cox, 1957). In the case where the blocking of incomplete block design was less

effective, the use of randomized blocks design (RCBD) analysis would be preferable (Cochran and Cox, 1957). The data collected for all quantitative characters were subjected to analysis of variance (ANOVA) using Agrobase (2000) software.

The variability of each quantitative morphological trait was estimated by simple statistical measures such as mean, range, and phenotypic and genotypic variances and coefficients of variation. The component and coefficients of variances were calculated following the formula suggested by Singh and Chaundhary (1977). Estimation of variance components for each location was made as follows.

a) Genotypic variance (δ^2_g)

$\delta^2_g = (MS_g - MS_e)/r$

Where, MS_g = mean square of genotype, MS_e is mean square of error and

r = number of replications

b) Environmental variance (δ^2_e)

δ^2_e = error mean square (MS_e)

c) Phenotypic variance (δ^2_p)

$\delta^2_p = \delta^2_g + \delta^2_e$

Where, δ^2_p = phenotypic variance, δ^2_g = genotypic variance and

δ^2_e = environmental variance

The components of variance including the variance due to genotype by environment interaction based on the combined analysis of variances over the two locations were obtained using the formula suggested by Singh and Chaundhary (1977) and Allard (1960) as follows,

a) Genotypic variance (δ^2_g)

$\delta^2_g = (MS_g - MSgl)/rl$

Where, MS_g = mean square of genotype,

MSgl is the mean square due to genotype by environment interaction,

l=number of locations, and r = number of replications

b) Genotype by environment interaction variance (δ^2_{gl})

$\delta^2_{gl} = (MSgl-MS_e)/r$

Where MSgl is the mean square due to genotype by environment interaction, and MSe = combined error mean square (δ^2_e)

c) Phenotypic variance (δ^2_p)

$$\delta^2_p = \delta^2_g + (\delta^2_{gl}/l) + (\delta^2_e/rl)$$

Estimates of coefficient of variation were obtained as follows.

a) Phenotypic coefficient of variation (PCV)

$$PCV = \frac{\sqrt{\delta^2_p}}{\bar{x}} \times 100$$

Where, PCV = phenotypic coefficient of variation,

δ^2_p = phenotypic variance and

$\bar{x}$ = population mean for the trait considered

b) Genotypic coefficient of variation (GCV)

$$GCV = \frac{\sqrt{\delta^2_g}}{\bar{x}} \times 100$$

Where, GCV = genotypic coefficient of variation, δ^2_g = genotypic variance and $\bar{x}$ = population mean for the trait considered

c) Genotype by environment interaction coefficient of variation (GECV)

$$GECV = \frac{\sqrt{\delta^2_{gl}}}{\bar{x}} \times 100$$

Where, δ^2_{gl} = genotypic x environment variance

$\bar{x}$ = population mean for the trait considered

Broad sense heritability was estimated according to the suggestion of Allard (1960). Heritability per location was calculated by dividing genotypic variances by phenotypic variance:

$$H^2 = (\delta^2_g/\delta^2_p) \times 100,$$

Where, δ^2_g = genotypic variance and δ^2_p = phenotypic variance

When heritability is calculated for combined analysis, combined over two locations, the phenotypic variance combined over location will be used.

Hence, $H^2 = (\delta^2_g/\delta^2_p) \times 100$,

Where $\delta^2_p = \delta^2_g + (\delta^2_{gl}/l) + (\delta^2_e/rl)$

Expected genetic advance under selection assuming a selection intensity of 5% was computed following the formula developed by Allard (1960) as:

$GA = (K)\ (\delta_p)\ (H^2)$,

Where GA = expected genetic advance

K=selection differential that varies depending upon the selection intensity and stands at 2.056 for selecting 5% of the genotypes.

δ_p = phenotypic standard deviation and

H^2= heritability (in broad sense)

Genetic advance as percent of mean was obtained as;

$$\text{GA (\% of mean)} = \left(\frac{GA}{\bar{x}}\right) \times 100\%:$$

Where, GA= genetic advance

$\bar{x}$ = population mean for the trait considered

RESULTS AND DISCUSSION

Analysis of variance

The analysis of variance for quantitative morphological trait showed highly significant ($P \leq 0.01$) genotype differences for days to panicle emergence, plant height, panicle length, number of panicle branches per main panicle, grain yield per plant and lodging index, both at Gute and Bako (Table 2 and 3). It also showed highly significant ($P \leq 0.01$) differences among genotypes for culm length, number of spikelet per main panicle, number of fertile floret per spikelet at middle of main panicle, harvest index and first culm diameter at Gute (Table 2); and for days to maturity, above ground weight and biomass per plant at Bako (Table 3).

Significant differences ($P \leq 0.05$) among genotypes were noted for traits such as days to maturity and shoot phytomass per plant at Gute (Table 2) and for numbers of internodes per main plant/culm, spikelet per panicle and fertile florets per spikelet at the base of the panicle at Bako (Table 3). However, there were no significant genotype differences for numbers of fertile floret per spikelet at top of the panicle and second culm internodes diameter at both locations (Table 2 and 3). The presence of significant variation

between tef genotypes for grain yield and some yield related traits was also reported by other workers (Haile-Melak Mengesha *et al.*, 1965; Hailu Tefera, 1988; Endashaw Bekele, 1996; Fufa Hundera *et al.*, 1999; Kebebew Asefa *et al.*, 2002; Temesgen Adnew, 2002).

Table 2 Mean squares from the analysis of variance of quantitative morphological traits of tef genotypes at Gute.

Source of variation	Df	DPE	DM	PLH	PAL	CL	N IN	NPB	SP/PN	LOG
Rep	1	164.00*	202.20	668.00*	78.00	373.70**	0.091	4.82	257044**	285.34*
Genotypes	80	96.70**	74.27*	240.00**	61.70**	79.58**	0.273	17.79**	9427.70**	173.36**
Error	80	40.30	53.30	108.00	28.60	50.10	0.273	6.76	4892.84	41.74
CV		7.10	7.10	15.30	16.40	19.80	15.200	18.20	27.60	40.62
LSD(0.05)		14.44	14.44	20.70	10.60	14.09	1.040	5.17	139.10	21.24
Mean		57.40	101.70	68.10	32.70	35.70	3.430	14.26	249.30	15.44

Table 2 Cont'd

Source of variation	Df	FCD	SCD	FFT	FFM	FFB	SHPL	BIOPL	Gy/pl	HI
Rep	1	0.003	0.009*	4.805	3.705	0.707	554.40*	41.877	0.940	27.8*
Genotypes	80	0.003**	0.003	3.670	2.660**	4.261	98.30*	53.736	4.48**	61.9**
Error	80	0.001	0.002	3.516	1.384	3.284	64.16	13.989	0.697	45.3
CV		22.700	24.200	26.960	15.720	22.890	36.92	28.800	25.400	23.0
LSD(0.05)		0.072	0.079	3.120	1.960	3.016	13.33	7.443	1.660	13.4
Mean		0.161	0.1633	6.955	7.485	7.915	21.69	12.988	3.280	17.1

Table 3 Mean squares from the analysis of variance of quantitative morphological traits of tef genotypes at Bako.

Source of variation	Df	DPE	DM	PLH	PAL	CL	N IN	NPB	SP/PN	LOG
Rep	1	27.700	28.54*	133.5**	44.87**	61.76*	2.469**	1.58	402.9**	213.88**
Genotypes	80	36.10**	19.05**	512.0**	585.60**	7.14	0.488*	46.2**	73.23*	2076.5**
Error	80	10.540	6.24	53.900	19.330	37.11	0.294	12.050	23.050	35.290
CV		8.200	3.17	8.660	12.950	11.98	13.110	16.650	12.770	24.240
LSD(0.05)		6.459	4.97	2.296	1.375	1.90	1.079	7.037	2.676	1.858
Mean		39.58	78.78	84.800	33.940	50.86	4.136	21.235	67.000	24.510

Table 3 Cont'd

Source of variation	Df	FCD	SCD	FFT	FFM	FFB	SHPL	BIOPL	Gy/pl	HI
Rep	1	0.0028	0.0025**	11.95*	5.56*	8.45**	56.84**	34.6**	4.396**	75.32**
Genotypes	80	0.002	0.0025	1.081	0.893	1.39*	283.50**	121**	48.020**	125.500
Error	80	0.001	0.0010	0.951	0.803	0.951	18.570	7.390	0.897	34.090
CV		18.680	19.9400	30.610	26.300	21.850	26.610	26.980	23.010	22.940
LSD(0.05)		0.008	0.0080	1.940	1.880	1.940	1.348	0.850	0.296	1.834
Mean		0.130	0.1310	3.185	3.590	4.460	16.194	10.074	4.111	25.569

@ KEY: DPE= days to panicle emergence, DM= days to maturity, PLH= plant height, PNL= panicle length, CL= length, NIN= number of culm internodes per main panicle, NPB= number of panicle branch per main shoot, SP/PN= number of spikelet per main shoot, LOG= lodging index, FCD= First culm diameter, SCD= second culm diameter, FFT=fertile floret per spikelet at top of the panicle, FFM= fertile floret per spikelet at middle of the panicle, FFB= fertile floret per spikelet at the base of the panicle, SHPL= shoot phytomass per plant, BIOPL= biomass weight per plant, TSW= Thousand seed weight, GY/PL = grain yield per plant and, HI= harvest index (%), df= degree of freedom

Combined analysis of variance locations showed significant location effect for all traits, indicating substantial differences between the two environments (Table 4). Temesgen Adnew (2002) reported that mean square due to location was significant for all the 14 quantitative traits of the tested tef genotypes. Kebebew Asefa *et al.* (1999) also noted significant location effects on days to maturity and spikelet per main panicle. The mean square of genotypes was highly significant (P≤0.01) for all traits except number of internodes per culm, spikelet per main panicle, and fertile florets per spikelet at the top, middle and base of the panicle and biomass weight per plant. Genotype x environment interaction effects were highly significant (P≤0.01) on number of panicle branch, lodging index, above ground biomass weight, grain yield per plant and harvest index, significant (P≤0.05) genotype *x* environment interaction was noted for number of spikelet per panicle. This implies that tef landraces responded differently over environments for these traits. These tef landraces showed no significant differences for the remaining 12 quantitative traits (Table 4)

Table 4 Mean squares from the combined analysis of variance of quantitative traits of tef landraces over two locations (Bako and Gute).

Source of variation	Df	DPE	DM	PLH	PAL	CL	N IN	NPB	SP/PN	LOG
Rep	1	25724*	430333**	22650**	114.1*	18632**	29.64*	3865.40**	8100	6302.60**
Genotypes	80	102.23**	66.81**	301.80**	88.7**	100.1**	0.463	48.12**	7115	258.96**
G *x* E	80	33.139	29.77	79.60	25.00	42.25	0.367	16.24**	9303*	128.30**
Error	160	25.130	26.52	76.90	22.20	41.53	0.341	10.113	6037	38.52
CV		10.340	6.04	11.67	15.18	15.02	15.230	17.890	31.80	30.88
LSD(0.05)		5.864	6.38	10.44	5.91	7.60	0.683	3.720	90.89	7.26
Mean		48.490	90.30	76.45	33.28	43.28	3.830	17.780	244.30	20.10

Table 4 Cont'd

Source of variation	Df	FCD	SCD	FFT	FFM	FFB	SHPL	BIOPL	Gy/pl	HI
Rep	1	0.086**	0.078**	1160.5**	1247.3**	969.63**	2535.1**	666**	31.090**	4883.7**
Genotypes	80	0.003**	0.003**	2.5370	1.898**	2.927*	84.25**	54.60*	5.139**	138.20**
G *x* E	80	0.0010	0.001	2.2260	1.443	2.713	71.36**	36.590	3.765**	115.78**
Error	160	0.0010	0.001	2.1860	1.114	2.106	41.22	32.330	0.772	22.780
CV		22.1600	22.350	29.4800	19.110	23.460	33.97	52.470	24.420	22.600
LSD(0.05)		0.0375	0.038	1.7456	1.234	1.697	7.51	7.077	1.030	5.584
Mean		0.1450	0.148	1.746	5.523	6.185	18.89	11.530	3.597	21.056

@ KEY: DPE= days to panicle emergence, DM= days to maturity, PLH= plant height, PNL= panicle length, CL= culm length, NIN= number of culm internodes per main panicle, NPB= number of panicle branch per main shoot, SP/PN= number of spikelet per main shoot, LOG= lodging index, FCD= First culm diameter, SCD= second culm diameter, FFT=fertile floret per spikelet at top of the panicle, FFM= fertile floret per spikelet at middle of the panicle, FFB= fertile floret per spikelet at the base of the panicle, SHPL= shoot phytomass per plant, BIOPL= biomass weight per plant, TSW= Thousand seed weight, GY/PL = grain yield per plant and, HI= harvest index (%), df= degree of freedom

Phenotypic and Genotypic coefficient of variation

The Genotypic Coefficient of Variation (GCV), phenotypic coefficient of variation (PCV), genotypic variance (GV), phenotypic variance (PV), environmental variance (EV), broad sense heritability (H^2), genetic advance (GA) and genetic advance (as % mean) at Gute, Bako and combined location are summarized in Tables 5, 6 and 7, respectively.

The PCV and GCV values of less than 10%, 10%-20% and greater than 20% are considered to be low, intermediate and high, respectively (Khorgade *et al.,* 1985). Maximum PCV values were observed for lodging index, grain yield per plant, biomass per plant, shoot phytomass yield per plant, panicle length, number of fertile florets per spikelet at the top and base of the panicle and number of panicle branches per main panicle both at Bako and Gute (Tables 5 and 6). Whereas, plant height, number of fertile florets per spikelet at the middle of the panicle, number of internodes per culm and days to panicle emergence showed intermediate PCV values and days to maturity resulted in the lowest PCV values both at Bako and Gute (Tables 5 and 6). Similarly, the study on variation, heritability and genetic advance in phenomorphic and agronomic traits of 120 tef germplasm lines (Kebebew Asefa *et al*., 2001) indicated that PCV was lowest for days to maturity.

Estimates of GCV were lowest for traits such as number of internodes per culm, days to maturity, days to panicle emergence, number of fertile florets per spikelet at the top and middle of the panicle both at Bako and Gute, number of fertile floret per spikelet at the base of the panicle at Gute, and harvest index at Bako (Tables 5 and 6). Such result indicates that selection is not effective for such traits because of the narrower genetic variability. Kebebew Asefa *et al*. (2001) reported that lower GCV were noted for days to 50% maturity, days to panicle emergence and number of internodes per culm. Fufa Hundera *et al.,* (1999) also noted relatively lower PCV and GCV for major traits such as days to panicle emergence, days to maturity, plant height, lodging index and harvest index.

Comparatively higher GCV values were noted for lodging index, grain yield per plant and biomass weight per plant at both location; harvest index at Gute; above ground shoot weight and panicle length for Bako (Table 5 and 6). PCV values were higher than the corresponding GCV values for all traits in this study. This implies that, in addition to the genetic factors, other factors such as environments have great contribution to the variations observed. The remaining quantitative traits have intermediate GCV values.

Overall, majority of the quantitative traits considered in this study had medium to high GCV values. This implies that there is genetic variability among tef populations. Several studies on tef also indicated higher GCV and PCV values for grain yield (Haile-Melak Mengesh *et al.*, 1965; Hailu Tefera *et al.*, 1990; Kebebew Asefa *et al.*, 1999 and Kebebew Asefa *et al*., 2001). Most of these authors also found that PCV values were higher than the corresponding GCV values for all quantitative traits considered in the different studies.

Table 5 Estimation of variability parameters (mean, genotypic variation (δ^2_g), phenotypic variation (δ^2_p), environmental variance (δ^2_e), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broader sense (H^2), genetic advance (GA) and genetic advance (as % mean) values for 18 quantitative traits of 81 tef genotypes at Gute.

Traits	$\bar{x}$	δ^2_g	δ^2_p	δ^2_e	GCV	PCV	H^2 (%)	GA	GA (%)
Days to panicle emergency	39.580	12.780	23.370	10.540	9.032	12.214	54.685	5.435	12.052
Days to maturity	78.780	6.410	12.640	6.240	3.214	4.513	50.712	3.707	4.113
Plant height	84.800	229.050	282.950	53.900	17.847	19.836	80.951	27.996	16.038
Panicle length	33.940	283.135	302.460	19.330	49.578	51.242	93.611	33.472	26.871
Culm length	50.860	12.330	49.440	37.110	6.904	13.825	24.939	3.605	5.682
Number of internodes per culm	4.136	0.097	0.391	0.294	7.530	15.118	24.808	0.319	6.093
Number of panicle branches	21.235	17.080	29.130	12.050	19.462	25.417	58.634	6.506	27.266
Number of spikelet per main panicle	67.000	25.090	48.140	23.050	7.480	10.400	52.120	15.210	22.600
Lodging indexs	24.540	1020.600	1055.890	35.290	130.183	132.414	96.658	64.576	83.741
First culm internodes diameter	0.130	0.0005	0.0015	0.001	17.251	29.792	33.330	0.026	20.420
Second culm internodes diameter	0.131	0.00075	0.00175	0.001	20.910	31.934	42.850	0.037	28.140
Number of fertile floret per spikelete (top)	3.185	0.065	1.016	0.951	8.005	31.647	6.398	0.133	2.826
Number of fertile floret per spikelete (mid)	3.590	0.046	0.847	0.801	5.970	25.600	5.440	0.071	1.190
Number of fertile floret per spikelete (bottom)	4.460	0.220	1.170	0.951	10.517	24.253	18.803	0.418	7.242
Shoot phytomass yield per plant (g)	16.194	132.460	151.030	18.570	71.070	75.889	87.704	22.160	59.343
Biomass weight per plant (g)	9.827	56.805	64.195	7.390	76.696	81.532	88.488	14.577	79.068
Grain yield per plant (g)	4.111	23.560	24.460	0.897	118.070	120.304	96.321	9.794	71.272
Harvest index	39.580	12.780	23.370	10.540	9.032	12.214	54.685	5.435	12.052

Table 6 Estimation of variability parameters (range, standard deviation, mean, genotypic coefficient of variation, genotypic variation (δ^2_g), phenotypic coefficient of variation (PCV), phenotypic variation (δ^2_p), environmental variance(δ^2_e), heritability in broader sense (H^2), genetic advance (as % mean) and genetic advance (GA) values for 18 quantitative traits of 81 tef genotypes at Bako.

Traits	$\bar{X}$	δ^2_g	δ^2_p	δ^2_e	GCV	PCV	H^2 (%)	GA	GA (%)
Days to panicle emergency	39.580	12.780	23.370	10.540	9.032	12.214	54.685	5.435	12.052
Days to maturity	78.780	6.410	12.640	6.240	3.214	4.513	50.712	3.707	4.113
Plant height	84.800	229.050	282.950	53.900	17.847	19.836	80.951	27.996	16.038
Panicle length	33.940	283.135	302.460	19.330	49.578	51.242	93.611	33.472	26.871
Culm length	50.860	12.330	49.440	37.110	6.904	13.825	24.939	3.605	5.682
Number of internodes per culm	4.136	0.097	0.391	0.294	7.530	15.118	24.808	0.319	6.093
Number of panicle branches	21.235	17.080	29.130	12.050	19.462	25.417	58.634	6.506	27.266
Number of spikelet per main panicle	67.000	25.090	48.140	23.050	7.480	10.400	52.120	15.210	22.600
Lodging indexs	24.540	1020.600	1055.890	35.290	130.183	132.414	96.658	64.576	83.741
First culm internodes diameter	0.130	0.0005	0.0015	0.001	17.251	29.792	33.330	0.026	20.420
Second culm internodes diameter	0.131	0.00075	0.00175	0.001	20.910	31.934	42.850	0.037	28.140
Number of fertile floret per spikelete (top)	3.185	0.065	1.016	0.951	8.005	31.647	6.398	0.133	2.826
Number of fertile floret per spikelete (mid)	3.590	0.046	0.847	0.801	5.970	25.600	5.440	0.071	1.190
Number of fertile floret per spikelete (bottom)	4.460	0.220	1.170	0.951	10.517	24.253	18.803	0.418	7.242
Shoot phytomass yield per plant (g)	16.194	132.460	151.030	18.570	71.070	75.889	87.704	22.160	59.343
Biomass weight per plant (g)	9.827	56.805	64.195	7.390	76.696	81.532	88.488	14.577	79.068
Grain yield per plant (g)	4.111	23.560	24.460	0.897	118.070	120.304	96.321	9.794	71.272
Harvest index	39.580	12.780	23.370	10.540	9.032	12.214	54.685	5.435	12.052

From combined analysis across locations, PCV was low for the first and the second culm internodes diameter, number of internodes per culm, number of fertile florets per spikelet at the middle of the panicle (Table 7). It was intermediate for plant height and number of fertile florets per spikelet at the base of the panicle, and maximum for the remaining traits. The GCV was minimum for first and second culm internodes diameter, number of internodes per culm, number of fertile floret per spikelet at the middle and the base of the panicle and grain yield per plant. Relatively, high GCV values were observed for plant height and lodging index.

Table 7 Estimation of variability parameters (mean, genotypic variation (δ^2_g), phenotypic variation (δ^2_p), environmental variance (δ^2_e), genotype by location variance (δ^2_{gl}), genotypic coefficient of variation (GCV), genotype by environment coefficient of variation (G *x* ECV) phenotypic coefficient of variation (PCV), heritability in broader sense (H^2), genetic advance (GA) and genetic advance (as % mean) values for 18 quantitative traits of 81 tef genotypes for combined data over two test locations.

Traits	$\bar{x}$	δ^2_g	δ^2_{gl}	δ^2_p	δ^2_e	GCV	G *x* ECV	PCV	H^2 (%)	GA	GA (%)
Days to panicle emergency	48.490	17.273	4.005	25.558	25.130	35.621	4.127	52.707	67.584	7.025	14.487
Days to maturity	90.300	9.260	1.625	16.703	26.520	10.255	1.412	18.497	55.441	4.658	5.159
Plant height	76.450	55.550	1.350	75.450	76.900	72.662	1.520	98.692	73.625	13.149	17.199
Panicle length	33.280	15.925	1.400	22.175	22.200	47.852	3.555	66.632	71.815	6.953	20.892
Culm length	43.280	14.463	0.360	25.025	41.530	33.416	1.386	57.821	57.792	5.944	13.734
Number of internodes per culm	3.830	0.024	0.013	0.116	0.341	0.627	2.977	3.022	20.734	0.145	3.787
Number of panicle branches per main panicle	17.780	7.970	3.064	12.030	10.113	44.826	9.844	67.660	66.251	4.724	26.572
Lodging index	20.100	32.665	44.890	64.740	38.520	62.512	33.333	322.09	50.456	8.347	41.526
First culm internodes diameter	0.150	0.001	0.000	0.001	0.001	0.345	0.000	0.517	66.667	0.038	25.888
Second culm internodes diameter	0.150	0.001	0.000	0.001	0.001	0.338	0.000	0.507	66.667	0.038	25.363
Number of fertile floret per spikelete (top)	1.750	0.078	0.020	0.634	2.186	4.453	8.100	36.326	12.259	0.201	11.496
Number of fertile floret per spikelete (mid)	5.520	0.114	0.165	0.475	1.114	2.060	7.344	8.591	23.973	0.340	6.147
Number of fertile floret per spikelete (bottom)	6.190	0.054	0.304	0.732	2.106	0.865	8.907	11.831	7.311	0.129	2.079
Shoot phytomass yield per plant (g)	18.890	3.223	15.070	21.063	41.220	17.059	20.551	111.501	15.300	1.444	7.642
Biomass weight per plant (g)	11.530	4.503	2.130	13.650	32.330	39.050	12.658	118.387	32.985	2.506	21.731
Grain yield per plant (g)	3.600	0.835	1.497	1.776	0.772	23.200	34.009	49.368	47.020	0.623	17.322
Harvest Index	21.060	5.605	46.500	34.550	22.780	26.619	32.385	164.086	16.223	1.961	9.311

The highest genotype *x* environment interaction coefficient of variation (G x ECV) of 34% was obtained for grain yield followed by lodging index (33 %) and harvest index (32%). These traits also have comparatively higher GCV at each of the two test locations and hence possible to improve them through selection breeding. The G x ECV values for most of the traits considered in this study were found to be less than the GCV values. This indicates that the variability observed in tef landrace populations are highly due to the genetic component than due to the interaction between genotype and environment. Kebebew Asefa *et al*. (2001) found that higher values of

PCV and GCV can be obtained in mono-environment than in multi-environment experiment due to high genotype *x* environment interaction effect noted for most of the traits evaluated in multiple environments.

Broad sense heritability (H^2) and Genetic advance

Heritability and genetic advance are important factors to determine the success of selection in breeding programs. Pandey and Tiwari (1983) indicated the importance of estimating heritability to know the inheritance of quantitative traits as it indicates the genetic gains that may be gained through selection. Genetic advance provides a prior quantitative estimate of the magnitude of the progress that could be achieved through selection (Panes, 1957).

Estimates of heritability (H^2) varied from 0.183% for number of culm internodes at Gute location to 96.32% (for grain yield per plant) at Bako. Hence, the highest heritability estimates were observed for grain yield per plant, lodging index and biomass weight per plant at both locations (Table 5 and 6). This indicates that improvement of these traits through selection is better than that for the remaining traits. Panicle length, plant height and shoot phytomass weight were also among the traits depicting high heritability at Bako. The fluctuation in heritability of some of the traits across environments implies that the utility of these traits for selection depends on the crosses and the environmental conditions. The least heritable traits were number of culm internodes (0.183%) at Gute and number of fertile florets per spikelet at top of the panicle (6.398%) at Bako site (Table 5 and 6).

Across locations lodging index, grain yield per plant and biomass yield per plant were the traits with maximum genetic advance as percent mean (Table 7). However, number of internodes per culm, number of fertile floret per spikelet at the top of the panicle and days to maturity were traits with minimum genetic advance across location. The higher heritability followed by higher genetic advance recorded for grain yield per plant, lodging index and biomass weight per plant in the current study indicated the ease of phenotype based selection and as it probably arose from additive gene effect. This also implied the possibility to improve the crop for its yielding capacity and its ability to resist lodging through selection. High heritability coupled with high expected genetic gain may result due to high additive gene effect and thus selection applied on such traits lead to yield improvement (Panes, 1957). At Bako, high heritability associated with low genetic advance was observed for plant height and panicle length. Such

result could be mainly due to dominance and epistasis (Panes, 1957). Comparatively, the lower heritability and genetic advance were recorded for culm length, number of culm internodes per main plant, number of fertile floret per spikelet at the top, middle and base of the panicle, days to maturity both at Bako and Gute; days to maturity, second culm internodes diameter, above ground shoot weight and harvest index at Gute. This implies that most of the variations for these traits were environmental; thus leading to low heritability and low expected genetic gains from selection.

Overall, the results for heritability and genetic advance in the current study provided information on the existence of wide genetic diversity in tef populations. This in turn offers high chances for improving several traits of the crop through selection and the need for hybridization to improve the characters with low heritability. Among previous studies on tef genetic diversity, Kebebew Asefa *et al*. (2001) reported low heritability (< 35%) for days to maturity, first basal culm internodes length, grain yield per plant and harvest index, intermediate heritability (35-54%) culm length, diameter of the first and the second basal culm, peduncle length and grain yield per panicle. But, days to panicle emergence, panicle length, average number of fertile florets per spikelet and number of panicle branches were relatively higher heritable traits.

Hailu Tefera (1988) noted high estimates of GCV, heritability and genetic advance as percent mean for number of spikelets per main panicle, 100 kernel weight, grain yield per main panicle, panicle length and kernel weight per main panicle and number of productive tiller per main plant there by indicating the possibility to improve these characters through single plant selection. Kebebew Asefa *et al*. (2001) found relatively high (>17%) estimate of GA (% of mean) for number of fertile tillers per plant, number of fertile florets per spikelet, length and grain yield of main shoot panicle; intermediate (10-17% GA) values for days to panicle emergence, length of the second and diameter of the first basal culm internodes, number of culm nodes, number of panicle branches and grain yield per plant. However, low GA (<10%) were estimated for harvest index, first and second basal culm internodes diameter, culm and peduncle length.

Hailu Tefera and Seyfu Ketema (2001) upon summarizing the results of narrow sense heritability (h^2) from three different studies, reported high h^2 values for days to grain filling period (48-74%), days to maturity (32-69%) and panicle length (40-68%); intermediate h^2 for grain yield per panicle (23%) with variation across studies, suggesting that this trait could be

reliable guide for selection. Low heritability values were reported for kernel weight (0.09), tiller number (0.15-0.52) and plant height (0.11-0.56).

CONCLUSIONS AND RECOMMENDATION

The significant variation ($P \leq 0.05$ and $P \leq 0.01$) between genotypes for most quantitative traits as revealed from analysis of variance indicated the existence of great genetic diversity among the tef populations. This in turn implies the possibility to improve traits such as yielding ability, resistant/tolerant to lodging and other important characters through selection breeding and through inter and intra-population crossing. This also gave a hint that diverse tef populations are grown within regions and within altitude classes.

The overall higher PCV than GCV implies that besides genetic factors, environmental factors have also great contribution to the gross variations observed. Comparatively higher G x E CV was obtained for grain yield, lodging index and harvest index. These traits also have comparatively higher GCV per location and hence are amendable to improvement through selection breeding. G x E CV values for most of the traits considered in this study were found to be less than the GCV values. This indicates that the variability observed in tef landrace populations were largely due to the genetic component than due to interaction between genotype and environment.

The relatively high heritability followed estimates by higher genetic advance noted for grain yield per plant, lodging index and biomass weight per plant in the current study indicated the ease of phenotype-based selection and this is probably due to additive gene effect. This also implies the possibility to improve the crop for its yielding capacity and its lodging resistance through selection breeding.

In order to overcome the problem of genetic erosion, the micro-center of origin/diversity for tef should be known to conserve, collect and utilize the tef genetic resources available. Hence, the regional and altitudinal distribution of the progenitors of tef should be known and tef populations from all tef growing region and agro-climates should be sampled proportionally and tested under multi-environments to predict the likely primary center of origin and diversity. Genetic information for tef especially at molecular level is limited, as compared to other cereal crops. Efficient utilization of the tef genetic resources and identification of superior genotypes for future breeding still urges morphological diversity studies supported by genotyping using molecular marker systems. Besides, further

biotechnology study should be conducted in order to induce desirable genes and create genetic diversity for utilization in solving major tef improvement constraints.

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