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Genetic Variability, Heritability and Genetic Advance of Some Tef (Eragrostis tef (Zucc.) Trotter) Varieties in Bench Maji Zone South Western, Ethiopia

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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 based on twelve morphological characters of tef (Eragrostis tef (Zucc**.)** Trotter.). The experiment was conducted in 2015 and 2016 main cropping seasons in three locations of Bench-Maji Zone by using randomized complete block design with three replications. The results revealed significant differences ($P < 0.05$) among genotypes for all characters considered in all locations except grain filling period at Guraferda. The maximum value between PCV and GCV was recorded forharvesting index both South Bench and Guraferda and by biomass yield at Sheko. High phenotypic coefficient of variation was recorded for days to emergency, grain yield, biomass yield and harvesting index in all environments in addition high PCV was recorded by number of primary panicle brunch at South Bench. GCV of high order was observed on grain yield, biomass yield and harvesting index in all locations. High heritability coupled with moderate genetic advance as percent of mean was observed for culm length and plant height at Guraferda and culm length, plant height, days to heading at Sheko. These traits are most likely controlled by both additive and non-additive gene actions. Therefore, any improvement of these characters would result in a substantial increment on grain yield. Evaluation for variability of tef using conventional approach still could provide vital information but using contemporary molecular genetic analysis approaches such as mapping of quantitative trait loci using molecular markers is helpful to understand variability at molecular level, improve selection knowledge and arrive at more comprehensive conclusions.

Keywords: Genetic advance, Heritability, Morphological Characters, Tef, Variability

Introduction

Tef (*Eragrostis Tef* (Zucc.) Trotter) is an annual grass crop and important cereal harvested for grain in Ethiopia. Ethiopia is not only the origin of tef but also the center of diversity [1].The exact date and location of domestication of tef is unknown. However, there is no doubt that it is a very ancient crop in Ethiopia, where domestication took place before the birth of Christ [2]. According to [3], tef originated in Ethiopia around 4000-1000 BC. It was probably cultivated in Ethiopia even before the ancient introduction of emmer wheat and barley [4].

In Ethiopia; the five major cereals (tef, wheat, maize, sorghum and barley) occupy almost three quarters of total area cultivated, and represent almost 70 percent of total value added in recent years [5]. Tef is adaptable to a wide range of ecological conditions in altitudes ranging from near sea level to 3000 masl and even it can be grown in an environment unfavorable for most cereal, while the best performance occurs between 1100 and 2950 masl in Ethiopia [6].

Tef is predominantly grown in Ethiopia as a food crop and not as a forage crop. However, when grown as a food, farmers highly value the straw of tef and it is stored and used as a very important source of animal feed, especially during the dry season. Farmers feed tef straw preferentially to lactating cows and working oxen. Cattle prefer tef straw to the straw of any other cereal and its price is higher than that of other cereals [2].

It has a fibrous root system with mostly erect stems, although some cultivars are bending or elbowing types [7]. The common name of the crop in Ethiopia is tef which seems to be derived from the Amharic word '*tefa*' to mean 'lost' to reflect the small size of the grain which disappears if scattered on the ground [2].

In Ethiopia, it is mainly produced in Amhara and Oromia, with smaller quantities in Tigray and South Nation Nationality People (SNNP) regions. However, the productivity of tef is low. The causes of low yield levels is low yielding varieties, low yielding potential of the landraces, poor management practices, moisture stresses, susceptibility to lodging which is the major bottleneck for tef mechanization, and lower variation in landraces. Therefore, assessing variability is fundamental to identify important traits for tef improvement. Knowledge of genetic variability, heritability and genetic advance provide more reliable information on variability, heritable trait, nature and level of interrelationship of tef yield and yield components. Therefore, the present study was conducted to understand the nature and extent of genetic variability, heritability and genetic advance in some important traits of tef genotypes.

Materials and Methods

Description of the study area

The experiment conducted at three locations of Bench Maji zone, namely South Bench, Guraferda and Shekoworeda during 2015 and 2016 main cropping season. The geographical study areas were characterized as semi tropical type with acidic nature of nitisols. The average annual rain fall of the area is wet moist for most months of the year with relative dry season in end of December up to beginning of March.

Table 1. Descriptions of Average temperate, altitude, latitude and longitude of testing locations

Location	Altitude (m.a.s.l)	Average temperate	Global positions	
			Latitude	Longitude
Sheko	950-1800	22.6 ^{0}C	N6^0 83' N	35^0 00' E
Debub Bench	980-1900	22.35 ^{0}C	N6^0 91' N	35° 16' 0' E
Guraferda	946-1800	23.1^{0}C	N6^0 25' N	35° 16' 0' E

***Sources**: Zone agricultural office*

Experimental materials

About 11 released tef varieties and one local that expected to perform better in the areas were used for this study. The varieties were selected based on average yield performance and agro ecological adaptation. The verities were obtained from Debrezeyt Agricultural Research center.

Table 2. List of tef (*Eragrostis tef*) genotypes used in this study

No	Code	Locale name	Released By	Year of release
1	DZ-Cr-354	Enatit	DZARC	1970
2	DZ-01-899	Gimbechu	MARC	2007
3	DZ-01-196	Magna	DZARC	1970
4	DZ-01-2675	Degatef	DZARC	2005
5	DZ-Cr-438	kora	MARC	2014
6	Ho-Cr-136	Amarach	DZARC	2006
7	DZ-Cr-387	Quncho	DZARC	2006
8	DZ-Cr-409	Boset	DZARC	2012
9	DZ-01-1285	Koye	DZARC	2002
10	DZ-01-255	Gibie	DZARC	1993
11	DZ-Cr-974	Dukem	DZARC	1995
12	Local Check			

Experimental Design

The experiment was laid out in RCBD with three replications and the plot size was 2m x 2m. A 1m space between plots and 1.5m between adjacent blocks were left for easy movement. Each genotype was sown at seed rate of 25 kg/ha by row planting. A recommended fertilizer rate 100kg/ha DAP and 53kg/ha urea were applied. All other trials management activities were carried out asdeemed necessary.

Data collection

The following quantitative datawere recorded from field observation:

a) Days to emergency
Number of days taken from date of sowing to 80 present of plants to emerge

b) Days to heading
Number of days from planting to 50% heading of the plants in a plot.

c) Days to maturity
Number of days taken from date of sowing to physiological maturity of the plants

d) Days to grain fill period
Number of days from 50% heading of the plants to maturity

e) Culm length (cm)
The heights of the five plants selected at random were measured at harvesting time in centimeter. The height was taken as the distance between the soil surfaces to the beginning of panicle.

f) Panicle length (cm)
Heights of the five plants selected at random measured at harvesting time in centimeter; height was taken as the distance between the ends of culm to tip of panicle

g) Plant height (cm)
Height of the main stem from the ground level to the tip of the main stem measured in centimeters at the time of harvesting

h) Number of primary branches per plant

Counting the total number of primary branches on main stem of each selected plant at the time of harvest

i) Grain yield per plot (kg)

Weight of the total grains on each plot of a particular variety obtained and recorded asgrain yield per plot

j) Biomass yield per plot (kg)

Total biological yield (biomass) produced at each plot recorded and expressed in kilogram

k) Harvest index (%)

Ratio of seed yield to the total biological yield per plot expressed in percentage

$$\text{Harvest index (HI)} = \frac{\text{Seed yield/plot (kg)}}{\text{Total biological yield/plot (kg)}} \text{ X } 100$$

Statistical Analysis

Analysis of variance (ANOVA)

The data were subjected to analysis of variance using SAS software program version 9.1.3 [8]. The significant differences among genotypes were tested by ‘F’ test at 1% and 5% levels of probability. The structure of analysis of variance (ANOVA) table is presented below.

Table 3. The structure of analysis of variance (ANOVA) **[9]**

Source	Df	(SS)	(MS)	F
Block	r-1	SSB	SSB/(r-1)	MSB/MSE
Treatment	t-1	SST	SST/(t-1)	MST/MSE
Error	(r-1)(t-1)	SSE = TSS-SST-SSB	SSE/(r-1)(t-1)	
Total	tr-1	TSS		

Where: r = Number of replications; t = Number of treatments / genotypes; SS =Sum of square; MS = Mean of square; S.Em = ± E.M.SS/r

$$\text{Coefficient of variation (CV \%)} = \frac{\sqrt{ErrorMS}}{Grandmean} X\ 100$$

The significance was tested by referring the table given by [10].

Components of variance

The genotypic and phenotypic components of variance were computed according to formulae given by [11] for the observed characters.

$$Vg = \frac{MST - MSE}{r}$$

Where: V_g ($\sigma^2 g$) = genetic variance; MST=mean square of treatment; MSE (Ve) = Error variance

r = Number of replications

Genotypic and Phenotypic variance

$\sigma^2 g = \sigma^2 p - \sigma^2 e$

Where: $\sigma^2 g$ = genetic variance; $\sigma^2 p$ = phenotypic variance; $\sigma^2 e$ = error variance

Genotypic and phenotypic Coefficient of variability

Genotypic and phenotypic coefficients of variability were computed according to[11].

$$\text{Genotypic coefficient of variability (GCV)} = \frac{\sqrt{\sigma 2g}}{x} \text{ x } 100$$

$$\text{Phenotypic coefficient of variability (PCV)} = \frac{\sqrt{\sigma 2p}}{x} \text{ x } 100$$

$$\text{Environmental coefficient of variability (ECV)} = \frac{\sqrt{\sigma 2e}}{x} \text{x } 100$$

Where, σ^2_g= Genotypic variance

σ^2_p = Phenotypic variance and

σ^2_e = Environmental variance

X = General mean of character

The PCV and GCV values are ranked as low, medium and high [12] as follows: 0-10% - Low; 10-20% - Moderate; >20% - High

Heritability

Broad sense heritability was estimated based on the ratio of genotypic variance to the phenotypic variance and was expressed in percentage [13].

$$h^2_{B=} \frac{Vg}{V_p} \times 100$$

Where: h^2_B= heritability in broad sense; V_g = Genotypic variance; V_p = Phenotypic variance

Heritability values are categorized as low, moderate and high [14] as follows: 0-30%: Low; 30-60%: Moderate; 60% and above: High

Genetic advance

The extent of genetic advance is expected by selecting certain proportion of the superior progeny was calculated by using the following formula given by [14].

Genetic advance (GA) = $k \sigma_p h^2$

Where: k = Intensity of selection at 5% (k – 2.06); σ_p = Phenotypic standard deviation; h^2 = Heritability in broad sense

The value of 'k' was taken as 2.06 assuming 5 % are selected.

Genetic advance is calculated by means of narrow sense heritability

Genetic advance expressed as percentage over Mean (GAM)

$$GAM = \frac{GA}{\bar{X}} \times 100$$

Where: GA = Genetic advance; x = General mean of the character

The GAM was categorized as suggested by [15] **as: 0-10 % = Low; 11-20 % = Moderate; >20 % High**

Results and Discussion

The present experiment was carried out to assess the nature and extent of genetic variability, heritability and genetic advance of twelve germplasm accessions of tef. The data recorded on the characters considered were subjected to statistical analysis to find out means and genetic parameters among the different characters.

The analysis of variance for different characters at South Bench, Guraferda and Sheko locations are presented in Table 4, 5 and 6, respectively. The results revealed significant differences ($p<0.05$) among genotypes for most characters among locations except grain filling period at Guraferda woreda**.** The results generally showed the existence of genetic variability with in yield and yield component in the population, which is desirable and can be utilized for developing or selection of the best genotypes. This difference may be due to the differences of genotypes used in the studies and environments used to test the genotypes. In general, the presence of variations among genotypes for the traits indicates the higher chance of improving the crop through selection. In agreement with the current study, [16] reported that presence of considerable variations among the 49 genotypes of tef. Similarly, [17] reported that significance differences between varieties for the characters like days to maturity, panicle length, plant height days to heading, days to maturity, grain yield. However, the results of the present study is in contrast to the findings of [18] that reported non-significant differences among tef genotypes tested in east Gojjam for yield, biomass yield and harvest index.

Table 4. Analysis of variance for different characters of tef Genotypes studied at South Bench

Sources of variation	df	CL	PL	PH	DE	DH	DM	GFP	PPB	GY	BM	HI
MSR	2	30.03	6.72	48.37	2.00	0.94	11.27	12.21	14.57	0.013	0.889	40.57
MST	11	68.4**	29.3*	55.2*	4.38*	13.4*	23.5*	28.9*	46.5**	0.088**	2.45**	130.05 **
MSE	35	13.17	12.01	21.26	1.10	4.37	9.64	9.24	8.04	0.015	0.5	24.41
F-value		5.19	2.44	2.6	4.00	3.07	2.44	3.12	5.79	5.67	4.87	5.33
CV (%)		6.25	10.67	5.09	19.40	2.89	2.74	7.38	13.1	23.26	23.73	25.73
SE		±2.1	±2.00	±2.66	±0.61	±1.21	±1.79	±1.75	±1.64	±0.07	±0.41	±2.85

** = Significant at 5% level of probability, ** = highly Significant at 1% level of probability, ns= Not significant, CL=Culm length, PL=panicle length, PH=plant height,DE days to emergency, DH=days to heading, DM days to maturity, GFP=grain filling period, PPB=primary panicle brunch, GY=grain yield, BMY=biomass yield, HI=harvest index, MSR=mean square of replication, MST= mean square of treatment, MSE =mean square of error, CV=coefficient of variation and SE=standard error.*

Table5. Analysis of variance for different characters of tef genotypes studied at Guraferda

Source of variatio	*df*	CL	PL	PH	DE	DH	DM	GFP	PPB	GY	BM	HI
MSR	2	55.7	18.01	135.2	0.78	0.33	10.58	11.08	2.41	0.01	0.14	12.93
MST	11	116.8*	28.3*	193.01**	5.4**	19.65*	27.28*	29.7^{ns}	18.5*	0.03**	1.36**	34.25 *
MSE	35	14.06	8.9	30.79	0.32	6.18	6.97	18.44	6.35	0.005	0.16	12.93
F-value		8.26	3.17	6.27	16.59	3.15	3.91	1.61	2.91	5.88	8.24	2.65
CV (%)		6.55	9.38	6.21	10.71	3.61	2.59	13.05	12.47	14.15	14.7	18.69
SE		±2.16	±1.7	±3.2	±0.33	±1.44	±1.52	±2.48	±1.45	±0.04	±0.23	±2.08

** = Significant at 5% level of probability, ** = highly Significant at 1% level of probability, ns= Not significant, CL=Culm length, PL=panicle length, PH=plant height,DE days to emergency, DH=days to heading, DM days to maturity, GFP=grain filling period, PPB=primary panicle brunch, GY=grain yield, BMY=biomass yield, HI=harvest index, MSR=mean square of replication, MST= mean square of treatment, MSE =mean square of error, CV=coefficient of variation and SE=standard error.*

Table6. Analysis of variance for different characters of tef genotypes studied at Sheko

Source of variatio	*df*	CL	PL	PH	DE	DH	DM	GFP	PPB	GY	BM	HI
MSR	2	58.6	7.79	103.04	4.36	6.86	15.36	28.69	4.6	0.003	0.4	21.9
MST	11	123.2**	37.6*	225.1**	5.68**	95.05**	50.02*	138.8**	21.2*	0.03*	1.73*	50.2*
MSE	22	14.06	11.14	33.51	0.9	4.89	14.51	19.36	7.92	0.01	0.53	16.4
‘F’ value		8.76	3.38	6.72	6.27	19.43	3.45	7.17	2.68	2.95	26.48	3.06
CV%		6	10.38	6.11	20.16	3.22	3.36	9.86	12.94	23.13	3.24	24.07
SE		±2.45	±3.22	±2.47	±4.49	±1.79	±1.83	±3.14	±3.6	±4.81	±1.8	±4.91

** = Significant at 5% level of probability, ** = highly Significant at 1% level of probability, ns= Not significant, CL=Culm length, PL=panicle length, PH=plant height,DE days to emergency, DH=days to heading, DM days to maturity, GFP=grain filling period, PPB=primary panicle brunch, GY=grain yield, BMY=biomass yield, HI=harvest index, MSR=mean square of replication, MST= mean square of treatment, MSE =mean square of error, CV=coefficient of variation and SE=standard error.*

Phenotypic and Genotypic Coefficient of Variation

The effectiveness of selection in any crop depends on the extent and nature of phenotypic and genotypic variability present in different agronomic traits of the population [19]. Generally, genetic parameters including genotypic coefficient of variation, heritability and genetic advance are prerequisite for genetic improvement of crops [20]. High genotypic coefficient of variation indicates availability of high genetic variation. The lower value of variation indicates that selection is not effective for particular character because of the narrow genetic variability [21, 19].

According to [11], PCV and GCV values great 20% are regarded as high, whereas values less than 10% are considered to be low and values between 10% and 20% to be moderate. Estimated variance components, PCV and GCV for the characters studied are presented in Tables (7, 8 and 9). In this study, PCV ranged from (3.34%) fordays to maturity to(40.22 %) forharvest index and the GCV ranged from 1.9% for days to maturity to 12.9 % for harvest index at South Bench, PCV ranged from (3.64%) for days to maturityto (27.11 %) for biomass yield and the GCV ranged from 2.56% for days to maturity to 24.46 % for days to emergency at Guraferda and also PCV ranged from (4.54%) for days to maturity to (35.07 %) for biomass yield and the GCV ranged from 3.04% for days to maturity to 26.72 % for days to emergency at Sheko. The maximum variability between PCV and GCV was recorded for harvesting index at both South Bench and Guraferda but at Sheko the maximum variability between PCV and GCV was recorded by trait biomass yield. It indicates that the expression of character relatively more influenced by environments. In agreement with the present study [18] reported that the maximum value between PCV and GCV for harvesting index.

PCV values were greater than GCV values across environments in all traits although the differences were small. The small differences indicated that the environmental effect was small for the expression of most characters (Table 7, 8 and 9). The present study was in agreement with the results reported by [22, 23]. In contrast to this, [24] reported high GCV than PCV for shoot biomass, above ground plant biomass, panicle seed weight and harvest index.

Generally, the GCV and PCV were similar in magnitude and direction in all locations which indicated that the genotypes were able to express their genetic potential for various traits. GCV of high order was observedgrain yield, biomass yield and harvesting index in all environments in addition of high order GCV was expressedin days to emergency at both Guraferda and Sheko environment.High values of GCV suggest better scope of improvement for these traits by selection. Therefore, selecting the tef genotypes having higher grain yield, biomass yield and harvesting indexcould help enhancing the productivity of tef. The present study is inconsistent with what reported by [25, 18] in which grain yield, biomass yield and harvesting index. But days to emergency and number of primary panicle brunch at South Bench and culm length at Guraferda and also days to grain fill period at Sheko had moderate GCV. Similar findings with relatively higher (moderate) GCV values were reported by [18] and number of primary panicle brunch by [26].

Other traits such as panicle length, plant height, days to heading and days to maturityamong location and culm length and days to grain fill periodat South Bench,days to grain fill perioddays to grain fill periodand number of primary panicle brunch at Guraferda and also culm length and number of primary panicle brunch at Sheko had low GCV. The lower GCV for phenological traits and culm length, panicle length, plant height, however, suggests the difficulty of manipulating these traits for improvement of tef. Similar results of lower GCV inculm length,panicle length, plant height, days to heading and days to maturity by [26] and days to maturity, days to grain fill period, panicle length [27, 28] were reported .

High PCV was recorded for days to emergency, grain yield, biomass yield and harvesting index in all environmentsin addition high PCV was recorded by number of primary panicle brunchat south bench (Table 7, 8 and 9). In these traits environment contributes more than the genes effect for phenotypic expression of the trait. This result was in close agreement with the findings of [28]; for grain yield, biomass yield and harvesting index. However this result disagrees with the findings with [25] for grain yield, biomass yield and harvesting index. Traits such aspanicle length at all environment and culm lengthplant height,days to grain fill period andnumber of primary panicle brunch at Guraferda and Sheko had moderate value of PCV. The moderate value of PCV for days to grain fill period (10.9), plant height (10.36), panicle length (14.08) and culm length (16.07) was reported by [29].

Lower PCV was observed for days to heading and days to maturity in all environments. Similar results showing low PCV were reported for days to maturity (9.02) and days to heading (4.35) by [18] and for days to maturity by [16] and days to heading by [25].

Among all traits, high GCV and PCV values (>20%) were observed for biomass yield and harvesting index in all environment and grain yield at South Bench and Guraferda and also days to emergency at Guraferda and Sheko environment. Moderate GCV and PCV values (>10%) were observed fornumber of primary panicle brunch in all environment and days to emergency at south Bench, culm length and grain yield at Guraferda and days to grain fill periodat Sheko environment. therefore further selection of these traits could improve the genotype. On the other hand, low PCV and GCV (<10%) were observed for days to heading and days to maturity across location and culm length, plant height and days to grain fill period at South Bench. This traits offered less scope of selectionas they under the influence of environments. Generally, the PCV values were greater than GCV values although the differences were not large suggesting that there was influence of the environment. The environmental coefficients of variation (ECV) of traits were lower than both genotypic and phenotypic coefficient of variations. This implies that the environmental role was less for the expression of such characters.

Table 7. Genotypic, phenotypic and environmental coefficient of variation, genotypic, phenotypic and environmental variance, heritability and genetic advance (GA as % of mean) of quantitative traits of 11 genotypes of tef= South Bench

№	Character	Vp	Vg	Ve	PCV	GCV	ECV	h^2%	GA	GAM
1	CL(cm)	31.57	18.4	13.17	9.69	7.4	6.26	58.28	6.75	11.63
2	PL(cm)	17.77	5.76	12.01	12.98	7.39	10.67	32.41	2.82	8.67
3	PH (cm)	32.57	11.31	21.26	6.31	3.72	5.1	34.73	4.09	4.51
4	DE	2.19	1.1	1.1	27.46	19.46	19.37	50.23	1.53	28.41
5	DH	7.38	3.01	4.37	3.77	2.41	2.9	40.79	2.29	3.17
6	DM	14.27	4.63	9.64	3.34	1.9	2.74	32.45	2.53	2.23
7	GFP	15.79	6.55	9.24	3.51	2.26	2.68	41.48	3.39	2.99
8	PPB	20.86	12.82	8.04	21.11	16.55	13.1	61.46	5.79	26.74
9	GY(kg/p)	0.04	0.02	0.015	35.3	26.68	23.11	57.14	0.22	42.2
10	BM (kg/ha)	1.15	0.65	0.5	35.87	26.96	23.65	56.52	1.25	41.67
11	HI (%)	59.62	35.21	24.41	40.22	30.91	25.73	59.06	9.39	48.92

CL=Culm length, PL=panicle length, PH=plant height, DH=days to heading, DM =days to maturity, GFP=grain filling period, PPB=primary panicle brunch, GY=grain yield, BMY= biomass yield, HI=harvest index, GV= Genotypic variance, GCV= Genotypic coefficient of variation, h^2 *= Heritability, PV=Phenotypic variance, PCV=Phenotypic coefficient of variation GAM=Genetic advance as per cent of mean, GA- genetic advance.*

Table 8. Genotypic, phenotypic and environmental coefficient of variation, genotypic, phenotypic and environmental variance, heritability and genetic advance (GA as % of mean) of quantitative traits of 12 genotypes of tef at Guraferda

№	Character	Vp	Vg	Ve	PCV	GCV	ECV	h^2%	GA	GAM
1	CL(cm)	48.31	34.25	14.06	12.11	10.2	11.84	70.90	10.15	17.68
2	PL(cm)	15.37	6.47	8.9	12.31	7.99	5.78	42.09	3.40	10.67
3	PH (cm)	84.86	54.07	30.79	10.32	8.24	24.58	63.72	12.09	13.54
4	DE	2.00	1.68	0.32	26.68	24.46	0.29	84.00	2.44	46.04
5	DH	10.67	4.49	6.18	4.75	3.08	4.01	42.08	2.83	4.12
6	DM	13.74	6.77	6.97	3.64	2.56	4.90	49.27	3.77	3.70
7	GFP	22.19	3.75	18.44	14.31	5.88	7.58	16.90	1.64	4.98
8	PPB	10.40	4.05	6.35	15.97	10.0	3.96	38.94	2.58	12.8
9	GY(kg/p)	0.015	0.01	0.005	24.01	19.91	0.00	66.67	0.17	33.00
10	BM(kg/ha)	0.56	0.40	0.16	27.11	22.92	0.14	71.43	1.10	39.99
12	HI(%)	20.04	7.11	12.93	23.28	13.87	7.70	35.48	3.27	17.03

CL=Culm length, PL=panicle length, PH=plant height, DH=days to heading, DM =days to maturity, GFP=grain filling period, PPB=primary panicle brunch, GY=grain yield, BMY= biomass yield, HI=harvest index, GV= Genotypic variance, GCV= Genotypic coefficient of variation, h^2 *= Heritability, PV=Phenotypic variance, PCV=Phenotypic coefficient of variation GAM=Genetic advance as per cent of mean, GA- genetic advance.*

Table 9. Genotypic, phenotypic and environmental coefficient of variation, genotypic, phenotypic and environmental variance, heritability and genetic advance (GA as % of mean) of quantitative traits of 12 genotypes of tef at Sheko

№	Character	Vp	Vg	Ve	PCV	GCV	ECV	h^2 %	GA	GAM
1	CL(cm)	50.44	36.38	14.06	11.36	9.65	6.0	72.13	10.55	16.88
2	PL(cm)	19.96	8.82	11.14	13.91	9.25	10.39	44.2	4.07	12.66
3	PH (cm)	97.38	63.87	33.51	10.43	8.45	6.12	65.59	13.33	14.09
4	DE	2.49	1.59	0.9	33.43	26.72	20.1	63.9	2.08	44.01
5	DH	34.94	30.05	4.89	8.63	8.0	3.23	86.01	10.47	15.28
6	DM	26.35	11.84	14.51	4.54	3.04	3.37	44.93	4.75	4.2
7	GFP	59.18	39.82	19.36	17.24	14.15	9.86	67.29	10.66	23.9
8	PPB	12.35	4.43	7.92	16.16	10.0	12.95	35.85	2.6	11.94
9	GY(kg/p)	0.02	0.01	0.01	32.89	23.26	23.26	40	0.12	27.1
10	BM (kg/ha)	0.93	0.4	0.53	35.07	23	26.47	43.01	0.85	31.07
11	HI(%)	27.66	11.26	16.4	31.27	19.95	24.08	40.71	4.41	26.22

CL=Culm length, PL=panicle length, PH=plant height, DH=days to heading, DM =days to maturity, GFP=grain filling period, PPB=primary panicle brunch, GY=grain yield, BMY= biomass yield, HI=harvest index, GV= Genotypic variance, GCV= Genotypic coefficient of variation, h^2 *= Heritability, PV=Phenotypic variance, PCV=Phenotypic coefficient of variation GAM=Genetic advance as per cent of mean, GA- genetic*

Estimates of Heritability (H_2B) In Broad Sense

Information on heritability in broad sense (h_2B) and genetic advance of yield attributing traits and their association helps plant breeder to identify characters for effective selection [30]. The concept of heritability explains whether differences observed among individuals rose as a result of differences in genetic makeup or due to environmental forces. According to [14], heritability values are categorized as low from 0-30%, moderate from 30-60% and 60% and above are high.Considering this benchmark, heritability estimate of this study are described as follows.

Heritability estimate for characters under study at south bench, Guraferda and Sheko are indicated in Table (7, 8and 9) respectively. PPB was the only character with high heritability value (80%) at south bench. Character such as culm length, panicle length, plant height, days to emergency, days to heading, days to maturity, grain yield, biomass yield and harvesting index exhibited moderately high heritability values. High heritability values for this traits indicated that the variation observed was mainly under genetic control and was less influenced by the environment and the possibility of progress from selection. This is in harmony with the findings of [18] reported similar moderate heritability in tef for panicle length, grain yield, biomass yield and harvesting index and also similar finding has been reported by[23] in panicle length (59%), days to maturity (37.2) and grain yield (56.7). Inconsistent with this finding, [31] noted lower heritability for grain yield (25.68), harvest index (19.6%) and shoot biomass (17.2%) recorded.

At Guraferda, some characters like culm length (70.9%), plant height (63.7%), days to emergency (84%), grain yield (66.6%) and biomass yield (71.4%) had exhibited relatively high heritability values. Other characters, Such as panicle length (42.09%), days to heading (42%), days to maturity (49.2%), number of primary panicle brunch (38.94%) and harvesting index (35.48%) shown moderate high heritability values. Likewise, culm length 72.13%), plant height (65.59%), days to emergency (63.9%), days to heading (86.01%) and days to grain fill period(67.29%) at Sheko showed very high heritability estimates in the broad sense. High heritability values for these traits indicated that the variation observed was mainly under genetic control and was less influenced by the environment and the possibility of progress from selection. This may be attributed due to uniform environmental conditions during the conduct of the experiment. Indicating that the possibility of success in selection. Earlier workers also reported relatively higher broad sense heritability values for culm length, plant height, days to heading and days to grain fill period by [18] and days to heading, grain yield and biomass yield by [25]. However, inconsistent with this findingculm length, plant height, days to heading, days to grain fill period, grain yield and biomass yield recorded low heritability [16].

Expected Genetic Advance (GAM %)

The expected genetic advance (GA) values for 12 characters of the genotypes evaluated are presented in table (7, 8 and 9). These values are also expressed as percentage of the genotypes mean for each character so that comparison could be made among various characters, which had different units of measurement. High h_2B along with high GA is an important factor for predicting the resultant effect of selecting the best individuals. Percentage of mean genetic advance (GAM) estimates varied from (6.8%) for days maturity to (48.92%) for harvesting index, from (3.70%) for days to maturity to (46.04%) for days to emergency and from (4.2%) for days to maturity to (44.01%) for days to emergency at South bench, Guraferda and Sheko environments, respectively.

According to [15], genetic advance as percent of mean was classified as low (<10%), moderate (10-20%) and high (>20%). In this study at south bench Higher GAM (> 20 per cent) was recorded for days to emergency (28.41%), number of primary panicle brunch (26.74%), grain yield (42.2%), biomass yield (41.67%) and harvesting index (48.92%) and also moderate GAM for culm length (11.63%) was recorded. [25] also found similar results with the present study results in Grain yield (20.25%) and biomass yield (27.81). Genetic advance values were low (<10%) for panicle length(8.67%, plant height (4.51%), days to heading (3.17%), days to maturity (2.23%) and days to grain fill period (2.99%). Similar work was noticed by [25] indicated the genetic advance was low (<10%) for traits like Panicle length (7.61%), Days to heading (7.22%) and, Days to maturity (9.34%).

At Guraferda, high genetic advance as a percent mean was observed for days to emergency (46%), grain yield (33%) and biomass yield (39.99%). But traits like culm length (17.68%), panicle length (10.67%), plant height (13.54%), number of primary panicle brunch (12.8%) and harvesting index (17.03%) showed moderate genetic advance as a percent mean. Similar finding has been reported by [28] lowest estimate was observed for both days to heading (4.12%) and days to maturity (3.7%).

The high genetic advance as a percent mean at Sheko was observed for days to emergency (46.04%, days to grain fill period (23.9%, grain yield (33%), biomass yield (39.99%) and harvesting index (26.22%). Moderate genetic advance as a percent mean culm length (16.88), panicle length (12.66%) plant height (14.09%), days to heading (15.28%) and number of primary panicle brunch (11.94%).

Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone. However, it is not necessary that a character showing high heritability will also exhibit high genetic advance [15]. In the present study, high heritability accompanied with high genetic advance values as percentage of the mean were observed for number of primary panicle brunchat South Bench, days to emergency, biomass yield and grain yield at Guraferda and also days to emergency and days to grain fill period at Sheko. Hence, selection for such traits is likely to be effective as high heritability values were associated with high genetic advance.This is in close agreement with the findings of [25] reported that, the high estimates of heritability with low genetic advance were detected for biomass yield, grain yield and number of primary panicle brunch. This is consistent with [32], where low heritability with low genetic advance values was found for biomass and grain yield.

High heritability coupled with moderate genetic advance as percent of mean was observed for culm length and plant height at Guraferda and culm length, plant height, days to heading at Sheko. These traits are most likely controlled by both additive (genes transmitted from parents to offspring) and non-additive (interaction between genes of the same or different loci) gene actions. Traits like culm length, days to emergency, grain yield and biomass yield at Sheko, panicle length, number of primary panicle brunch and harvesting index at Guraferda and panicle length, number of primary panicle brunchgrain yield, biomass yield and harvesting index at Sheko showed moderate heritability and genetic advance.

As opposite to the above, the traits panicle length, plant height, days to heading, days to maturity and days to grain fill periodat south bench, days to heading and days to maturity at Guraferda and days to maturity at Sheko depicted moderate heritability coupled with low genetic advance as percent of mean compared to other traits; this makes the improvement program of important traits or characters of sesame makes difficult. In agreement with the current finding, [33; 34] and [25] reported that, the moderate estimates of heritability with low genetic advance were detected for panicle length, days to maturity days to heading and days to grain fill period.

Therefore, any improvement of these characters would result in a substantial increment on grain yield. Thus, evaluation for variability of tef using conventional approach still could provide vital information but using contemporary molecular genetic analysis approaches such as mapping of quantitative trait loci using molecular markers is helpful to understand variability at molecular level, improve selection knowledge and arrive at more comprehensive conclusions. Repeating the experiment is advisable to better estimate environmental effects.

CONCLUSIONS

The objective of present investigation was to provide information for the improvement of grain yield and related traits in tef by obtaining estimates of the amount of genetic variation, and heritability and genetic advancement of traits. The results revealed that there is highly significant difference for all characters considered in the tested genotypes. Such variability is desirable and can be utilized for developing or selection of the best genotypes.

The GCV and PCV were similar in magnitude and direction in all locations which indicated that the genotypes were able to express their genetic potential for various traits. GCV of high order was observed grain yield, biomass yield and harvesting index in all environments. High values of GCV suggest better scope of improvement for these traits by selection. High PCV was recorded for days to emergency, grain yield, biomass yield and harvesting index in all environments in addition high PCV was recorded by number of primary panicle brunch at south bench. In these traits environment contributes more than the genes effect for phenotypic expression of the trait. Lower PCV was observed for days to heading and days to maturity in all environments.

High heritability coupled with moderate genetic advance as percent of mean was observed for culm length and plant height at Guraferda and culm length, plant height, days to heading at Sheko. These traits are most likely controlled by both additive (genes transmitted from parents to offspring) and non-additive (interaction between genes of the same or different loci) gene actions. As opposite to the above, the traits panicle length, plant height, days to heading, days to maturity and days to grain fill period at south bench, days to heading and days to maturity at Guraferda and days to maturity at Sheko depicted moderate heritability coupled with low genetic advance as percent of mean compared to other traits; this makes the improvement program of important traits or characters of sesame makes difficult.It can be concluded that the importance of continuing the study of variability in tef genotypes at different location to identify which traits can be used for causal selection of genotypes for grain yield.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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