

Correlation and path coefficient analysis among yield and yield related traits of Tef [*Eragrostis tef* (Zucc.) Trotter] genotypes

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ABSTRACT

Aim: The aim of this study was to determine the nature and strength of association between yield and yield related traits as well as to obtain information on path coefficient for yield and contributing traits.

Materials and Methods: The experiment was conducted in central Ethiopia during main cropping season at two locations (Bishoftu and Akaki) and arranged in 7x7 simple lattice designs. The planting material consisted of 49 tef recombinant inbred line along with standard check.

Results: Number of primary panicle branches per main shoot, above ground biomass and harvest index had a positive direct effect on the grain yield at both phenotypic and genotypic levels. According to path coefficient analysis, above ground biomass, harvest index, number of spikelets per panicle and number of florets per spikelets are the primary component traits affecting grain yield. Grain yield and other yield related traits have significance positive correlation.

Conclusion: It was concluded that above ground biomass and harvest index had highest positive direct effect on grain at both genotypic and phenotypic levels and direct selection of genotypes with high mean values of above ground biomass and harvest index to increase tef yield is important in tef improvement program.

Keywords: Direct effect, *Eragrostis tef*, genotypic correlation, indirect effect, phenotypic correlation.

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Introduction

Tef [*Eragrostis tef* (Zucc.) Trotter] is an allotetraploid ($2n=4x=40$) plant whose diploid ancestors (s) in not yet identified. The allotetraploid species *Eragrostispilosa* is closet relative and potentially direct wild progenitor of tef (Ingram and Doyle, 2003). The tef chromosome are extremely small (0.8-2.9m), even by standard of genus. The largest tef chromosome is around three times smaller than smallest (1D) wheat chromosome. Unlike several allied *Eragrostis* species, chromosomal race and aneuploidy have not yet been detected in tef (Tavassoli, 1989). Tef can grow in a variety of ecological conditions from sea level up to 3000 m.a.s.l. Production of tef accounted for about 25.93 % of nationwide grain-cultivated area, and more than 6.66 million smallholder farmers grew it on 2.93 million ha of land. Tef is the most important economic crop cultivated by 40% of

smallholder farmers' households in Ethiopia and 17.12 % of the total grain production, with an overall average productivity of 1.94 t/ha (CSA, 2022). The environment and genotype have a significance impact of tef yield and yield component. Breeders therefore investigate the correlation between yield and its component as generate new variety through breeding process (Mecha *et al.*, 2017). The studies on the direct and indirect effects of yield components serves as the basis for a successful breeding program that increase yield, as a result the issue of yield increase can be addressed more successfully due to the effectiveness of yield component and closely related traits (Chowdhry *et al.*, 2000).

Breeder can better understand the cause of association between two variables through path coefficient analysis, which quantifies the direct and indirect effect of independent variable on dependent variables (Baranwal *et al.*, 2012). Path coefficient analysis separates correlation coefficients into components of direct and indirect effect, measuring the direct effect of one variable on the other.

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During the selection process in breeding program, it is essential to understand the direct and indirect effect of various components on dependent traits, such as yield and yield related traits as well as the interaction between various components (Vijayabharathi et al., 2009). Path coefficients analysis minimize the breeding time during the selection procedure in addition to offering a selection criteria (Qaizar et al., 1991). For instance, selection is only allowed for a small number of important traits, when the breeder focuses primary on traits that have a significant direct effect on dependent traits like maturity and yield.

In plant breeding, information of the extent of the correlation between the traits is critical for identifying the magnitude and degree of interaction between physiological traits, yield and yield related traits. Plant breeder can distinguish between direct and indirect effects through characteristics by partitioning the relationships using path coefficient analysis. Correlation and path coefficient studies are utilized as the base for selection in order to understand the yield contributing variable affecting yield in tef. Therefore the objective of the current study was to determine the correlation between various agronomic traits and their direct and indirect effect on tef yield and yield related traits.

Materials and Methods

Descriptions of Experimental Locations

The field experiment was conducted during the 2021/22 main cropping season at two locations in the central high land of Ethiopia (Bishoftu and Akaki). Akaki was located at (8° 53' N, 38° 58' E, and 2400 m.a.s.l) latitude, longitude and altitude, whereas Bishoftu is found at (8° 44' N, 38° 58' E, and 1900 m.a.s.l) latitude, longitude and altitude, respectively. The two locations share a common moist tropical climate and experience a long rainy season extending from June to September. Bishoftu experience maximum and minimum mean annual temperature of 24.3 °C and 8.9 °C, respectively and 832 mm of annual rainfall. On the other hand, Akaki frequently has 1254 mm of annual rainfall and with maximum and minimum mean annual temperature of 30 °C and 10 °C, respectively. The field experiment for two sites characterized by vertisols (heavy black soil) with a very high water holding capacity.

Experimental Planting Materials: The experimental plant material consisted of 49 tef recombinant inbred line (RILs), including the standard check. RILs are offspring of the inter-specific cross that have been continuously maintained through progenies up to the seventh filial generation (F7) through selfing using a single seed descent breeding method that is developed from F2.

Experimental Design, Layout and Management: The study was layout in 7x7 simple lattice with two replication. Each plot consisted of five rows spaced 20 cm apart, covering an area of 2m² (1 m x 2 m). Plots were arranged 1.5 m apart within incomplete blocks and 1 m apart between incomplete blocks. Genotypes were randomly assigned to plots within each replicate. Standard crop management techniques and recommendations were uniformly applied to all genotypes based on crop recommendation.

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, grain yield, harvest index and thousand seed weight data were collected as recommended for the tef and subjected to analysis using appropriate software.

Correlation coefficient (r): The estimation of the genotypic and phenotypic correlation coefficient between yield and yield related traits was carried out based on the standard methods describes below and the correlation coefficient (r) between pairs of quantitative traits was estimated according to Singh and Chaudhary, (1977).

$$r_{p_{xy}} = \frac{Cov_{p_{xy}}}{\sqrt{\sigma_{p_x}^2 \sigma_{p_y}^2}}$$

Where: $r_{p_{xy}}$ = Phenotypic correlation coefficient

between character x and y, $Cov_{p_{xy}}$ = Phenotypic

covariance between character x and y, $\sigma_{p_x}^2 =$

Phenotypic variance for character x, $\sigma_{p_y}^2 =$

Phenotypic variance for character y

$$r_{g_{xy}} = \frac{Cov_{g_{xy}}}{\sqrt{\sigma_{g_x}^2 \sigma_{g_y}^2}}$$

Where: $r_{g_{xy}}$ = genotypic correlation coefficient between character x and y, $Cov_{g_{xy}}$ = Genotypic covariance between character x and y, $\sigma^2_{g_x}$ = Genotypic variance for character x, $\sigma^2_{g_y}$ = Genotypic variance for character y.

Using the t-test, the resulting phenotypic correlation coefficient values were evaluated for significance: $t = SE(r_{ph})/r_{ph}$, Where, r_{ph} = Phenotypic correlation; $SE(r_{ph})$ = Standard error of phenotypic correlation obtained using the following formula (Sharma, 2001).

$SE(r_{ph}) = \sqrt{\frac{1-r^2_{ph}}{n-2}}$ Where r^2_{ph} is the phenotypic correlation coefficient and n is the number of genotype used. The Robertson (1959) formula is shown below, and it was used to determine the significance of the Correlation of coefficients at genotypic level. $t = \frac{r_{g_{xy}}}{SE_{r_{g_{xy}}}$

The calculated "t" was compared with the tabulated "t" value at (n-2) degree of freedom at 5% level of significance. Where, n is number of genotypes.

$SE_{r_{g_{xy}}} = \sqrt{\frac{1-r^2_{g_{xy}}}{h^2_x}}$ Where, h^2_x = Heritability of trait x, h^2_y = Heritability of trait y

Path coefficient analysis: Path coefficient analysis, which considers the correlation coefficient for both genetic and phenotypic traits, was employed to assess the association between traits and to quantify their influence on yield component of tef genotype (Dewey and Lu, 1959).

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

Where; r_{ij} = is the correlation coefficients evaluation of the mutual association between the independent character (i) and dependent character (j), P_{ij} stand for direct effect component of and independent character (i) on the dependent character (j) as measured by the path coefficient and $\sum r_{ik} p_{kj}$ = summation of components of indirect effect of a given independent character (i), through every other independent character (k) and the specific independent character (j)

The residual effect, which determines how best the causal factors account for the variability of the dependent factor yield was computed using the formula;

$1 = p^2R + \sum p_{ij} r_{ij}$, where, p^2R is the residual effect, $p_{ij} r_{ij}$ = the product of direct effect of any variable and its correlation coefficient with yield.

Residual effect = $\sqrt{1 - R^2}$, where $R^2 = \sum P_{ij} r_{ij}$

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

No.	Recombinant Inbred Lines	No.	Recombinant Inbred Lines
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 cultivar

Results and Discussion

Understanding how traits relate to each other and to other desired characteristics is crucial for devising effective selection strategies. The correlations observed in this experiment among yield and yield-related traits are detailed below. The experiment presents estimates of genotypic (rg) and phenotypic (rp) correlation coefficients for each pair of studied traits averaged across two locations (Table 2). Generally, the genotypic correlation coefficients were higher in magnitude than their corresponding phenotypic correlation coefficients, with a few exceptions. This pattern clearly demonstrates that there is an inherent association among the traits under consideration.

Correlation of grain yield with other traits: Above ground biomass, harvest index and the number of primary panicle branches per main shoot showed positive and highly significant genotypic and phenotypic correlation with a grain yield. The correlation coefficient analysis also revealed that grain yield had positive and significant genotypic correlation with panicle length and number of spikelets per panicle. Grain yield also showed positive and highly significance phenotypic correlation with days to physiological maturity, grain filling period and culm length, whereas positive and significant phenotypic correlation with number of florets per spikelet. On other hand, there was a negative and highly significance correlation of grain yield with days to heading and lodging index (Table 2).

The importance of correlation between traits is to ascertain whether the selection for one traits have an impact on the selection of another traits. According to Kelsey and Pooni (1996), traits that exhibit a positive and significance correlation may be the consequence of strong coupling linkage between genes, or they may be the result of pleiotropic genes that governs these traits in the same direction. The number of florets per spikelets, number of primary panicle branches per main shoot, panicle length, culm length, above ground biomass and harvest index all exhibited a positive correlation with grain yield, which help in the breeder identification of better performing genotypes based on the selection for these traits. The improvement of one trait would lead to the decrease of another for traits that have a significance and negative correlation. However, lodging index which is necessary attributes for the improvement of tef, showed a significance and negative correlation with grain yield.

Many authors (Solomon, 2010, Abel *et al.*, 2013, Dagnachew and Girma, 2014, Habte *et al.*, 2015 and Chekole *et al.*, 2016) reported that their is positive correlations of grain yield with above ground biomass and harvest index. Similarly, Habte and Likyelesh (2013) reported that above ground biomass, panicle length and harvest index had positive and highly significance correlation with grain yield. Contrary to our result, Wondewosen *et al.* (2012) also describe negative correlation between grain yield and grain filling period under stress environment.

Similar to the current finding, Solomon (2010) and Habte *et al.* (2015) also reported significant negative genotypic and phenotypic correlation between lodging index and grain yield. The negative correlation could be due to the effect of different genes or pleiotropic genes that have dominance on the characters and control the characters in different directions (Kearsey and Pooni, 1996).

Correlation among phenological traits

Number of spikelets per panicle and number of primary panicle braches per main shoot exhibited a positive and highly significance genotypic and phenotypic correlation with days to heading and physiological maturity. Days to heading and physiological maturity also showed highly significant and positive genotypic correlation with plant height and panicle length. Grain filling period, culm length and thousand seed weight showed positive and highly significance correlation with days to physiological maturity, whereas number of florets per spikelets and harvest index showed highly significant and positive genotypic correlation with days to heading.

The number of spikelets per panicle and number of primary branches per main shoot exhibited a highly significance and positive genotypic and phenotypic correlation with days to heading and physiological maturity. Days to heading and physiological maturity also showed highly significant and positive genotypic correlation with plant height and panicle length. Number of florets per spikelets and harvest index showed highly significant and positive genotypic correlation with days to heading, whereas grain filling period, culm length and thousand seed weight showed highly significant and positive genotypic correlation with days to physiological maturity.

Table 2. 2Estimates of genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients of 49 tef genotypes based on average data of 17 traits over two test locations.

Traits	DTH	DTM	GFP	PH	PL	CL	PDL	NSPP	NPBPMS	NFPS
DTH	1.00	0.65**	-0.11	0.57**	0.60**	0.34*	-0.12	0.65**	0.76**	-0.44**
DTM	0.65**	1.00	0.66**	0.70**	0.67**	0.47**	-0.02	0.65**	0.50**	-0.10
GFP	-0.24**	0.45**	1.00	0.37**	0.28	0.31*	0.13	-0.06	-0.08	0.31*
PH	0.01	0.15*	0.34**	1.00	0.74**	0.84**	0.10	0.54**	0.59**	-0.23
PL	0.17*	0.26**	0.27**	0.75**	1.00	0.29	-0.10	0.73**	0.70**	-0.32*
CL	-0.10	0.04	0.29**	0.90**	0.38**	1.00	0.23	0.20	0.29*	-0.08
PDL	-0.03	-0.00	0.09	0.17*	0.08	0.18*	1.00	-0.27	-0.03	0.34*
NSPP	0.37**	0.27**	0.03	0.46**	0.64**	0.22**	-0.13	1.00	0.82**	-0.57**
NPBPMS	0.32**	0.20**	0.08	0.56**	0.67**	0.34**	0.05	0.71**	1.00	-0.45**
NFPS	-0.29**	-0.06	0.28**	-0.12	-0.22**	-0.04	0.21**	-0.35**	-0.27**	1.00
NTTPP	0.05	0.01	-0.08	-0.19**	-0.09	-0.20**	-0.13	-0.05	-0.12	0.01
NFTPP	0.14	0.12	-0.05	-0.22**	-0.10	-0.24**	-0.12	-0.08	-0.13	-0.01
LI	-0.70**	-0.57**	0.08	-0.06	-0.28**	0.11	-0.04	-0.36**	-0.36**	0.24**
BY	-0.16*	0.01	0.19**	0.28**	0.17*	0.28**	-0.03	0.01	-0.04	0.01
GY	-0.43**	0.22**	0.27**	0.12	-0.02	0.19**	-0.04	-0.14	0.21**	0.17*
HI	-0.38**	0.29**	0.15*	-0.12	-0.19**	-0.04	-0.02	-0.18*	-0.21**	0.20**
TSW	-0.03	0.15*	0.20**	0.06	0.04	0.06	0.10	-0.00	-0.03	0.05

*, ** Significant at 0.05 and 0.01 probability level respectively, 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.

Table 2. Continued...

Traits	NTTPP	NFTPP	LI	BY	GY	HI	TSW
DTH	-0.15	-0.16	-0.75**	-0.20	-0.49**	-0.41**	0.00
DTM	-0.20	-0.12*	-0.60**	0.10	-0.21	-0.34*	0.43**
GFP	-0.09	0.04	-0.02	0.28	0.21	0.00	0.58**
PH	-0.19	-0.10	-0.63**	0.18	-0.20	-0.41**	0.30*
PL	-0.12	-0.03	-0.76**	0.07	0.32*	-0.45**	0.04
CL	-0.18	-0.11	-0.30*	0.20	-0.04	-0.23	0.40**
PDL	-0.31*	-0.31*	-0.14	-0.19	-0.21	-0.07	0.03
NSPP	-0.11	-0.11	-0.61**	-0.06	0.30*	-0.29*	-0.11
NPBPMS	-0.13	-0.12	-0.76**	-0.15	0.48**	-0.43**	-0.09
NFPS	-0.01	0.00	0.35*	0.08	0.21	0.20	0.07
NTTPP	1.00	0.93**	0.30*	0.17	0.16	0.04	-0.14
NFTPP	0.90**	1.00	0.18	0.20	0.10	-0.07	-0.06
LI	-0.01	-0.12	1.00	0.24	-0.61**	0.52	0.08
BY	0.00	0.04	0.27**	1.00	0.60**	-0.19	0.33
GY	-0.07	-0.11	-0.55**	0.62**	1.00	0.68**	0.20
HI	-0.09	-0.19**	0.42**	-0.21**	0.63**	1.00	-0.06
TSW	-0.12	0.04	-0.00	0.16*	0.09	-0.05	1.00

*, ** Significant at 0.05 and 0.01 probability level respectively, 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.

Additionally there was a highly significance and positive phenotypic correlation of grain filling period with panicle length, culm length, number of florets per spikelets, above ground biomass, grain yield and thousand seed weight. In line with present finding Habte and Likyelesh (2013) also reported significance and positive phenotypic correlation between plant height and grain filling period. Plant height and panicle length showed highly significant and positive genotypic and phenotypic correlation with number of spikelets per panicle and number of primary panicle branches per main shoot. The current study also in line with the finding of Ayalneh *et al.* (2012) and Chekole *et al.* (2016) who reported positive and significant correlation of lodging index with harvest index at genotypic and phenotypic level.

On the other hand lodging index showed significance and negative genotypic correlation with culm length, whereas highly and negative genotypic correlation with days to heading, days to physiological maturity, panicle length, number of spikelets per panicle and number of primary panicle braches per main shoot. Number of spikelets per panicle and number of primary panicle branches per main shoot inhibited highly significant and negative genotypic and phenotypic correlation with number of florets per spikelet and harvest index, whereas number of florets per spikelet was significant and negative genotypic correlation with days to heading and panicle length. Harvest index showed a highly significance and negative genotypic and phenotypic correlation with panicle length and days to heading, whereas highly significant and negative genotypic correlation with days to physiological maturity and plant height

In line with the current finding Ayalneh *et al.* (2012) also reported that days to heading showed significance and negative correlation with above ground biomass, while significance and negative correlation with panicle length and harvest index. Chekole *et al.* (2016) also reported that lodging index showed highly significance and negative correlation with days to maturity and plant height at genotypic and phenotypic level, and highly significance and negative correlation with plant height. Habte *et al.* (2015) also reported that lodging index had negative correlation with days to heading, days to physiological maturity, plant height and culm length.

Path Analysis: To execute the path coefficient analysis based on average of data over two locations, seven and nine traits were selected as causal (independent) variables when grain yield is selected as dependent variable for genotypic and phenotypic correlation, respectively.

Genotypic direct and indirect effects of various traits on grain yield

Genotypic path coefficient analysis showed that, above-ground biomass (0.424), number of spikelets per panicle (0.285) and harvest index (0.122) has the moderate positive direct effect on grain yield, whereas days to heading (0.063) and number of primary panicle branches per main shoot (0.018) has the weak positive direct effect on grain yield. However, the weekly negative direct effect on grain yield was exerted by panicle length (-0.095) and lodging index (-0.022) (Table 3). Previous study conducted by Habtamu *et al.* (2011a) indicated that harvest index and biomass yield had significant direct influence on grain yield. According to these authors, selecting of traits that have positive direct effect help to increase grain yield. In agreement with the current findings, Ayalneh *et al.* (2012) and Mizan *et al.* (2017) found that harvest index and above-ground biomass had a strong significant direct effect on grain yield in tef landrace and positive correlation with it. In accordance with the present findings, Solomon *et al.* (2006) found that harvest index and shoot biomass had high significance and positive direct effect on grain yield of tef recombinant inbred lines.

Days to heading and panicle length exerted the moderate positive indirect effect on grain yield via number of primary panicle branches per main shoot, whereas number spikelets per panicle has moderate positive indirect effect on grain yield through number of primary panicle branches per main shoot. Days to heading, panicle length, number of spikelets per panicle and number of primary panicle braches per main shoot all had a positive indirect effect on grain yield via lodging index. But days to heading, number of spikelets per panicle and number of primary panicle branches per main shoot has negative indirect effect on grain yield via above-ground biomass. Negative indirect effect was observed on grain yield by days to heading, panicle length, number of spikelets per panicle, number primary panicle branches per main shoot and above-ground biomass through harvest index (Table 3). Corresponding to the present

findings Chekole *et al.* (2016) reported days to heading had negative and highest indirect effect via harvest index on grain yield, but positive and high indirect effect through above ground biomass on grain yield. The residual effect was 0.078, suggesting that all the study includes explain a high percentage of variation in grain yield (92.20), while other factors that were not included in the study contributed to 7.80 of the variation (Table 3).

Selection of characters that had positive direct effect on grain yield boosts the tef yield in succeeding generation. The strong and positive correlation along with positive direct effect was indicated the true relationship between above ground biomass and harvest index with grain yield. Moreover, traits that had both positive direct effects and positive and significant correlation with grain yield are the most preferred traits for selection. Harvest index and

above-ground biomass can both be seen as significant contributors to grain yield, indicating that they should be selected as breeding criteria for tef in order to increase grain yield

Phenotypic direct and indirect effects of various traits on grain yield

Phenotypic path coefficient analysis revealed that, above-ground biomass (0.794) had positive highest direct effect on grain yield, whereas harvest index (0.481) and number of florets per spikelet (0.324) exerted positive moderate direct effect on grain yield. Days to physiological maturity (0.098), culm length (0.048), and the number of primary panicle branches per main shoot (0.039) had a weak positive direct effect on grain yield, but days to heading and grain filling period had a negative direct impact. The greatest direct effect on grain yield is caused by the lodging index (Table 4).

Table 3. 3Estimates of direct (bold diagonal) and indirect effect (off diagonal) at genotypic level of seven traits on grain of 49 tef genotypes based on average data of 17 traits over two test locations.

Traits	DTH	PL	NSPP	NPBPMS	LI	BY	HI	r _g
DTH	0.063	-0.856	0.181	0.235	0.894	-0.346	-0.424	-0.253
PL	-0.856	-0.095	0.035	0.138	0.932	0.121	-0.904	0.370**
NSPP	0.131	-0.042	0.285	0.533	0.354	-0.104	-0.583	0.574**
NPBPMS	0.235	-0.999	0.039	0.018	0.932	-0.759	-0.864	-0.398**
LI	0.894	0.085	-0.029	-0.235	-0.022	0.815	0.045	0.553**
BY	-0.346	-0.100	-0.003	-0.044	-0.526	0.424	-0.082	-0.676**
HI	-0.024	0.042	-0.014	-0.099	-0.006	-0.329	0.122	-0.307**

** , * indicates highly significant at 1% and significant at 5% probability levels, respectively. r_g: genotypic correlations with the grain yield, DTH = PL= panicle length, NSPP= number of spikelets per panicle, days to heading, NPPBPMS=number of primary panicle branches per main shoot, LI= lodging index, BY=biomass yield, HI = harvest index and Residual effect =0.078.

Table 4. 4Estimates of direct (bold and underlined diagonal) and indirect effect (off diagonal) at phenotypic level of seven traits on grain yield in 49 tef genotypes tested at Bishoftu during 2021/22.

Traits	DTH	DTM	GFP	CL	NPBPMS	NFPS	LI	BY	HI	r _p
DTH	-0.050	0.359	0.384	-0.005	0.150	-0.094	0.114	-0.127	0.038	0.770**
DTM	-0.113	0.098	-0.721	0.082	0.094	-0.149	0.907	0.188	-0.149	0.237
GFP	0.780	0.541	-0.002	0.014	0.058	0.091	-0.127	0.151	-0.015	0.590**
CL	0.425	0.084	-0.465	0.048	0.159	-0.013	-0.175	0.022	0.204	0.290*
NPBPMS	-0.040	0.418	-0.128	0.016	0.039	-0.087	0.573	-0.032	0.721	0.480**
NFPS	0.943	-0.025	-0.448	-0.002	-0.127	0.324	-0.382	0.118	-0.020	0.380**
LI	0.275	-0.192	-0.128	0.005	-0.169	0.078	-0.059	0.214	-0.042	0.450**
BY	0.520	0.021	-0.304	0.013	-0.019	0.003	-0.430	0.794	0.021	0.620**
HI	0.435	0.606	-0.240	-0.002	-0.098	0.065	-0.668	-0.167	0.481	0.411**

** , * indicates highly significant at 1% and significant at 5% probability levels respectively. r_p: phenotypic correlations with the grain yield, DTH = days to heading, DTM= days to physiological maturity, GFP = grain filling period, CL= culm length, NPPBPMS=number of primary panicle branches per main shoot, NFPS= number of florets per spikelet, LI= lodging index, BY=biomass yield, HI = harvest index and Residual effect =0.088.

Days to heading exerted moderate positive direct effect on grain yield via days to physiological maturity and grain filling period. The positive indirect effect was observed on grain yield by days to heading, days to physiological maturity, grain filling period and culm length through number of florets per spikelets. The positive indirect effect was observed on grain yield by days to heading, days to physiological maturity and number of primary panicle branches per main shoot through lodging index, whereas grain filling period, culm length and number of florets per spikelets has negative indirect effect on grain yield via lodging index. Days to physiological maturity, grain filling period, culm length, number of florets per spikelet and lodging index has positive indirect effect on grain yield via above-ground biomass, whereas days to heading and number of primary panicle branches per main shoot has negative indirect effect on grain yield through above-ground biomass. The positive indirect effect was exerted on grain yield by days to heading, culm length, number of primary panicle branches per main shoot and above-ground biomass through harvest index, whereas days to physiological maturity, grain filling period, number of florets per spikelet and lodging index has negative indirect effect on grain yield via harvest index (Table 4). The residual effect was 0.088, indicating that all the traits included in the study explained high percentage of variation in grain yield (91.2%), while other factors not included in the study explained 8.8%.

Conclusions

The genotypic correlation coefficients were found to be higher than the corresponding phenotypic correlation coefficients for the majority of traits indicating that genetic factors played major role in the expression of the traits. At both phenotypic and genotypic correlation level, the number of primary panicle branches per main shoot, above-ground biomass, and harvest index were found to highly significance and positively correlated with grain yield. Additionally there was a positive and significance correlation of numbers of spikelets per panicle, panicle length and numbers of florets per spikelets with grain yield, suggesting that selection for these traits would indirectly increase grain yield. Path coefficient analysis showed that above ground biomass and harvest index had highest positive direct effect on

grain at both genotypic and phenotypic levels. Thus to increase tef yield direct selection of genotypes with high mean values of above ground biomass and harvest index is important in tef improvement program. This indicate that attention should be given for these traits which have positive correlation with grain yield in the process of selection as these traits are helpful for indirect selection. The present study examined the traits association between grain yield and yield component and showed varying degree of association, which may be further investigated and used to promote desirable traits in tef breeding through selection.

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