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# Correlation and Path Coefficient Studies of Agronomic Traits for Bread Wheat (*Triticum aestivum* L.) Genotypes at Korem, North Ethiopia

**Adhiena Mesele [a*]**

[a] *Tigray Agricultural Research Institute, Alamata Agricultural Research Centre, Alamata, Ethiopia.*

***Author's contribution***

*The sole author designed, analyzed, interpreted and prepared the manuscript.*

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## ABSTRACT

For crop improvement, the association between inherited plant characters and their direct and indirect effects on yield are crucial. To create such evidences, a field study was done at Korem, Northern Ethiopia in 2014. 26 bread wheat genotypes were sown using RCB design with 3 replications. A genetic analysis was done for the traits studied. The correlation of yield with number of tillers per plant, number of kernels per spike and biomass were positive. Biomass had strong and positive direct effect on yield. However, the direct effect of number of tillers per plant and number of kernels per spike were low. Positive and strong genotypic and phenotypic indirect effect on yield via biomass suggested that selection on biomass would lead to improving of yield directly and selection on number of tillers per plant and number of kernels per spike indirectly via biomass. This result is based at one location with no repetition. Therefore, replication of this trial is crucial for conformation.

**Corresponding author: E-mail: adhienam@gmail.com;*

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*Keywords: Bread wheat; correlation; path coefficient; agronomic characters; Ethiopia.*

## 1. INTRODUCTION

In Ethiopia during 2013, wheat stands 4$^{th}$ in both area cultivation and total production. Total area of cultivation and national average productivity during 2013 cropping season were 1627647 ha and 2.10 tons ha$^{-1}$ respectively [1]. Wheat import in Ethiopia is rising at an average of 9% annually while production is increasing at an average of 7% in the last decade [1]. Thus, there is a need to balance the gap between the import and production by improving the productivity of the crop and this can be achieved through varietal development. Studying genetic variability for the traits of interest is the primary precondition for improvement of varieties [2].

Yield is polygenic inherited trait which is highly influenced by environment. Because of this, direct selection for yield resulted little progress. Indirect selection through yield components is the best and effective way of selection. Selection for yield based on highly correlated characters becomes easy if the contribution of different characters to yield is quantified using path coefficient analysis [3]. Therefore, this study was initiated to estimate correlation of characters, direct and indirect contribution of characters to yield.

## 2. METHODOLOGY

### 2.1 Study Site

A field trial was done at Awliegara research station of Korem district, Northern Ethiopia. Which is located at 39$^{o}$33'E and 12 $^{o}$31'N and is 160km South of Mekele and 620km North of Addis Ababa at an altitude of 2490masl. The average annual rainfall ranges from 450 to 1200mm at main cropping season and from 180 to 250mm at Belg (winter season).

### 2.2 Genotypes used for Experiment

Twenty three bread wheat genotypes which were under preliminary variety trial and three released variety (Hidase, Danda'a and Digalu) were included in the experiment.

### 2.3 Design of the Experiment

The RCB design with 3 replications was used. Seeds were drilled in 5 rows with row spacing of 20cm and plot length of 2.5m. A seed rate of 150 kg ha$^{-1}$ was used. The source of $P_2O_5$ and N were di ammonium Phosphate and Urea respectively with application rate of 100 kg ha$^{-1}$ for both.

### 2.4 Data Collection and Analysis

Data collection was made from plot basis and plant basis. Analysis of variance was computed using the procedures outlined by Gomez [4]. Variance components were derived by described by Cochran [5].

The procedure of Dabholkar [6] was used to estimate genotypic and Phonotypic coefficient of variation. Sharma [7] and Robertson [8] formulas were used to test significance of correlation values at phenotypic and genotypic level respectively. The path coefficient analysis and the residual factor ($P^2R$) were computed using the formula of Dewey [3] and with statistical package described by Doshi [9].

## 3. RESULTS AND DISCUSSION

### 3.1 Analysis of Variance

There was significant ($P<0.01$) differences among genotypes for ten of twelve traits studied (Table 1). It is indicated from the result that the genotypes tested had significance variations for traits. This showed presence of sufficient scope of selection for traits studied for the enhancement of the crop and the need to undertake further genetic analysis on the genotypes.

### 3.2 Correlation Coefficients at Genotypic and Phenotypic Levels

#### 3.2.1 Correlation coefficient of yield with other parameters

Genotypic correlation of grain yield with biomass is positive and highly significant ($r_g$=0.90). Hence, improvements of biomass will result in a substantial increase in grain yield. Some previous studies also reported same result [10, 11]. Besides, grain yield has no significant genotypic correlation with grain filling period, number of tillers per plant, spike length, number of kernels per spike and thousand kernel weight

(Table 2). These results suggest that selection based on these traits will not improve grain yield as suggested earlier by Ahmadi [11].

Phenotypic association of grain yield with number of tillers per plant (r = 0.46) and with biomass (r = 0.91) is positive and highly signifcant (P<0.01) (Table 2). Therefore, these traits can be considered when selection is made for grain yield. Previous studies also reported same result [12,13,14].

Yield and days to heading showed negative and significant genotypic and phenotypic correlation. The negative association of the traits may be due to late season rainfall. Hence, selection for more number of days to heading might reduce yield. Same outcome was reported by Ahmadi in moisture deficit condition [11]. However, these results contradicted with some previous studies [15]. This might be attributed to the area of the study site, where late heading genotypes might have been favored for yield.

#### 3.2.2 Correlation coefficient of biomass with other traits

Biomass and harvest index had negative and high significant genotypic correlation ($r_g$=-0.52) (Table 2). The other traits had not significant genotypic correlation with biomass. Same result was reported [16].

Biomass phenotypic correlation coefficients with number of fertile titters per plant (r=0.47) and spike length (r=0.31) were positive and highly significant. These correlation coefficient results emphasizes the importance of these traits to biomass. Ahmadi [11] and Bagrei [10] reported same findings.

### 3.3 Path-Coefficient Analysis

#### 3.3.1 Phenotypic path coefficient analysis of yield with other traits

The direct effect of biomass on yield is the highest and positive whereas, the indirect effects were negligible (Table 3). Phenotypic correlation between biomass and yield is high significant. This indicated that the correlation with yield was largely due to the direct effect. Therefore, direct selection through this trait will improve yield. Similar findings were reported by Bargei [10], Dawit [17] and Abderrahmane [18].

The phenotypic correlation between days to heading and yield is significant and negative. The direct effect of days to heading is negative and the indirect effect is also negative through biomass and harvest index. Therefore, both the direct effect and the indirect effect through biomass and harvest index contributed for phenotypic correlation of this trait with yield. Hence, when selection is made for improving yield, days to heading accompanied by biomass and harvest index should be considered. Mohammad [19] also reported same result.

**Table 1. Mean squares of parameters of bread wheat genotypes tested at Awliegara in 2014**

| Parameters | Replication (2) | Genotype (25) | Error (50) | CV (%) |
|---|---|---|---|---|
| Degree of freedom | 2 | 25 | 50 | |
| Days to heading | 7.540** | 38.270** | 1.450 | 2.100 |
| Days to maturity | 26.320ns | 135.020** | 8.611 | 2.570 |
| Grain filling period (days) | 5.861** | 52.450** | 7.051 | 4.65 1 |
| Tillers per plant | 0.321ns | 0.550** | 0.482 | 31.681 |
| Plant height (cm) | 34.441ns | 53.681ns | 47.830 | 7.972 |
| Spike length (cm) | 0.201ns | 1.081** | 0.283 | 7.222 |
| Number of spikelet per spike | 6.610** | 3.821ns | 0.950 | 7.170 |
| Number of seeds per spike | 17.801ns | 54.680** | 17.980 | 10.600 |
| Thousand seed weight (g) | 57.640ns | 223.941** | 67.701 | 10.250 |
| Biomass(t $ha^{-1}$) | 1.991ns | 17.470** | 7.721 | 27.061 |
| Yield (t $ha^{-1}$) | 0.972ns | 2.231* | 1.080 | 24.440 |
| Harvest index (%) | 14ns | 36.27** | 9.67 | 7.381 |

**= significant (P<0.05) and **=highly significant (P<0.01). ns = non-significant at P<0.05.*

**Table 2. Estimate of genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients estimation for yield contributing traits of bread wheat genotypes grown at Korem in 2014**

| Traits | DH | DM | GFP | NT | SL | NKS | TSW | BY | HI | GY |
|---|---|---|---|---|---|---|---|---|---|---|
| DH | 1 | 0.842** | 0.493* | -0.130 | 0.072 | 0.022 | 0.013 | -0.131 | -0.330 | -0.330 |
| DM | 0.801** | 1 | 0.892** | 0.170 | -0.051 | 0.081 | 0.052 | 0.021 | -0.181 | -0.112 |
| GFP | 0.432** | 0.881** | 1 | 0.380 | -0.130 | 0.106 | 0.071 | 0.140 | 0.000 | 0.112 |
| NT | -0.040 | 0.131 | 0.241* | 1 | -0.070 | -0.24 | -0.270 | 0.384 | -0.121 | 0.340 |
| SL | 0.050 | 0.010 | -0.032 | 0.203 | 1 | 0.260 | 0.292 | 0.123 | -0.10 | 0.101 |
| NKS | -0.042 | 0.020 | 0.061 | 0.033 | 0.23 | 1 | 0.993** | 0.162 | 0.030 | 0.192 |
| TSW | -0.043 | 0.000 | 0.030 | 0.011 | 0.091 | 0.983** | 1 | 0.121 | 0.022 | 0.140 |
| BY | -0.120 | 0.062 | 0.180 | 0.470** | 0.034 | 0.221 | 0.184 | 1 | -0.523** | 0.903** |
| HI | -0.260* | -0.161 | -0.040 | -0.071 | 0.470 | -0.014 | 0.000 | -0.452** | 1 | -0.112 |
| GY | -0.260* | -0.041 | 0.152 | 0.471** | 0.016 | 0.250* | 0.213 | 0.910** | -0.073 | 1 |

**= significant (P<0.05) and **=highly significant (P<0.001), DH=Number of days to heading, DM= Number of days to maturity, GFP= Number of days for grain filling, NT=Number of tillers per plant, SL=Spike length(cm), NKS= number of kernels per spike, TKW=Thousand kernel weight(g), BY=biomass (tone per hectare), GY=yield (tone per hectare), HI=Harvest index.*

Number of tillers per plant and number of kernels per spike had positive and high indirect effect on yield through biomass but negligble phenotypic direct effect. Therefore, phenotypic correlations of these traits with yield were due to the indirect effects through biomass. These traits may improve yield of bread wheat through the increased biomass. Therefore, selection for high number of tillers per plant and number of kernels per spike cannot guarantee for high yield. Similarly Bagrei [10] reported same result.

Direct effect of days to maturity and harvest index on yield is positive and high and their indirect effects through grain filling period and biomass were also negative and high. So their direct effects were counter balanced by the indirect effects. Therefore, correlation of these traits remained non-significant. So that late mature genotypes may not give raise yield.

From phenotypic path analysis residual effects was 0.056 (Table 3), this suggested that traits used for the study explained high percentage of variation in yield (94.4%).

### 3.3.2 Genotypic path coefficient analysis of yield with other traits

Biomass exerted maximum positive genotypic direct effect on yield (1.17) followed by harvest index (0.54), days to maturity (0.13). Traits with highly negative direct effects on yield were grain filling period (-0.16), days to heading (-0.05) and number of tillers per plant (-0.04). Other traits' direct effects were insignificant.

**Table 3. Direct (underlined diagonal) and indirect (off diagonal) effects of traits on yield at phenotypic level in 26 bread wheat genotypes tested at Korem (2014)**

| Traits | DH | DM | GFP | NT | SL | NKS | TSW | BY | HI | $r_p$ |
|---|---|---|---|---|---|---|---|---|---|---|
| DH | <u>-0.130</u> | 0.201 | -0.091 | 0.000 | 0.000 | -0.000 | 0.000 | -0.131 | -0.111 | -0.261* |
| DM | -0.101 | <u>0.252</u> | -0.171 | -0.000 | 0.000 | 0.002 | 0.000 | 0.051 | -0.071 | -0.041 |
| GFP | -0.052 | 0.221 | <u>-0.201</u> | -0.011 | -0.000 | 0.011 | -0.001 | 0.200 | -0.020 | 0.151 |
| NT | 0.011 | 0.031 | -0.050 | <u>-0.042</u> | 0.000 | 0.001 | -0.002 | 0.512 | -0.030 | 0.47** |
| SL | -0.012 | 0.000 | 0.011 | -0.011 | <u>0.021</u> | 0.020 | -0.021 | 0.342 | -0.071 | 0.011 |
| NKS | 0.013 | 0.010 | -0.011 | -0.000 | 0.011 | <u>0.081</u> | -0.070 | 0.241 | -0.000 | 0.251* |
| TSW | 0.013 | 0.000 | -0.010 | 0.000 | 0.012 | 0.080 | <u>-0.071</u> | 0.202 | 0.000 | 0.210 |
| BY | 0.022 | 0.010 | -0.041 | -0.021 | 0.012 | 0.020 | -0.010 | <u>1.091</u> | -0.201 | 0.910** |
| HI | 0.031 | -0.041 | 0.011 | 0.000 | -0.001 | -0.000 | 0.001 | -0.490 | <u>0.441</u> | -0.071 |

*Residual = 0.056, $r_p$=phenotypic coefficient of correlation*

**Table 4. Direct (underlined and diagonal) and indirect (off diagonal) effects of traits on yield at genotypic level in 26 bread wheat genotypes tested at Korem (2014)**

| Traits | DH | DM | GFP | NT | SL | NKS | TSW | BY | HI | $r_g$ |
|---|---|---|---|---|---|---|---|---|---|---|
| DH | -0.051 | 0.112 | -0.081 | 0.012 | 0.001 | 0.002 | 0.001 | -0.150 | -0.181 | -0.333 |
| DM | -0.041 | 0.130 | -0.140 | -0.013 | -0.001 | -0.003 | -0.002 | 0.020 | -0.102 | -0.111 |
| GFP | -0.023 | 0.123 | -0.160 | -0.024 | -0.002 | -0.001 | -0.001 | 0.161 | 0.001 | 0.111 |
| NT | 0.012 | 0.022 | -0.060 | -0.041 | -0.002 | 0.002 | 0.010 | 0.451 | -0.061 | 0.340 |
| SL | -0.001 | -0.011 | 0.012 | 0.003 | 0.023 | -0.001 | -0.010 | 0.142 | -0.051 | 0.101 |
| NKS | -0.002 | 0.013 | -0.021 | 0.012 | 0.012 | -0.012 | -0.030 | 0.191 | 0.022 | 0.190 |
| TSW | 0.001 | 0.011 | -0.013 | 0.012 | 0.013 | -0.011 | -0.030 | 0.140 | 0.011 | 0.142 |
| BY | 0.013 | 0.002 | -0.024 | -0.020 | 0.001 | -0.002 | -0.001 | 1.170 | -0.282 | 0.901** |
| HI | 0.021 | -0.021 | 0.004 | 0.010 | -0.002 | 0.001 | -0.000 | -0.611 | 0.542 | -0.111 |

*Residual = 0.116, $r_g$=genotypic coefficient of correlation.*

Genotypic correlation coefficient of biomass with grain yield was positive and highly significant. In addition its direct effect on yield was the highest. It had also negative indirect effect via harvest index. Therefore, grain yield can be improved by selecting genotypes with high biomass. Besides, the negative indirect effect of harvest index needs to be handled wisely. Abderrahmane [18] also reported similar findings on durum wheat.

From genotypic path analysis residual effects was 0.116 (Table 4), this suggested that traits used for the study explained high percentage of variation in yield (88.6%).

## 4. CONCLUSION AND RECOMMENDATIONS

In main season of 2014, 26 bread wheat genotypes were tested in RCBD at Awliegara research station of Korem district, South Tigray, Ethiopia. Genotypic correlation of grain yield with biomass is positive and highly significant ($r_g$=0.90). Hence, improvements of biomass will result in a substantial increase in grain yield. Yield and days to heading showed negative and significant genotypic and phenotypic correlation. The negative association of the traits may be due to late season rainfall. Hence, selection for more number of days to heading might reduce yield.

The direct effect of biomass on yield is the highest and positive whereas, the indirect effects were negligible. Phenotypic correlation between biomass and yield is high significant. This indicated that the correlation with yield was largely due to the direct effect. Therefore, direct selection through this trait will improve yield.

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## COMPETING INTERESTS

Author has declared that no competing interests exist.

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