

## Interrelationship and Path Coefficient Analysis of Yield Components in F<sub>4</sub> Progenies of Tef (*Eragrostis tef*)

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**Abstract:** This experiment was conducted at Debre Zeit and Akaki during 2004-2005 cropping season on F<sub>2</sub>-derived F<sub>4</sub> bulk families of 3 crosses, viz, DZ-01-974 x DZ-01-2786, DZ-01-974 x DZ-Cr-37 and Alba x Kaye Murri. To estimate the correlations and path coefficients between yield and yield components, 63 F<sub>4</sub> families were taken randomly from each of the 3 crosses. The 189 F<sub>4</sub> families, five parents and 2 checks were space planted following in 14×14 simple lattice design. Study of associations among traits indicated that yield was positively associated with shoot biomass, harvest index, lodging index and panicle kernel weight at phenotypic level at Debre Zeit. At Akaki, yield had significant positive correlation with shoot biomass, harvest index, plant height and panicle length and panicle weight. At genotypic level, grain yield per plot exhibited positive association with harvest index, shoot biomass, lodging index and panicle kernel weight at Debre Zeit. By contrast, days to heading, days to maturity, plant height and panicle length showed negative association with yield. At Akaki, kernel yield per plot was positively correlated at genotypic level with all the traits considered where lodging index had the highest correlation followed by shoot biomass, panicle kernel weight and harvest index. Path coefficient analysis at both phenotypic and genotypic levels for both the locations suggested those shoot biomass and harvest indexes are the two important yield determining traits. These two traits might be useful in indirect selection for yield improvement in the material generated from the three crosses under consideration.

**Keywords:** Correlation, path coefficient analysis, tef (*Eragrostis tef*)

### INTRODUCTION

Tef (*Eragrostis tef*) is a high value crop and is primarily grown for its grain that is used for preparing injera, which is a staple and very popular food in the national diet of Ethiopians (Hailu *et al.*, 2003). Tef has many prospects outside Ethiopia also due to its gluten-freeness, tolerance to biotic and a biotic stress, animal feed and erosion control quality (Hailu and Seyfu, 2001). Tef is an allotetraploid with  $2n = 4x = 40$  (Tavassoli, 1986). However, the 2 diploid parents that contributed to its genome have not been identified. However, several wild species of *Eragrostis* were identified to be close relatives or progenitors of the present-day tef based on morphological and biochemical marker analysis (Likyelesh and Mengiste, 1999).

The breeding program of Debre Zeit Agricultural Research Center has made 3 crosses and the segregating generations are handled by modified bulk method, i.e., raising bulk families in F<sub>3</sub>-F<sub>4</sub> generations that are derived from individual F<sub>2</sub> plants. According to Stoskopf *et al.* (1999) it is possible to evaluate yield

trials still the families are segregating and superior yielding lines so that it is possible to reduce number of years to develop and release cultivars as well as the information generated on associations among characters in the crosses will be useful to apply for indirect selection to achieve higher responses. This interrelationship may be estimated by correlation analysis. This can be done at individual plant level and family level (Stoskopf *et al.*, 1999). Association of characters can be done at F<sub>4</sub> family level as 87.7% of the populations have attained homozygous (Hailu, 1988). However, correlation analysis alone becomes insufficient to explain relationships among characters and path analysis permits identification of direct and indirect causes of association and measures the relative importance of each character (Rao *et al.*, 1997). Correlation coefficient whilst provides basic criteria for selection and leads to directional model base on yield and its components in field experiments yet, the information it supplies about the nature of association is often incomplete (Fraser and Eaton, 1983). Path coefficient analysis, on the other hand, is an efficient statistical technique specially designed to quantify the

inter-relationships of different components and their direct and indirect effects on kernel yield. Through this technique, yield-contributing characters can be ranked and specific traits producing a given correlation can be headed (Rao *et al.*, 1997). Thus, path-coefficient analyses have been deemed more informative and useful than simple correlation coefficients (Kang, 1994; Gravois and McNew, 1993).

So information on the extent and nature of interrelationship character help to formulate multiple trait selection procedure. Hence, the present study was conducted to find out the information on nature and magnitude of gene action for yield and yield related traits.

The study was aimed at generating the information on those specific crosses made at Deber Zeit Agricultural Research Center (DZARC). The information generated on associations among characters in the crosses will be useful to apply for indirect selection to achieve higher responses.

Therefore, the objectives of the present study were:

- To estimate the nature and magnitude of associations among yield and yield related traits
- To obtain information on path coefficient for yield and its contributing characters

## MATERIALS AND METHODS

The experiment was conducted in 2004/05 cropping season at 2 locations, Debre Zeit and Akaki. The experimental materials comprised of F<sub>2</sub>-derived F<sub>4</sub> bulk families developed from 3 tef crosses, DZ-01-974 x DZ-01-2786, DZ-01-974 x DZ-Cr-37 and Alba x Kaye Murri. They were obtained by bulking kernel from each F<sub>3</sub> family derived from each single F<sub>2</sub> plant for each F<sub>2</sub> population. DZ-01-974 and DZ-Cr-37 are released varieties. The former is a late maturing, high yielding variety and the latter is an early maturing white-kerneled variety. Alba and Kaye Murri are cultivars described by Tadesse (1975). From F<sub>1</sub> plants of the crosses indicated above, 1200 individual F<sub>2</sub> plants were grown on the field in 1.5 m long rows spaced 0.5 m at the Debre Zeit Agricultural Research Center with intra-row spacing of 0.1 m. About 200 plants were randomly selected from each F<sub>2</sub> population and advanced to F<sub>3</sub> by field planting of kernels of each individual F<sub>2</sub> panicle in 1m long rows spaced 0.5 m apart. About 63 plants were randomly taken from each F<sub>3</sub> population and advanced to F<sub>4</sub>. A total of 189 F<sub>4</sub> (F<sub>2</sub>-derived F<sub>4</sub> families) from 3 crosses were produced and field grown along with the five parents and 2 standard checks. DZ-01-1285 was used as a late maturing standard check and DZ-01-1681 was used as an early maturing standard check.

The genotypes were sown at Debre Zeit and Akaki in 14×14 simple lattice designs. Each plot consisted of 2 rows of 2 m length spaced 0.2 m apart. A distance of 50 cm between plots was maintained and the distance

between blocks and replications was 1 m. The recommended kerneling rate of 30 kg/ha and fertilizer rate of 60/60 kg ha<sup>-1</sup> N/P<sub>2</sub>O<sub>5</sub> were used at both locations. Weeds were controlled manually and at early tillering all the stands were thinned to 10 cm-intra-row spacing. Thus plants row<sup>-1</sup> (40 plants plot<sup>-1</sup>) was maintained. In each row 5 plants (10 plants plot<sup>-1</sup>) were tagged for data to be taken on individual plant basis.

Data on the following traits were taken on the basis of the 2 rows in each plot. Namely, Days to 50% heading, Days to 75% maturity, hundred kernel weight, biological yield, grain yield, harvest Index and Lodging index which was recorded using the method of Caldicott and Nuttall (1997). Ten randomly per-tagged plants were used for recording data on 4 characters, Panicle length, Panicle weight, Yield per panicle and Plant height.

Estimates of association of characters at phenotypic and genotypic levels as well as path coefficients analyses were done based on RCBD ANOVA using INDOSTAT computer program. RCBD ANOVA was used to derive variance components used in the following format (Sharma, 1998). Phenotypic correlation, the observable correlation between variables, which includes genotypic and environmental effects, was calculated from the variance covariance components. Based on genotypic correlation, path coefficient which refers to the direct and indirect effects of the yield attributing traits (independent character) on grain yield (dependent character) were calculated following the method used by Dewey and Lu (1959).

## RESULTS

**Correlation of traits:** At Debre Zeit (Table 1) yield per plot exhibited positive and significant correlation with shoot biomass (0.836, 0.745), harvest index (0.965, 0.831), panicle kernel weight (0.556, 0.135), lodging index (1.102, 0.517) and panicle weight (0.283, 0.017) at both genotypic and phenotypic levels. Similar results of positive correlation of these traits with yield were reported by Hailu (1988), Fufa *et al.* (2000) and Kebebew *et al.* (2002). This indicated that selection for higher shoot biomass, harvest index, panicle kernel weight, lodging index and panicle weight is computed to bring about improvement in grain yield. However in this study, plant height, days to heading, days to maturity and panicle length showed negative correlation with yield. Similar to this finding (Fufa *et al.*, 2000) observed negative association of panicle length with yield per plot.

At Akaki (Table 2), yield per plot showed positive correlation at both genotypic and phenotypic levels with all characters studied but relatively high and significant positive correlation was observed with shoot biomass (0.664, 0.766), harvest index (0.378, 0.612), panicle kernel weight (0.613, 0.128), panicle length (0.389, 0.182), plant height (0.28, 0.231) and panicle weight (0.598, 0.230) at both genotypic and

Table 1: Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients in 196 F4 families of tef crosses tested at Debre Zeit

Characters	1	2	3	4	5	6	7	8	9	10
1. Days to heading		0.743*	-0.441*	-0.725*	-0.771*	0.495	0.542*	-0.045	-0.428**	-0.729*
2. Days to maturity	0.569**		-0.694*	-0.821*	-0.743*	0.558*	0.728*	-0.226	-0.500	-0.770*
3. Shoot biomass (gm)	-0.257**	-0.294**		0.836*	0.665	-0.674**	-0.871*	0.497*	0.772**	0.952*
4. Grain yield	-0.438**	-0.493**	0.745**		0.965**	-0.842*	-1.069**	0.283*	0.556**	1.102**
5. Harvest index	-0.412**	-0.452**	0.271**	0.831**		-0.737*	-0.960**	0.094	0.344**	1.022**
6. Plant height	0.184*	0.254**	0.055	-0.075	-0.134		0.948**	-0.624*	-1.095**	-0.748*
7. Panicle length	0.217**	0.267**	0.009	-0.098	-0.128	0.696**		-0.664*	-1.643**	-0.825*
8. Panicle weight	0.036	-0.033	0.031	0.017	0	0.145	0.245**		0.860**	0.268*
9. Panicle kernel weight	-0.019	-0.098	0.087	0.135	0.123	0.101	0.173*	0.688**		0.873*
10. Lodging index	-0.413**	-0.489**	0.350**	0.517**	0.457**	-0.208**	-0.229**	0.068	0.086	

\*\*, \*: Significant at 1 and 5% probability levels, respectively

Table 2: Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients in 196 F4 families of tef crosses tested at Akaki

Characters	1	2	3	4	5	6	7	8	9	10
1. Days to heading		0.718**	0.566*	0.234	-0.379*	0.739*	0.720*	0.619*	0.678*	-0.500*
2. Days to maturity	0.549**		0.721	0.239	-0.592*	0.874*	0.766*	0.369*	0.331*	-0.785*
3. Shoot biomass (gm)	0.178*	0.332**		0.664*	-0.460*	0.655*	0.645*	0.281*	0.308*	-0.204*
4. Grain yield	0.056	0.110	0.766**		0.378*	0.280*	0.389*	0.598*	0.613*	0.666*
5. Harvest index	-0.125	-0.233**	-0.015	0.612**		-0.447*	-0.250*	0.456*	0.457*	1.285**
6. Plant height	0.397**	0.475**	0.429**	0.231**	-0.191*		0.952*	0.559*	0.593*	-0.689*
7. Panicle length	0.416**	0.425**	0.345**	0.182*	-0.146	0.792**		0.531*	0.572*	-0.508*
8. Panicle weight	0.186*	0.176*	0.155*	0.230**	0.179*	0.283**	0.313**		1.203**	-0.134
9. Panicle kernel weight	0.238**	0.149*	0.127	0.128	0.051	0.275**	0.308**	0.676**		-0.291*
10. Lodging index	-0.274**	-0.380**	-0.198**	0.064	0.330**	-0.290**	-0.166	0.045	-0.034	

\*\*, \*: Significant at 1 and 5% probability levels, respectively

Table 3: Phenotypic direct (bold face and diagonal) and indirect effects of various characters on grain yield/plot in 196 genotypes of tef crosses tested at Debre zeit

Characters	$r_p$	1	2	3	4	5	6	7	8	9
1. Days to heading	<b>-0.438**</b>	-0.005	-0.012	-0.143	-0.274	-0.001	-0.001	0.000	0.000	-0.002
2. Days to maturity	<b>-0.493**</b>	-0.003	-0.021	-0.163	-0.300	-0.001	-0.002	0.000	-0.001	-0.002
3. Shoot biomass (gm)	<b>0.745**</b>	0.001	0.006	0.556	0.180	0.000	0.000	0.000	0.001	0.001
4. Harvest index	<b>0.831**</b>	0.002	0.009	0.151	0.664	0.001	0.001	0.000	0.001	0.002
5. Plant height	<b>-0.075</b>	-0.001	-0.005	0.031	-0.089	-0.005	-0.005	-0.001	0.001	-0.001
6. Panicle length	<b>-0.098</b>	-0.001	-0.006	0.005	-0.085	-0.003	-0.007	-0.001	0.001	-0.001
7. Panicle weight	<b>0.017</b>	0.000	0.001	0.017	0.000	-0.001	-0.002	-0.004	0.005	0.000
8. Panicle kernel weight	<b>0.135</b>	0.000	0.002	0.048	0.082	0.000	-0.001	-0.003	0.007	0.000
9. Lodging index	<b>0.517**</b>	0.002	0.010	0.194	0.304	0.001	0.002	0.000	0.001	0.004

Residual: 0.017; \*\*, \*: Significant at 1 and 5% probability levels

Table 4: Phenotypic direct (bold face and diagonal) and indirect effects of various characters on grain yield/plot in 196 genotypes of 3 tef crosses tested at Akaki

Characters	$r_p$	1	2	3	4	5	6	7	8	9
1. Days to heading	<b>0.056</b>	-0.005	0.001	0.138	-0.078	-0.003	0.007	-0.001	0.000	-0.003
2. Days to maturity	<b>0.110</b>	-0.003	0.002	0.258	-0.145	-0.004	0.007	-0.001	0.000	-0.005
3. Shoot biomass (gm)	<b>0.766**</b>	-0.001	0.001	0.777	-0.010	-0.004	0.006	-0.001	0.000	-0.002
4. Harvest index	<b>0.612**</b>	-0.001	-0.001	-0.012	0.622	0.002	-0.002	-0.001	0.000	0.004
5. Plant height	<b>0.213**</b>	-0.002	0.001	0.333	-0.119	-0.009	0.013	-0.001	0.000	-0.004
6. Panicle length	<b>0.182*</b>	-0.002	0.001	0.268	-0.090	-0.007	0.017	-0.001	0.000	-0.002
7. Panicle weight	<b>0.230**</b>	-0.001	0.000	0.120	0.112	-0.002	0.005	-0.005	0.000	0.001
8. Panicle kernel weight	<b>0.128</b>	-0.001	0.000	0.098	0.032	-0.002	0.005	-0.003	0.000	0.000
9. Lodging index	<b>0.064</b>	0.001	-0.001	0.153	0.205	0.003	-0.003	0.000	0.000	0.012

Residual: 0.0237; \*\*, \*: Significant at 1 and 5% probability levels

phenotypic levels respectively. These observations are in agreement with that of Fufa *et al.* (1999) who observed positive correlation of all the traits with yield per plant. High genotypic correlations suggest that selection directed to one character would directly affect the other.

#### Phenotypic and genotypic path coefficient analysis:

The phenotypic path coefficient analysis at Debre zeit (Table 3) revealed that harvest index had the maximum positive direct effect followed by shoot biomass. Others traits observed negligible direct effect. On the other hand, days to heading, days to maturity, plant height,

panicle length and panicle weight had negative direct effect on grain yield at this location.

The phenotypic path coefficient analysis studies at Akaki revealed that shoot biomass had the maximum positive direct effect on yield followed by harvest index (Table 4). These 2 traits also had highly significant phenotypic correlation with yield. Though, panicle weight and plant height had significant phenotypic correlation with yield, their direct effect were negligible. The positive association of plant height with yield was due to considerable positive indirect effect via shoot biomass. These observations suggested that like Debre Zeit, at Akaki also shoot

Table 5: Genotypic direct (bold face and diagonal) and in direct effects of various characters on grain yield/plot in 196 genotypes of three tef crosses tested at Debre Zeit

Characters	$r_g$	1	2	3	4	5	6	7	8	9
1. Days to heading	<b>-0.725*</b>	0.007	-0.052	-0.190	-0.566	-0.104	0.009	0.003	0.001	0.166
2. Days to maturity	<b>-0.821*</b>	0.005	<b>-0.070</b>	-0.298	-0.546	-0.117	0.012	0.016	0.002	0.176
3. Shoot biomass (gm)	<b>0.836*</b>	-0.003	0.048	<b>0.430</b>	0.488	0.142	-0.014	-0.035	-0.002	-0.217
4. Harvest index	<b>0.965*</b>	-0.005	0.052	0.286	<b>0.734</b>	0.155	-0.016	-0.007	-0.001	-0.233
5. Plant height	<b>-0.842*</b>	0.003	-0.039	-0.290	-0.541	-0.210	0.016	0.044	0.003	0.171
6. Panicle length	<b>-1.069**</b>	0.004	-0.051	-0.375	-0.705	-0.199	0.017	0.047	0.005	0.188
7. Panicle weight	<b>0.283*</b>	0.000	0.016	0.214	0.069	0.131	-0.011	-0.071	-0.003	-0.061
8. Panicle kernel weight	<b>0.556*</b>	-0.003	0.035	0.332	0.252	0.230	-0.027	-0.061	-0.003	-0.199
9. Lodging index	<b>1.102**</b>	-0.005	0.054	0.410	0.750	0.157	-0.014	-0.019	-0.003	-0.228

Residual: -0.0061; \*\*, \*: Significant at 1 and 5% probability levels, respectively

Table 6: Genotypic direct (bold face and diagonal) and in direct effects of various characters on grain yield/plot in 196 genotypes of three tef crosses tested at Akaki

Characters	$r_g$	1	2	3	4	5	6	7	8	9
1. Days to heading	<b>0.234*</b>	-0.175	0.034	0.569	-0.206	-0.060	-0.021	0.095	0.044	-0.045
2. Days to maturity	<b>0.239*</b>	-0.126	0.047	0.726	-0.322	-0.071	-0.023	0.056	0.021	-0.070
3. Shoot biomass (gm)	<b>0.664*</b>	-0.099	0.034	1.007	-0.250	-0.053	-0.019	0.043	0.020	-0.018
4. Harvest index	<b>0.378*</b>	0.066	-0.028	-0.463	0.544	0.036	0.007	0.070	0.030	0.115
5. Plant height	<b>0.280*</b>	-0.129	0.041	0.659	-0.243	-0.081	-0.028	0.086	0.038	-0.061
6. Panicle length	<b>0.389*</b>	-0.126	0.036	0.649	-0.136	-0.077	-0.030	0.081	0.037	-0.045
7. Panicle weight	<b>0.598*</b>	-0.108	0.017	0.283	0.248	-0.045	-0.016	0.153	0.078	-0.012
8. Panicle kernel weight	<b>0.613*</b>	-0.119	0.015	0.310	0.249	-0.048	-0.017	0.184	0.065	-0.026
9. Lodging index	<b>0.666*</b>	0.088	-0.037	-0.205	0.700	0.056	0.015	-0.021	-0.019	0.089

Residual: -0.0004; \*\*, \*: Significant at 5% probability levels

biomass and harvest index are important yield determining traits.

In the genotypic path coefficient analysis at Debre Zeit (Table 5) harvest index had the maximum positive direct effect followed by shoot biomass. As observed at phenotypic level, these 2 traits had highly significant positive genotypic correlation with yield. Though lodging index had highly significant positive association with yield, it had low negative direct effect on yield; its positive association with yield was due to its positive indirect effect via shoot biomass and harvest index. Similarly, significant genotypic correlation of panicle kernel weight was due to the indirect effect via shoot biomass and harvest index. Highly significant negative genotypic correlation of panicle length, plant height, days to maturity and days to heading were mainly due to their negative indirect effect via shoot biomass and harvest index. This analysis indicated that harvest index and shoot biomass are important determinants of yield. This implies that yield improvement can be used by indirect selection. This is in agreement with (Fufa *et al.*, 1999) who observed positive direct effect of shoot biomass, however, in their study lodging index showed positive direct effect where as the direct effect of this traits on yield is negative in the present study. The genotypic path coefficient analysis at Akaki (Table 6) showed that shoot biomass had the highest positive direct effect on yield followed by harvest index. These traits had highly significant and significant association with yield, respectively. Other traits like panicle weight, lodging index, panicle kernel weight and panicle length while had highly significant or significant association with yield, they did not show positive direct effect on yield

except panicle weight that had low positive direct effect (0.153). These traits had positive association with yield mainly due to their positive indirect effect via shoot biomass and/or harvest index. In contrary to Debre Zeit, where days to heading and days to maturity had negative association with yield, low positive genotypic correlation of these 2 traits with yield was due to this positive indirect effect via shoot biomass. However, days to heading had low (-0.175) direct effect.

## DISCUSSION

At both locations, phenotypic and genotypic correlations of yield with shoot biomass and harvest index were high and positive suggesting that these yield components could be used as selection criteria in these materials. This result is in agreement with (Kebebew *et al.*, 2000; Fufa *et al.*, 1999) who observed high correlation of shoot biomass with yield. Moreover, at Akaki days to heading and maturity are positively correlated with yield suggesting that the possibility of improving both traits simultaneously. At both locations the positive relation between lodging index and yield implied that the high yielders are more likely to lodge. These observations are in agreement with that of Kebebew *et al.* (2000) and Fufa *et al.* (2000).

The phenotypic path coefficient analysis at Debre zeit showed that harvest index and shoot biomass were important components of selection for higher yield as they had high genotypic correlation with yield as well as high direct effect. Similarly, (Fufa *et al.*, 1999) observed a positive direct effect of shoot biomass and harvest index. Even though, lodging index showed high phenotypic association with yield its direct effect is

low. It is, because, this trait exerted high positive indirect effect via shoot biomass and harvest index. Though, days to heading had negligible negative direct effect, its indirect effect via shoot biomass and harvest index was negative and therefore it exhibited negative association with yield. The same is true for the association of days to maturity with yield. However, this analysis showed that harvest index and shoot biomass are important in indirect selection for yield. At Akaki also shoot biomass and harvest index are important yield determining traits.

At Debre Zeit, the residual value of 0.0177 showed that the variables considered accounted for almost 100% of the variability observed. While at Akaki, the residual effect of 0.0237 showed that the variables considered accounted for 100% of the variability observed.

### CONCLUSION

In this study, an intensive selection for harvest index, shoot biomass and panicle kernel weight will improve seed yield. Since these traits are highly correlated among themselves also selection in one of the traits will result in improvement of the other. Based on path coefficient an analysis the direct effect of shoot biomass and harvest index contribution on seed yield were highest. This implies that emphasis should be given on these traits while exercising selection for yield improvement. Thus harvest index and shoot biomass can be used as selection criteria at both location as these traits showed strong genetic correlation and high direct effect on yield per plot.

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