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Genetic variability, heritability and genetic advance among yield and yield related traits of advanced Tef [*Eragrostis tef (Zucc.)* Trotter] breeding lines

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In Ethiopia, tef is one of the most significant crops that are grown extensively as a staple cereal crop. The evaluation of genetic variability in crop species is one of the key activities in plant breeding, which supports in the creation of breeding strategies to meet a diversify objectives. A field experiment was therefore conducted to determine genetic variability, heritability, and genetic advanced for yield and yield-related traits of tef genotypes. The experiment was laid out in 7x7 simple lattice designs at two locations (Bishoftu and Akaki) in central Ethiopia during the 2021/22 main cropping season. For the majority of the parameters, the combined analysis of variance over locations revealed significance differences in location, genotype, and genotype x location interactions. The genotypic coefficient of variation (GCV) ranged from 2.96% for the number of primary panicle branches per main shoot to 15.82% for days to physiological maturity, while the phenotypic coefficients of variation (PCV) ranged from 3.62% for days to physiological maturity to 18.42% for the number of primary panicle branches per main shoot. Genetic advanced as a percentage of mean ranges from 2.43% (number of total tillers per plant) to 28.03% (number of primary panicle branches per main shoot) and heritability in the broadest sense ranges from 14% (number of total tillers per plant) to 88.67% (day to heading), respectively. High heritability coupled with high genetic advance as percentage of mean was recorded for the number of spikelets per panicle, number of primary panicle branches per main shoot and panicle length. Generally, the variation observed among the tested genotypes confirmed the possibility of improving tef genotypes for better yield through selection and hybridization.

Key words: Genotypic coefficient of variation, genetic advance, genetic variability, heritability, phenotypic coefficient of variation.

INTRODUCTION

Tef [*Eragrostis tef (Zucc.)* Trotter] (2n =4x =40] belongs to the family Poaceae and the genus *Eragrostis*. In Ethiopia, tef is the most significant crop grown for a different use. Because of the tef grain's nutritional and health advantages, as well as the fact that it doesn't contain gluten, the substance that causes celiac disease,

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the production of tef grain is gaining popularity on a global scale (Spaenij-Dekking et al., 2005; Hopman et al., 2008; Bergamo et al., 2011). In terms of production and consumption, it is the most significant staple cereal crop that thrives in various climatic and soil environments (Neela and Solomon, 2018).

Tef is a cereal crop that can grow in several of ecological conditions, from below the sea level to 3000 m above sea
level (m. a. s. l.). More over 7.1 million smallholder farmers produced tef on 3.1 million hectares of land in 2019/20, making up around 24.1% of the total area used for grain cultivation in the country. In Ethiopia, 40% of smallholder farmer households cultivated tef, which accounts for 17% of all grain production (CSA, 2020) and is the most significant economically important crop. Amhara and Oromia are the two main tef producing regions in Ethiopia, and together they account for 85.3% of the country's land area and 87.2% of its production, with an overall average productivity of 1.85 t/ha (CSA, 2020).

According to Allard (1960) and Falconer and Mackay (1996), variability is the occurrence of differences between individuals as a result of their genetic make-up and/or the environment in which they are raised. Differences in character expression between two individuals would be caused by genetic control if it were possible to measure these differences in an environment that was the same for both individuals (Falconer and Mackay, 1996).

For the crop to be further improved, understanding the degree and pattern of genetic variability present in a population is crucial. Understanding genetic variation is critical for improving yield and its components in any crop, as observable variability results from a combination of genetic, environmental, and numerous interactions between genes and environments. Thus, there is a need to evaluate the available genotypes for genetic variability and identify the best performing genotypes for future use in the breeding program. Therefore, the present study was, conducted, to assess genetic variability, heritability, and genetic advance for yield and yield-related traits in advanced tef breeding lines.

MATERIALS AND METHODS

Descriptions of experimental locations

The field experiment was carried out at the Debre Zeit Agricultural Research Center (DZARC) main station (Bishoftu) and the Akaki sub-station during the 2021/22 main cropping season. Bishoftu is located at (8° 44' N, 38° 58' E, and 1900 m.a.s.l) whereas Akaki at (8^{o} 53' N, 38° 58' E, and 2400 m.a.s.l) latitude, longitude, and altitude, respectively. The two locations are characterized by a moist tropical climate and experience a long rainy season extending from June to September. Bishoftu receives a mean annual rainfall of 832 mm during the main growing season, with maximum and minimum mean annual temperatures of 24.3 and 8.9°C, respectively. In contrast, Akaki often receives annual total rainfall of 1254 mm with maximum and minimum mean annual temperatures of 30 and 10°C, respectively. The experimental field at both locations is characterized by heavy black soil (vertisoil) with a very high moisture retention capacity.

Experimental plant materials

The experimental tef plant materials were obtained from Debre Zeit Agricultural Research Center of the National Tef Breeding Program. Forty-nine genotypes (48 advanced lines and 1 standard check (Dagim)) were used in the experiment. Table 1 shows the list and description of tef genotypes used for the study.

Experimental design, layout and management

The experiment was set up using a 7x7 simple lattice design with two replications. Each experimental plot measured 2 m^2 (1 m × 2 m) and had five rows that were 20 cm apart. Distances between incomplete blocks and between plots within incomplete blocks were 1.5 and 1 m, respectively. Within each replication, the genotypes were distributed randomly to plots. All additional crop management practices and recommendations were uniformly implemented to all genotypes as recommended for the crop.

Data collection and analysis

Days to 50% heading, days to 90% physiological maturity, grain filling period, plant height, panicle length, peduncle length, culm length, number of spikelets per panicle, number of primary panicle branches per main shoot, number of florets per spikelet, number of total tillers per plant, number of fertile tillers per plant, lodging index, above-ground biomass per plot, grain yield per plot, harvest index and thousand seed weight data were collected and subjected to analysis using appropriate software.

In addition to phenotypic and genotypic coefficients of variation, the variability of each quantitative trait was evaluated using simple metrics like mean, range, and standard deviation. The formula presented by Singh and Chaudhary (1977) was used to estimate the phenotypic (PCV) and genotypic (GCV) coefficients of variations.

Genotype variance ($\sigma^2 g$) = $\frac{MS_g - MS_e}{r}$

Phenotypic variance ($\sigma^2 p$) = $\sigma^2 g + \sigma^2 e$

Where, $\sigma^2 g$ = genotypic variance MS_g= mean square of genotype MS_e = mean square of error r = number of replications $\sigma^2 e$ = Environmental variance and $\sigma^2 p$ = phenotypic variance.

$$PCV = \frac{\sqrt{phenotypic\ \text{var}iance}}{population\ mean\ for\ the\ trait} x100$$

$$GCV = \frac{\sqrt{genotypic\ \text{var}iance}}{population\ mean\ for\ thet\ rait} x100$$

Heritability (H^2) in broad sense for all characters was computed using the formula adopted by Allard (1960).

$$H^2 = \left[\sigma^2{}_g \Big/ \sigma^2{}_p \right] x100$$

Where; H^2 = heritability in broad sense

Table 1. List and description of tef genotypes used for the study.

No.	Pedigree (Genotype)	No.	Pedigree (Genotype)
1	DZ- Cr-387xRosea (RIL 162)	26	DZ-01-1681 x Alba (RIL 147)
2	DZ- Cr-387xRosea (RIL 14)	27	DZ-01-1681x Alba (RIL 142)
3	DZ- Cr-387xRosea (RIL 106)	28	DZ-01-1681x Alba (RIL 144)
4	DZ- Cr-387xRosea (RIL 196)	29	DZ-01-1681 x Alba (RIL 31)
5	DZ- Cr-387xRosea (RIL 173)	30	DZ-01-1681 x Alba (RIL 87)
6	DZ- Cr-387xRosea (RIL 6)	31	DZ-01-1681 x Alba (RIL 175)
7	DZ- Cr-387xRosea (RIL 132)	32	DZ-01-1681 x Alba (RIL 103)
8	DZ- Cr-387xRosea (RIL 92)	33	DZ-01-1681 x Alba (RIL 76)
9	DZ- Cr-387xRosea (RIL 96)	34	DZ-01-1681 x Alba (RIL 121)
10	DZ- Cr-387xRosea (RIL 117)	35	DZ-01-1681 x Alba (RIL 32)
11	DZ- Cr-387xRosea (RIL 138)	36	DZ-01-1681 x Alba (RIL 78)
12	DZ- Cr-387xRosea (RIL 163)	37	DZ-01-1681 x Alba (RIL 47)
13	DZ- Cr-87xRosea (RIL 7)	38	DZ-01-1681 x Alba (RIL 70)
14	DZ- Cr-387xRosea (RIL 58)	39	DZ-01-1681 x Alba (RIL 97)
15	DZ- Cr-387xRosea (RIL 107)	40	DZ-01-1681 x Alba (RIL 116)
16	DZ- Cr-387xRosea (RIL 53)	41	DZ-01-1681 x Alba (RIL 46)
17	DZ- Cr-387xRosea (RIL 122)	42	DZ-01-1681 x Alba (RIL 30)
18	DZ- Cr-387xRosea (RIL 119)	43	DZ-01-1681 x Alba (RIL 15)
19	DZ- Cr-387xRosea (RIL 1)	44	DZ-01-1681 x Alba (RIL 100)
20	DZ- Cr-387xRosea (RIL 98)	45	DZ-01-1681 x Alba (RIL 134)
21	DZ- Cr-387xRosea (RIL 157)	46	DZ-01-1681 x Alba (RIL 185)
22	DZ- Cr-387xRosea (RIL 155)	47	DZ-01-1681 x Alba (RIL 2)
23	DZ- Cr-387xRosea (RIL 166)	48	DZ-01-1681 x Alba (RIL 48)
24	DZ-Cr-387xRosea (RIL 91)	49	Dagim (DZ-Cr-438 RIL91)
25	DZ-01-1681 x Alba (RIL 120)		

DZ- Debre Zeit, Cr- Cross, Rosea and Alba- Tef cultivars.

The heritability estimates were categorized as low (0-30%), moderate (30- 60%) and high (60% and above) as suggested by Robinson et al. (1949).

Genetic advance under selection (GA) for each character was computed using the formula adopted by Johnson et al. (1955).

$GA = (k)(SDp)(H^2)$, and GA (as % of the mean) = $\left[\frac{(GA)}{\bar{x}}\right] x100$

Where; k = selection differential (with a value of 2.06 at 5% selection intensity), SDp= phenotypic standard deviation, H^2 = heritability in broad sense, $\bar{x}$ = Grand mean. Genetic advance as a percentage mean was categorized as low (0-10%), moderate (10-20% and high (≥20%) as suggested by Johnson et al. (1955).

RESULTS AND DISCUSSION

Analysis of variance

Tests were conducted to check the homogeneity of error variances prior to doing the combined analysis of variance over locations, and all of the traits showed homogeneity of error variances. Consequently, the data were pooled across locations and analyzed, and the results of the combined analysis of variance across the two test locations are presented in Table 2. The mean squares from the pooled analysis of variance over the two locations showed a highly significant location (P≤0.01) effect for almost all traits except for peduncle length and thousand seed weight. The mean squares from the pooled analysis of variance over the two locations also showed highly significant (P≤ 0.01) effects of genotypes for all traits except for number of fertile tillers per plant and thousand seed weight (Table 2). Similar significant results were reported for most traits in earlier studies (Solomon et al*.,* 2009; Jifar et al*.,* 2015; 2017; Tsion, 2016).

The mean squares resulting from the genotype x location interaction were statistically significant (P 0.05) for the number of florets per spikelet and the total number of tillers per plant, but highly significant (P 0.01) for the grain filling period, number of spikelets per panicle, lodging index, above ground biomass, and harvest index. Days to heading, panicle length, culm length, peduncle length, number of primary panicle branches per main shoot, number of florets per spikelet, number of fertile tillers per plant, harvest index, and thousand seed weight

Table 2. Mean squares from the combined analysis of variance of 17 traits of 49 tef genotypes tested at two locations during the 2021/22 main season.

Trait	MSl	MSr(l)	MSg	MSgl	MSE	CV (%)	R^2
	(df=1)	(df=2)	(df=48	(df=48)	(df=72)		
DTH	408.62**	8.49**	15.44**	0.52ns	0.72	1.63	0.97
DTM	519.19**	15.07*	41.96**	6.22ns	4.19	1.84	0.92
GFP	358.29**	1.66ns	25.41**	15.75**	5.75	4.06	0.84
PH	5247.14**	601.60**	129.52**	28.68ns	22.69	4.65	0.91
PL	659.02**	136.56**	42.12**	4.88ns	4.56	5.17	0.92
CL	2187.03**	248.17**	69.38**	21.55ns	20.25	7.36	0.85
PDL	14.28ns	22.20**	8.84**	3.80ns	3.81	9.45	0.75
NSPP	73247.56**	6669.41**	31633.28**	6495.23**	1153.71	5.43	0.97
NPBPMS	393.43**	56.14**	32.44**	3.22ns	4.57	10.18	0.90
NFPS	3.30**	7.17**	1.08**	0.56*	0.33	10.00	0.83
NTTPP	27.19**	16.50**	4.78**	4.14*	2.39	12.09	0.77
NFTPP	95.93**	23.50**	4.28ns	3.82ns	2.99	16.04	0.74
LI	7044.01**	178.13**	437.39**	149.03**	6.44	3.78	0.99
BY	2212656.25**	2389595.03**	1685890.73**	1994820.90**	57757.2	1.78	0.98
GY	1251753.40**	23494.58**	110401.01**	125128.47**	3077.62	2.12	0.99
HI	41.04**	1.93**	4.4089**	3.83**	0.22	2.44	0.97
TSW	0.0015ns	0.018**	0.0017ns	0.0014ns	0.0014	12.68	0.70

*,** Significant at $p \leq 0.05$, and $p \leq 0.01$ probability level respectively and ns= non-significant, Figures in parenthesis indicate degrees of freedom, MSl= Mean Squares of locations, MSr (l) =mean squares of block (location), MSg= Mean squares of genotypes, MSgl = Mean square of genotype x location interaction, MSE = Mean squares of error, CV = Coefficient of variation, R^2 = coefficient of determination. DTH =days to heading, DTM = days to physiological maturity, GFP = grain filling period, PH= Plant height, PL=panicle length, CL= culm length, PDL= peduncle length, NSPP=number of spikelets per panicle, NPPBMS = number of primary panicle branches per main shoot, NFPS =number of florets per spikelet, NTTPP= number of total tillers per plant, NFTPP= number of fertile tillers per plant, LI= lodging index, BY=biomass yield, GY= grain yield, HI = harvest index and TSW= thousand-seed weight.

did not show statistically significant genotype x location interaction (Table 2).

The findings of the current study agree with those of Kebede et al. (2019) which found no significant genotype x location interaction for days to heading, panicle length, culm length, peduncle length, number of florets per spikelet, total number of tillers per plant and thousand seed weight. Similar results were found by Solomon et al. (2009) and Assefa et al. (1999) regarding the genotype x location interaction effect on panicle length. The significant differences observed among the genotypes for grain yield and yield-related traits suggest the presence of substantial variation in the inherent genetic potential of the advanced lines/genotypes studied depicting the possibility of selecting high yielding tef genotypes.

Phenotypic and genotypic coefficient of variation

Genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV) are used to measure the variability that exists in a given population. High genotypic coefficients of variation indicate availability of high genetic variation. The GCV ranged from 2.96% for days to physiological maturity to 15.82% for number of primary panicle branches per main shoot, whereas the PCV ranged from 3.62% for days to physiological maturity to 18.42% for number of primary panicle branches per main shoot (Table 3). Sivasubramaniah and Menon (1973) suggested that the values of PCV and GCV can be categorized as low (0-10), moderate (10-20) and high (> 20).

According to this classification the estimates of PCV were moderate for peduncle length (11.18%), number of spikelets per panicle (18.29%), number primary panicle branches per main shoot (18.42%), number of florets per spikelet (13.84%), number of fertile tillers per plant (11.18%), lodging index (17.79%), grain yield (12.27%), harvest index (13.59%) and thousand seed weight (15.17) (Table 3). Previous findings by Solomon *et al*. (2009), Solomon (2010), Ayalew et al. (2011), Habte et al. (2015), Nigus et al. (2016) and Tsion (2016) were also similar to the present results for estimates of phenotypic coefficients of variation for most the tef traits.

On the other hand, GCV were relatively moderate for number of primary panicle branches per main shoot (15.82%), number of spikelets per panicle (14.73%) and lodging index (13.33%). In contrast to the present

Table 3. Estimates of variance components, phenotypic and genotypic coefficients variance, broad sense heritability and expected genetic advance for 17 traits of 49 tef genotypes based on analysis of variance over two test locations.

Traits	Range	Mean ±SE	σ^2g	σ^2p	GCV (%)	PCV (%)	H^2 (%)	GA	GAM (%)
DTH	48-57.50	52.17 ± 0.58	5.32	6.00	4.42	4.70	88.67	4.48	8.59
DTM	105.25-117.50	111.43 ±1.39	10.93	16.24	2.96	3.62	67.31	5.60	5.02
GFP	50.50-64.75	59.04 ±1.66	3.07	13.95	2.97	6.33	22.03	1.70	2.88
PH	91.05-116.80	102.48 ±3.33	31.61	58.29	5.49	7.45	54.24	8.54	8.34
PL	34.30-48.95	41.31 ±1.47	11.44	16.21	8.19	9.75	70.56	5.86	14.19
CL	51.40-69.70	61.17 ±3.09	13.49	35.19	6.00	9.70	38.33	4.69	7.67
PDL	16.30-26.05	20.70 ±1.4	1.60	5.36	6.11	11.18	29.88	1.43	6.89
NSPP	400.33-816.17	625.33 ±23.97	8485.70	13080.00	14.73	18.29	64.88	153.07	24.48
NPPBPMS	16.17-28.42	20.99 ±1.48	11.03	14.95	15.82	18.42	73.78	5.88	28.03
NFPS	4.55-7.03	5.76 ±0.46	0.21	0.64	7.90	13.84	32.59	0.54	9.30
NTTPP	10.05-14.95	12.79 ±1.14	0.16	1.11	3.12	8.26	14.26	0.31	2.43
NFTPP	8.85-13.30	10.77 ±1.25	0.25	1.45	4.66	11.18	17.42	0.43	4.02
LI	38.50-88.25	67.21 ±1.94	80.25	142.88	13.33	17.79	56.17	13.85	20.61
BY	10750-14750	13415.18±548.53	586283.90	1593897.86	5.69	9.38	37.00	956.63	7.10
GY	2222.20-2904.7	2615.49 ±38.92	46017.32	103030.91	8.20	12.27	45.00	295.33	11.29
HI	16.78-37.57	19.78 ±3.26	3.53	7.22	9.49	13.59	48.80	2.71	13.68
TSW	0.24-0.34	0.29 ±0.03	0.001	0.002	8.26	15.17	29.64	0.03	9.28

DTH =days to heading, DTM = days to physiological maturity, GFP = grain filling period, PH= Plant height, PL=panicle length, CL= culm length, PDL= peduncle length, NSPP=number of spikelets per panicle, NPPBPMS = number of primary panicle branches per main shoot, NFPS =number of florets per spikelet, NTTPP= number of total tillers per plant, NFTPP= number of fertile tillers per plant, LI= lodging index, BY=biomass yield, GY= grain yield, HI = harvest index and TSW= thousand-seed weight, SE=Standard error of mean, σ^2g = Genotypic variance, σ^2p=Phenotypic variance, PCV=phenotypic coefficients of variation, GCV= genotypic coefficients variation, H^2 =heritability in broad sense, GA= genetic advance, GAM= genetic advance as percentage of mean.

findings, Nigus et al. (2016) and Kebede et al. (2019) reported high value of GCV for lodging index and number of spikelet per panicle, respectively. Solomon (2010) and Ayalew et al. (2011) reported low value of GCV for day to maturity, harvest index and grain filling period.

PCV is usually the reflection of the effects of genotypes and environment and if PCV is greater than GCV, it indicates that the environment has a greater influence on the phenotypic expression of the trait than the gene effect (Habte et al., 2015). High GCV values imply greater potential for these traits to be improved through selection. Since improvement efforts typically concentrate on traits with higher values of GCV estimates, GCV provides a better measure of the extent of genetic variation. The number of spikelets per panicle, the number of primary panicle branches per main shoot and lodging index in this study all had moderate GCV values, indicating it opportunity for improvement. As a result, GCV allows for a better assessment of the extent of genetic variation among genotype (Solomon et al., 2013).

Heritability and expected genetic advance

Broad sense heritability values of the different traits based on the combined analyses of variance ranged from 14.26% for number of total tillers per plant to 88.67% for days to heading (Table 3). High heritability estimate was observed for days to heading (88.67%), days to physiological maturity (67.31%), panicle length (70.56%), number of spikelets per panicle (64.88%) and number of primary panicle branches per main shoot (73.78%). In line with the current findings similar results were reported by Solomon (2010) and Habte et al. (2015). Genetic advance as percentage of mean in present study ranged from 2.43% for number of fertile tillers per plant to 28.03 % for number primary panicle branches per main shoot (Table 3). In the present study, the number of primary panicle branches per main shoot (28.03%), number of spikelets per panicle (24.48%) and lodging index (20.61%) recorded high genetic advance as percentage of mean. For most traits' similar findings to that of the present study were also reported by Abel Debebe et al. (2012), Jifar and Gugssa (2013), Jifar et al. (2015, 2017) and Kebede et al. (2019).

The estimate of genetic advance as percentage of mean is more useful as a selection tool when considered jointly with heritability estimates (Johnson et al., 1955). Therefore, a high heritability together with a high genetic advance as a percentage of mean imply the importance of additive genes for the development of the traits, and this might make selection more successful. Both the number of spikelets per panicle and the number of primary panicle branches per main shoot showed high

heritability estimates in the current study along with high genetic advance as a percentage of mean, whereas panicle length showed high heritability values along with moderate genetic advance as a percentage of mean. For grain yield and harvest index, it was observed that there was a moderate heritability value along with a moderate genetic advance as a percentage of the mean. Similar to this, Solomon (2010) also noted a greater heritability value along with genetic advance as a percentage of mean for lodging index and panicle length.

To improve traits of interest, estimates of genotypic and phenotypic coefficients of variation, heritability, and genetic progress as a percentage of mean are crucial (Denton and Nwangburuka, 2011). The high heritability estimates along with low genetic advance as percentage of mean indicate that non-additive type of gene action and genotype x environment interaction play a significant role in the expression of the trait (Fatema et al., 2011). High GCV, heritability and genetic advance as percentage of mean for traits could be an excellent tool for improvement through selection of high performing genotypes (Akbar et al., 2003).

Conclusion

The current study showed a presence of significant genetic variations among tef genotypes for grain yield and yield-related traits, which allows plant breeders to develop improved varieties for the traits of interest and use them in the breeding program. The higher heritability estimate coupled with high genetic advance as percentage of mean found for important agronomic traits in the present study suggest the possibility of improving tef grain yield through direct selection of superior genotypes through phenotypic based selection. Thus, there is an opportunity of exploiting the existing variability in tef improvement programs through selection and hybridization.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

REFERENCES

Abel Debebe A, Singh H, Tefera H (2012). Genetic Variability and Heritability Studies in F_4 Progenies of Tef (Eragrostis tef). Asian Journal of Agricultural Sciences 5(4):225-228.

Allard RW (1960). Principles of Plant Breeding. John Wiley and Sons. Inc. New York, USA P 485.

Akbar M, Mahmood T, Yaqub M, Anwar M, Ali M, Iqbal N (2003). Variability, correlation and path coefficient studies in summer mustard (*Brassic juncea.* L). Asian Journal of Plant Science 2(9):696-698.

Bergamo P, Maurano F, Mazzarella G, Iaquinto G, Vocca I, Rivelli AR, De Falco E, Gianfrani C, Rossi M (2011). Immunological evaluation of the alcohol-soluble protein fraction from gluten-free grains in relation to celiac disease. Molecular Nutrition and Food Research 55(8):1266-1270.

Nigus C, Mohammed W, Damte T (2016). Genetic variation, correlation and path coefficient analysis in tef [*Eragrostis tef (Zucc.)* Trotter] genotypes for yield, yield related traits at Maysiye, Northern Ethiopia. American Journal of Research Communication 4(11):73-102.

Central Statistical Agency (CSA) (2020). Agricultural sample survey 2019/2020 (2013 E, C,). Vol I. Report on area and production of major crops (Private Peasant Holdings, Meher season). Statistical Bulletin 578 Addis Ababa, Ethiopia.

Denton OA, Nwangburuka CC (2011). Heritability Genetic Advance and Character Association in Six Yield Related Characters of *Solanum anguivi*. Asian Journal of Agricultural Research 5(3):201-207.

Falconer DS, Mackay TF (1996). Introduction to Quantitative Genetics. Essex. UK: Longman Group P 12.

Fatema K, Rasul MG, Mian MA, Rahman MM (2011). Genetic Variability for grain quality traits in aromatic rice (*Oryza sativa* L.). Bangladesh. Journal of Plant Breeding and Genetics 24(2):19-24.

Ayalew H, Genet T, Wondale L 2011. Correlation and Path Coefficient Analysis among Yield Component Traits in Tef [*Eragrostis tef (Zucc)*. Trotter] Landraces. Libyan Agriculture Research Center Journal International 2(4):180-185.

Jifar H, Gugssa L (2013). Variation in Major Traits of Gynogenically derived tef [*Eragrostis tef (Zucc.)* Trotter] lines Evaluated in the Central highlands of Ethiopia. Ethiopian Journal of Applied Science and Technology 4(1):50-64.

Jifar H, Tesfaye K, Assefa K, Chanyalew S, Tadele Z (2017). Semi-dwarf tef lines for high seed yield and lodging tolerance in Central Ethiopia. African Crop Science Journal 25(4):419-439.

Jifar H, Assefa K, Tadele Z (2015). Grain yield variation and association of major traits in brown-seeded genotypes of tef [*Eragrostis tef (Zucc.)* Trotter]. Agriculture and Food Security 4(1):1-9.

Hopman E, Dekking L, Blokland ML, Wuisman M, Zuijderduin W, Koning F, Schweizer J (2008). Tef in the diet of celiac patients in The Netherlands. Scandinavian Journal of Gastroenterology 43(3):277-282.

Johnson HW, Robinson HF, Comstock RF (1955). Genotypic and phenotypic correlation in Soya bean and their implication in selection. Agronomy Journal 47(10):477-483.

Assefa K, Ketema S, Tefera H, Nguyen HT, Blum A, Ayele M, Bai G, Simane B, Kefyalew T (1999). Diversity among germplasm lines of the Ethiopian cereal tef [*Eragrostis tef (Zucc.)* Trotter]. Euphytica 106:87-97.

Neela S, Solomon WF (2018). Review on structural, nutritional and anti-nutritional composition of tef (*Eragrostis tef*) in comparison with quinoa (*Chenopodium quinoa* Willd.). Cogent Food and Agriculture 4(1):1546942.

Robinson HF, Comstock RE, Harvey PH (1949). Estimates of heritability and the degree of dominance in corn. Agronomy Journal 41:353-359.

Singh RK, Chaudhary BD (1977). Biometrical Methods in Quantitative Genetic Analysis, Kalyani Publishers New Delhi-Ludhiana, India P 318.

Solomon C, Tefera H, Harjit S (2009). Genetic variability, heritability and trait relationships in recombinant inbred lines of tef [*Eragrostis tef (Zucc.)* Trotter]. Research Journal of Agriculture and Biological Sciences 5(4):474-479.

Solomon C, Assefa K, Metaferia G (2013). Phenotypic and molecular diversity in tef. Achievements and Prospects of Tef Improvement pp. 21-31.

Solomon C (2010). Genetic analyses of agronomic traits of tef (*Eragrostis tef*) genotypes. Research Journal of Agriculture and Biological Sciences 6(6):912-916.

Spaenij-Dekking L, Kooy-Winkelaar Y, Koning F (2005). The Ethiopian cereal tef in celiac disease. The New England Journal of Medicine 353(16):1748-1749

Tsion F (2016). Variability Genetic Diversity of Ethiopian Tef [*Eragrostis tef (Zucc.)* Trotter] Varieties as Revealed by Morphological and Microsatellite Markers. MSc. Thesis, Addis Ababa University, Addis Ababa, Ethiopia.

Kebede W, Assefa K, Tesso B, Asfaw M (2019). Study of broad sense heritability and genetic advance for grain yield and yield components of drought tolerant tef [*Eragrostis tef (Zucc.)* Trotter] genotypes. Crop Research 54(3/4):94-100.