

# Path Coefficient and Correlation Studies of Yield and Yield Associated Traits in Bread Wheat (*Triticum Aestivum* L.) Genotypes at Kulumsa Agricultural Research Center, South East Ethiopia

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## Abstract

Yield and yield contributing traits were studied in sixty four bread wheat genotypes using a simple lattice design in order to find out the genetic contribution of different characters towards grain yield at Kulumsa Agricultural Research Center during 2014/15 main cropping season. The genotypes showed significant variation for all the traits studied except for biomass yield ha<sup>-1</sup>. Results showed that grain yield had positive and significant correlation with 1000 kernel weight, harvest index and hectoliter weight at both levels. Days to 50% heading exerted highly significant and positive association with days to maturity (0.79\*\*), biomass yield per plot (0.55\*\*), number of productive tillers per plant (0.47\*\*) and number of grains per plant (0.43\*\*) at genotypic level. Days to 50% heading had significant positive phenotypic correlation with days to 75% maturity and significant negative phenotypic association with grain filling period. It had non-significant association with the rest of the traits. Thousand kernel weight had positive and highly significant phenotypic correlation with harvest index (0.48\*\*), hectoliter weight (0.51\*\*) and grain yield (0.51\*\*). Harvest index showed positive and highly significant correlation with 1000 kernel weight (0.48\*\*), hectoliter weight (0.41\*\*) and grain yield per hectare (0.86\*\*) and non-significant association with the rest traits at phenotypic level irrespective of direction. Maximum positive direct effect was exhibited by days to 75% maturity (1.189) followed by harvest index (1.057). This suggests the correlation revealed true relationship and direct selection through these characters is effective.

**Keywords:** Phenotypic correlation, genotypic correlation, direct effect & indirect effects

## 1. INTRODUCTION

Being a staple food, wheat has occupied a lot of area in Ethiopia. The need and importance of wheat is increasing day by day due to increase in human population. It is grown at an altitude ranging from 1500 to 3000 meters above sea level, between 6-16° N latitude and 35-42° E longitude in our country. The most suitable agro-ecological zones, however, fall between 1900 and 2700m.a.s.l (Abu Tefera, 2012). The major wheat producing areas in Ethiopia are located in Oromiya (Arsi, Bale, Shewa, Ilubabor, and Western Harerge), in SNNPR (Hadiya, Sidamo, Silte, Guraghe, Kambata), Tigray, Amhara (Northern Gondar and Gojam zones). Due to population growth and the increasing need for food, increasing yield is one of the most important goals of wheat breeding. Increasing yield and improving crop cultivation conditions can be realized by applying agronomic principles and using plant Breeding Research. The objective of wheat breeding is to obtain varieties that are winter-friendly, and resistant to draught and lodging and are free of seed abscission and spike density, from and early maturing are significant, and totally it will lead to a higher yield per unit area (Karimi, 1993). Yield is a complex quantitative trait that is greatly influenced by environmental factors such as soil fertility, light and temperature. Due to the large number of controlling genes, yield and the impact of environmental factors on it the yield heritability is low so in order to increase yield in breeding procedures. The selection based on related components and traits with yield is highly important (Valesh, 1992).

In order to increase yield in breeding methods we can use topics on quantitative genetics and understand yield components that are important in its improvement (Ehdaei, 1996 and Farshadfar, 1998). Before that we should compute yield relation with its components, in the other hands, the correlation between yield trait and its related traits and components and due to effective factors in variation that is genotype and environment yield components effect should be determined (Falcoer, 1999 and Fashadfar, 1999). Understanding the genetic characteristics of train, their relation and how traits affect each other to gain desired goals in breeding are important. We can determine the best breeding method and the most effective traits through understanding these relations (Allah Gholipour and Salehi, 2004). With regards to the relationship between grain yield and main agronomic traits, finding appropriate indicators can be considerably important for yield improvement. Genotypic and phenotypic correlation between different traits helps the modifier in indirectly selection of main traits through less important traits. Path analysis was proposed by right for the first time and is a method that makes clear the relationship between traits and their direct or indirect effects on

yield (Honar Najad, 2003).

Due to the use of traditional production systems, use of low level of production inputs, the influence of biotic and abiotic factors, environmental fluctuations, shortage of improved varieties and more importantly genetic factors the productivity of wheat per hectare in Ethiopia is low as compared to that of most of the countries of the world like Germany (7.9 tons/ha), France (7.6 tons/ha), Egypt (6.4 tons/ha). A wide gap in the yield is attributed to shortage of improved varieties for different agro ecological zone of the country; poor agronomic practices, drought, poor soil fertility, diseases and insect pests, etc. are the major constraints of wheat production in Ethiopia.

## 2. MATERIALS AND METHODS

### 2.1. Description of the study area

The field experiment was conducted at Kulumsa Agricultural Research Center (KARC). KARC is located in Oromiya Regional State Arsi Zone, 160 km South East of Addis Ababa and 8 kms to the North of Asella town. It is located in latitude of 8°17'N and longitude of 39°9'35"E. Its altitude and annual rainfall are 2,200 m.a.s.l and 832 mm respectively. The annual average temperature of the study area is 17°C with maximum and minimum temperature of 22.8°C and 10.5°C respectively. The soil type classified as clay loam soil with a pH of 6.

### 2.2. Experimental Material

A total of sixty four released & elite bread wheat genotypes (52 released and 12 Pipe lines) were grown at Kulumsa in 2014 cropping season.

### 2.3. Field Experimental Design, Trail management and Season

The experiment was carried out in 8 x 8 Simple Lattice Design. The genotypes were grown under uniform rain fed conditions. The plot/block dimension was six rows of 2.50 m length with 0.20m row spacing. Planting was done by hand drilling on July 08, 2014 with the seed rate of 150 kg/ha (45 g/plot).

### 2.4. Statistical Analysis

The mean values of the genotypes were subjected to analysis of variance based on simple lattice design using SAS procedure.

The generalized genetic distance between clusters was calculated using the generalized Mahalanobis' D<sup>2</sup> statistics equation:  $D^2_{ij} = (x_i - x_j)S^{-1}(x_i - x_j)$

#### 2.4.1. Analysis of variance (ANOVA) Structure /Model

The Mathematical Model for Simple Lattice Design is:

$Y_{ijr} = \mu + A_r + G_{ij} + B_{ir} + B_{jr} + e_{ijr}$ , where  $Y_{ijr}$  = the value observed for the plot in the  $r^{\text{th}}$  replication containing the genotype  $G_{ij}$ ,  $\mu$  = grand mean,  $G_{ij}$  = genotype effect in the  $i^{\text{th}}$  row &  $j^{\text{th}}$  column,  $A_r$  = replication effect,  $B_{ir}$  =  $i^{\text{th}}$  block effect,  $B_{jr}$  =  $j^{\text{th}}$  block effect,  $e_{ijr}$  = the plot residual effect\*

#### 2.4.2. Correlation Coefficient Analysis

Estimation of correlation coefficients (r) was computed using GENRES Statistical Software Package (Pascal Intl Software Solutions, 1994) to study positively and negatively correlated characters with yield and among themselves. Genotypic coefficient of correlation ( $r_g$ ) and phenotypic coefficient of correlation ( $r_p$ ) were computed as per Robinson *et al.* (1955) and tested for statistical significance against the correlation table values at 5% and 1% levels of significance (Fischer and Yates, 1963). The statistical procedures were as follows:

$$r_g = \frac{\text{Covg}(X,Y)}{\sqrt{\text{VargX}} \cdot \sqrt{\text{VargY}}} \qquad \text{Cov}_{gxy} = \frac{MSPg - MSPE}{r}$$

Where, Covg(X.Y) is genotypic covariance between characters X and Y; Var gX is genotypic variance of character X; Var gY is genotypic variance of character Y.

$$r_p = \frac{\text{Covp}(X,Y)}{\sqrt{\text{VarpX}} \cdot \sqrt{\text{VarpY}}} \qquad \boxed{\text{Cov}_{pxy} = \text{Cov}_{(gxy)} + \text{Cov}_{(exy)}}$$

Where, Covp(XY) is phenotypic covariance between characters X and Y; Var pX is phenotypic variance of character X; Var pY is phenotypic variance of character Y.

The correlation coefficients were done to determine the degree of association of a character with yield and among the yield components. Estimates of genotypic and phenotypic correlation coefficients were compared against r-values given in Fisher and Yates (1963) table at n-2 degrees of freedom, at the probability levels of 0.05 and 0.01 to test their significance, where n is the number of genotypes. To test the significance of correlation coefficients, the following formula was adopted (Sharma, 1998):

$$t = \frac{r}{SE(r)} \text{ And } SE(r) = \frac{1-r^2}{\sqrt{n-2}}$$

Where,  $r$  is correlation coefficient;  $n$  is number of genotypes. To test the significance of correlation coefficient, the calculated  $t$ -value can be compared with tabulated  $t$ -value at  $(n-2)$  degree of freedom at 0.05 and 0.01 levels of probability (Snedecor and Cochran, 1989).

#### 2.4.3. Path coefficient analysis

The path coefficient analysis was carried out using GENRES Statistical Software Package (Pascal Intl Software Solutions, 1994) to study the direct and indirect contributions of the traits to the associations. A measure of direct and indirect effects of each character on grain yield was estimated using a standardized partial regression coefficient known as path coefficient analysis, as suggested by Dewey and Lu (1959). Thus, correlation coefficient of different characters with grain yield was partitioned into direct and indirect effects adopting the following formula.

$$r_{iy} = r_{1iP1} + r_{2iP2} + \dots + r_{iiP_i} + \dots + r_{niP_n}$$

where  $r_{iy}$  is correlation of  $i^{\text{th}}$  character with grain yield;  $r_{1iP1}$  is indirect effects of  $i^{\text{th}}$  character on grain yield through first character;  $r_{ni}$  is correlation between  $n^{\text{th}}$  character and  $i^{\text{th}}$  character;  $n$  is number of independent variables;  $P_i$  is direct effect of  $i^{\text{th}}$  character on grain yield;  $P_n$  is direct effects of  $n^{\text{th}}$  character on grain yield.

Direct effect of different component characters on grain yield were obtained by solving the following equations:

$$(r_{iy}) = (P_i) (r_{ij}); \text{ and } (P_i) = (r_{ij})^{-1} (r_{1iP_i})$$

where,  $(P_i)$  is matrix of direct effect;  $(r_{ij})$  is matrix of correlation coefficients among all the  $n^{\text{th}}$  component characters;  $(r_{iy})$  is matrix of correlation of all component characters with grain yield;  $(r_{1iP_i})$  is indirect effect of  $i^{\text{th}}$  character on seed yield through first character.

### 3. RESULT AND DISCUSSION

#### 3.1. Analysis of Variance (ANOVA)

Mean squares of the 13 characters from analysis of variance (ANOVA) are presented in Table 1. Highly significant differences among genotypes ( $P < 0.01$ ) were observed for nine characters (days to 50% heading, days to 75% maturity, grain filling period, 1000 kernel weight, plant height, spike length, number of productive tillers per plant, number of spikelet's per spike and number of grains per plant). Significant differences at ( $p < 0.05$ ) were observed for three characters namely; grain yield per plot, harvest index and hectoliter weight whereas biomass yield showed non-significant difference among the bread wheat genotypes under study. Asaye Demelash *et al.* (2013) reported similar work in which biomass yield was non-significant in twelve alternative varieties of bread wheat, which supports the present study.

Several researchers reported significant differences among wheat genotypes studied. Shashikala (2006) reported significant differences among 169 genotypes for 11 morphological traits such as days to 50% heading, days to 75% maturity, plant height, spike length, peduncle length, number of tillers per  $m^2$ , number of spikelets per spike, 1000 grain weight, protein content and grain yield per plot. Similarly, works of Kumar *et al.* (2011) showed that significant differences among 30 genotypes of bread wheat for 8 quantitative characters and among 21 genotypes of bread wheat for 11 quantitative characters respectively. Kalimullah *et al.* (2012) reported that grains per spike, number of tillers per plant, 1000 grain weight, spike density and grain yield per plant showing highly significant differences between forty one bread wheat genotypes studied. Thus, it indicated that there was sufficient variability in the material used for their study, which provides ample scope for selecting superior and desired genotypes by the plant breeders for further improvement.

#### 3.2. Range and Mean Values

The mean performances of the sixty four bread wheat genotypes for 13 characters are presented in Table 5. The mean values for days to 50% heading ranged from 56.5 (ETBW-8532) to 80 (ET13-A2), days to 75% maturity ranged from 112.5 (Dure) to 130 (Mitikie). Grain filling period is an important trait that ultimately affects the overall grain yield by increasing grain weight. Therefore, it was ranged from 47.5 (Dodota) to 66.5 (Dashen) with a mean value of 56.34. Thousand kernel weight was ranged from 21.39 (Sirbo) to 37.84 (Dinknesh) and grain yield per plot showed a wide variation which ranged from 2115 (Menze) to 5955 (Alidoro). Biomass yield ranged from 13,750 (Simba) to 18,945 (Sanate) with a mean value of 16,008.9  $kg\ ha^{-1}$  and harvest index ranged from 12.71 (Millennium) to 35.28 (Alidoro) with a mean value of 25.59. Hectoliter weight varied from 64.58 (ETBW-8532) to 74.31 (K6295-4A), plant height ranged from 71.9 (KBG-01) to 105.6 (K6290-Bulk) and spike length ranged from 7.25 (Digelu) to 10.5 (Sulla). Similarly, the mean values for number of productive tillers per plant, number of spikeletes per spike and number of grains per plant were ranged from 3.25 (ETBE-5879) to 5.38 (ETBW-8540), 16.6 (Hidasse) to 22.0 (Sirbo) and 25.5 (ETBE-5879) to 49.7 (ETBW-8530) respectively.

**Table 1:** Analysis of variance (Mean squares) for the 13 characters of 64 bread wheat genotypes grown at Kulumsa (2014/15)

Characters	Replication (D.F.=1)	Genotype (D.F.=63)	Intra Block Error (D.F.=49)	C.V (%)	Efficiency Relative to RCBD
Days to 50% heading	0.781250	64.347803**	11.542621	5.201	1.136%
Days to 75% maturity	6.125000	25.014016**	9.323817	2.501	1.938%
Grain filling period (days)	10.125000	40.577139**	16.033475	7.107	1.863%
1000 kernel weight per plot(g)	1.746113	29.226132**	7.515515	9.449	1.428%
Grain yield per plot (kg/ha)	3841645.51	985027.36*	574163.7	18.65	0.436%
Biomass yield per plot (kg/ha)	56465236.1	2793695.4	2283935.0	9.440	1.797%
Harvest index per plot (%)	672.436128	36.956978*	20.197455	17.5	0.8679%
Hectoliter weight per plot (kg/hL)	2.5792883	11.3431088*	6.922708	3.822	0.772%
Plant height (cm)	6.480000	80.732619**	24.676632	5.608	1.476%
Spike length (cm)	25.0278125	0.91613831**	0.3329242	6.675	2.373%
Number of productive tillers/plant	0.04205000	0.47278197**	0.22463951	11.291	1.503%
Number of spikelet's/ spike	0.0312500	2.4277316**	0.6529676	4.168	1.150%
Number of grains/plant	22.194453	49.23018**	21.446217	12.055	1.884%

D.F.=degrees of freedom, \*=significant at 5% probability level and \*\*=highly significant at 1% probability level, C.V= Coefficient of Variation, RCBD=Randomized Complete Block Design.

From the result it was clearly observed that those characters with the higher range of values also had higher mean values and vice versa. Accordingly, the mean performance analysis indicated that 33 (51.56%) of the evaluated genotypes exhibited mean values above the grand mean for grain yield per hectare.

From the fifty two released varieties, 26 (50%) of them showed better yield performance whereas 7 (58.3%) of the pipelines were characterized by higher yield than the grand mean value. Furthermore, most of the pipelines were found to be better yielders than most of those released varieties (Table 2).

### 3.3. Character Association Studies

#### 3.3.1. Correlation of grain yield with other traits

Phenotypic ( $p_r$ ) and genotypic ( $g_r$ ) correlation between the various characters are presented in Table 3. Correlation studies showed that grain yield had positive and significant correlation with 1000 kernel weight (0.78\*\*, 0.51\*\*), harvest index (0.96\*\*, 0.86\*\*) and hectoliter weight (0.55\*\*, 0.46\*\*) at both phenotypic and genotypic levels. But it had positive, significant correlation with biomass yield per plot (0.29\*) and number of productive tillers plant<sup>-1</sup> (0.24\*) at genotypic level and negative correlation with the number of productive tillers plant<sup>-1</sup> (-0.01ns) at phenotypic level. Belay *et al.* (1993) and Aycecik and Yildirim (2006) reported positive correlation of grain yield with number of grains per spike, plant height and 1000 grain weight, which support the present study. Ali and Shakor (2012) and Peymaninia *et al.* (2012) also reported strong positive correlation and direct effect of total biomass and harvest index on grain yield.

Generally, in those characters in which grain yield showed positive and significant correlation, there were component interactions in which a gene conditioning an increase in one character will also influence another character provided other conditions are kept constant. Grain filling period showed positive association with grain yield plot<sup>-1</sup> at genotypic level (0.01) and it showed negative association with grain yield plot<sup>-1</sup> (-0.05) phenotypic level. However, the associations were non-significant at both levels. Negative correlation indicated inverse relationship between earliness characters and grain yield that is desirable if stresses such as terminal heat and drought are expected. This is in agreement with the findings of Tsegaye *et al.* (2012), Zafarnaderi *et al.* (2013) and Gelalcha and Hanchinal (2013), who reported negative relationship between days to flowering and grain yield per plant in their studies in advanced wheat lines.

#### 3.3.2. Correlation among characters

##### Phenotypic correlation (rp)

Days to 50% heading had significant positive phenotypic correlation with days to 75% maturity and significant negative phenotypic association with grain filling period. It had non-significant association with the rest of the traits. The works of Anwar *et al.* (2009), and Gelalcha and Hanchinal (2013) support these findings. Days to 75% maturity showed positive and non-significant correlation with grain filling period (0.21), biomass yield (0.13), harvest index (0.10) plant height (0.12), spike length (0.02), number of productive tillers (0.20), number of grains (0.22) and grain yield (0.06) whereas it showed negative non-significant phenotypic correlation with the rest traits. Thousand kernel weight had positive and highly significant phenotypic correlation with harvest index (0.48\*\*), hectoliter weight (0.51\*\*) and grain yield (0.51\*\*). However, the trait exhibited insignificant

phenotypic associations with the rest characters. Biomass yield had negative non-significant association with spike length (-0.03), number of spikelet's spike<sup>-1</sup>(-0.14) and number of grains per plant (-0.01) whereas it had positive non-significant association with the rest traits at phenotypic level.

**Appendix 1:** Genotypes that had greater mean yield than the Grand Mean

From the Released Varieties				
Entry	Name of genotype	Code	Yield mean ± Std. Dev.	Rank
2	Dereselign	-	4145.0 ± 502.04 <sup>c-n</sup>	25
3	Enkoy	-	4432.5 ± 45.96 <sup>b-l</sup>	16
4	K6290-Bulk	-	4355.0 ± 721.24 <sup>b-m</sup>	19
5	K629-4A	-	4472.5 ± 300.52 <sup>b-l</sup>	15
7	Pavon-76	-	4875.0 ± 339.41 <sup>a-f</sup>	6
10	Kubsa	HAR 1685	4240.0 ± 120.21 <sup>b-n</sup>	21
12	Abolla	HAR 1522	4730.0 ± 1265.72 <sup>a-g</sup>	12
13	Tusie	HAR 1407	4102.5 ± 470.22 <sup>c-n</sup>	11
15	Hawi	HAR 2501	4595.0 ± 650.53 <sup>a-j</sup>	26
19	Dodota	HAR 2508	4635.0 ± 806.10 <sup>a-i</sup>	8
20	Dure	HAR 1008	5627.5 ± 604.57 <sup>ab</sup>	2
23	Bobicho	HAR 2419	4162.5 ± 293.45 <sup>c-n</sup>	22
28	Alidoro	HK-14-R251	5955.0 ± 480.83 <sup>a</sup>	1
29	Dinknesh	HAR 3919	5320.0 ± 84.85 <sup>abc</sup>	4
31	Millennium	ETBW 4921	4392.5 ± 187.38 <sup>b-m</sup>	18
32	Sulla	HAR710/RBC	4300.0 ± 1166.72 <sup>b-m</sup>	20
38	Kakaba	Picaflor#1	4145.0 ± 834.39 <sup>c-n</sup>	24
42	Mekelle-02	HI-1418	4147.5 ± 1191.47 <sup>c-n</sup>	23
43	Shorima	ETBW 5483	4687.5 ± 95.46 <sup>a-h</sup>	9
44	Hidasse	ETBW 5795	4590.0 ± 49.49 <sup>a-j</sup>	13
45	Huluka	ETBW 5496	4740.0 ± 1216.22 <sup>a-g</sup>	7
46	Jefferson	NA	4662.5 ± 915.70 <sup>a-i</sup>	10
49	Ogolcho	ETBW 5520	4570.0 ± 0.00 <sup>a-k</sup>	14
50	ETBE-5879	-	4410.0 ± 763.67 <sup>b-m</sup>	17
51	ETBE-6095	-	5227.5 ± 222.74 <sup>a-d</sup>	5
52	Sanate	-	5322.5 ± 781.35 <sup>abc</sup>	3
From the Pipelines				
Entry	Name of genotype	Code	Yield mean ± Std. Dev.	Rank
53	King Bird	-	4567.5 ± 484.37 <sup>a-k</sup>	3
54	ETBW-8520	-	4380.0 ± 1103.08 <sup>b-m</sup>	5
56	ETBW-8525	-	4780.0 ± 134.35 <sup>a-g</sup>	2
57	ETBW-8526	-	5037.5 ± 830.85 <sup>a-e</sup>	1
59	ETBW-8530	-	4520.0 ± 70.71 <sup>b-l</sup>	4
63	ETBW-8538	-	4220.0 ± 360.6 <sup>b-n</sup>	6
64	ETBW-8540	-	4205.0 ± 35.36 <sup>c-n</sup>	7
<b>Grand Mean</b>			<b>4062.23</b>	

Harvest index showed positive and highly significant correlation with 1000 kernel weight (0.48\*\*), hectoliter weight (0.41\*\*) and grain yield per hectare (0.86\*\*) and non-significant association with the rest traits at phenotypic level irrespective of direction (Table 3).

Hectoliter weight showed highly significant and positive association with grain yield per plot (0.46\*\*) and 1000 kernel weight (0.51\*\*) but it showed insignificant negative correlation with characters like spike length (-0.06), number of spikelet's per spike (-0.095), days to 50% heading (-0.10), days to 75% maturity (-0.16) and grain filling period (-0.037) at phenotypic level. This character had non-significant positive phenotypic correlations with the rest characters. Works of Kumar *et al.* (2010), and Gelalcha and Hanchinal (2013) indicate the existence of strong positive correlation of number of productive tillers per plant with grain yield. Spike length had non-significant positive association with number of spikelet's per spike (0.12), number of grains per plot (0.03), days to heading (0.01) and days to maturity (0.02) having non-significant negative associations with the rest characters at phenotypic level.

Number of productive tillers plant<sup>-1</sup> exhibited non-significant positive association with almost all characters except plant height (-0.04), spike length (-0.03) and grain yield per hectare (-0.006) which were negatively correlated at phenotypic level. Number of spikelet's per spike had shown negative non-significant association with days to 50% heading (-0.006), days to 75% maturity (-0.09), 1000 kernel weight (-0.12), biomass yield (-0.14), harvest index (-0.196), hectoliter eight (-0.095), number of grains per plant (-0.01) and grain yield per hectare (-0.12) while it had positive and non-significant correlation for the rest traits at phenotypic level. Significant negative association was observed for grain filling period with days to 50% heading (-0.59\*\*). It had non-significant negative association with 1000 kernel weight (-0.05), harvest index (-0.04), hectoliter weight (-0.037), plant height (-0.02) spike length (-0.04) and grain yield (-0.05) at phenotypic level whereas it was correlated to the rest traits positively but non-significant. The association of plant height and spike length with all other traits was non-significant in both directions (Table 3).

### Genotypic correlation

The yield components exhibited varying trends of association among themselves. Days to 50% heading exerted highly significant and positive association with days to maturity (0.79\*\*), biomass yield per plot (0.55\*\*), number of productive tillers per plant (0.47\*\*) and number of grains per plant (0.43\*\*) at genotypic level. However, the trait revealed negative but highly significant correlation with grain filling period (-0.80\*\*) and number of spikelet's per spike (-0.31\*\*). It showed a non-significant positive genotypic correlation with harvest index (0.14), plant height (0.18) and grain yield hectare<sup>-1</sup>(0.08). Days to 75% maturity showed significant and negative genotypic correlation with grain filling period (-0.28\*), hectoliter weight (-0.29\*) and number of spikelet's spike<sup>-1</sup> (-0.24\*) whereas it had highly significant and positive correlation with biomass yield (0.52\*\*), plant height (0.35\*\*) and number of productive tillers plant<sup>-1</sup> (0.31\*\*) at genotypic level. Grain filling period had highly significant and negative correlation with number of productive tillers plant<sup>-1</sup> (-0.33\*\*), days to 50% heading (-0.80\*\*) and number grains spike<sup>-1</sup> (-0.42\*\*) while it had negative and significant association with days to 75% maturity (-0.28\*) at genotypic level. It exhibited non-significant association with the rest traits including grain yield per hectare regardless of directions. Thousand kernel weight had a highly significant and negative association with biomass yield (-0.322\*\*), but it exhibited highly significant positive association with harvest index (0.71\*\*), hectoliter weight (0.84\*\*) and grain yield (0.78\*\*) indicating that selection for the improvement of the grain yield based upon these characters will be effective. Significant and negative association was observed for the trait with number of spikelet's spike (-0.26\*) at genotypic level (Table 3).

**Table 3:** Estimates of phenotypic (below diagonal & bold) and genotypic (above diagonal & not bold) correlation coefficients among yield and yield components in 64 bread wheat genotypes tested at Kulumsa (2014)

Character	HD	MD	GFP	TKW	BY	HI	HLW	PH	SL	NPT	NSPS	NGP	GY
HD	<b>1.0</b>	0.79**	-0.80**	-0.036	0.55**	0.14	-0.22	0.18	-0.12	0.47**	-0.31**	0.43**	0.08
MD	<b>0.62**</b>	<b>1.0</b>	-0.28*	-0.081	0.52**	0.095	-0.29*	0.35**	-0.05	0.31**	-0.24*	0.19	0.09
GFP	<b>-0.59**</b>	<b>0.21</b>	<b>1.0</b>	-0.011	-0.13	-0.079	0.05	0.14	0.09	-0.33**	0.20	-0.42**	0.01
TKW	<b>-0.07</b>	<b>-0.11</b>	<b>-0.05</b>	<b>1.0</b>	-0.322**	0.71**	0.84**	0.11	-0.21	0.005	-0.26*	0.12	0.78**
BY	<b>0.02</b>	<b>0.13</b>	<b>0.09</b>	<b>0.04</b>	<b>1.0</b>	-0.96**	-0.34**	0.32**	-0.329**	0.45**	-0.99**	-0.77**	0.29*
HI	<b>0.11</b>	<b>0.10</b>	<b>-0.04</b>	<b>0.48**</b>	<b>0.08</b>	<b>1.0</b>	0.55**	-0.09	0.06	0.26*	-0.25*	-0.04	0.96**
HLW	<b>-0.10</b>	<b>-0.16</b>	<b>-0.037</b>	<b>0.51**</b>	<b>0.16</b>	<b>0.41**</b>	<b>1.0</b>	-0.03	-0.28*	0.40**	-0.27*	-0.27*	0.55**
PH	<b>0.13</b>	<b>0.12</b>	<b>-0.02</b>	<b>0.096</b>	<b>0.14</b>	<b>-0.03</b>	<b>0.12</b>	<b>1.0</b>	-0.42**	0.01	0.09	-0.16	0.03
SL	<b>0.01</b>	<b>0.02</b>	<b>-0.04</b>	<b>-0.05</b>	<b>-0.03</b>	<b>-0.024</b>	<b>-0.06</b>	<b>-0.17</b>	<b>1.0</b>	0.10	0.08	-0.04	0.10
NPT	<b>0.22</b>	<b>0.20</b>	<b>0.01</b>	<b>0.06</b>	<b>0.05</b>	<b>0.09</b>	<b>0.02</b>	<b>-0.04</b>	<b>-0.03</b>	<b>1.0</b>	0.16	0.31**	0.24*
NSPS	<b>-0.20</b>	<b>-0.09</b>	<b>0.17</b>	<b>-0.12</b>	<b>-0.14</b>	<b>-0.196</b>	<b>-0.095</b>	<b>0.02</b>	<b>0.12</b>	<b>0.09</b>	<b>1.0</b>	0.003	-0.19
NGP	<b>0.15</b>	<b>0.22</b>	<b>0.034</b>	<b>-0.01</b>	<b>-0.01</b>	<b>-0.001</b>	<b>0.09</b>	<b>-0.09</b>	<b>0.03</b>	<b>0.11</b>	<b>-0.01</b>	<b>1.0</b>	0.11
GY	<b>0.07</b>	<b>0.06</b>	<b>-0.05</b>	<b>0.51**</b>	<b>0.06</b>	<b>0.86**</b>	<b>0.46**</b>	<b>0.05</b>	<b>-0.06</b>	<b>-0.01</b>	<b>-0.12</b>	<b>0.03</b>	<b>1.0</b>

t=0.24 (P<0.05) and t=0.31 (P<0.01) for df=n-2, where n is the number of genotypes, HD= Days to heading, MD= Days to maturity, GFP= Grain filling period, TKW=1000 kernel weight (g), BY= Biomass yield plot<sup>-1</sup>, HI = Harvest index, HLW= Hectoliter weight, PH= Plant height (cm), SL= Spike length (cm), NPT= No. of productive tiller plant<sup>-1</sup>, NSPS = No. of spikelet's spike<sup>-1</sup>, NGP= No. of grains spike<sup>-1</sup> and GY= Grain yield plot<sup>-1</sup>.

Biomass yield plot<sup>-1</sup> had highly significant and positive association with days to 50% heading (0.55\*\*), days to 75% maturity (0.52\*\*), plant height (0.32\*\*) and number of productive tillers per plant (0.45\*\*). It had highly significant negative association with 1000 kernel weight (-0.322\*\*), harvest index (-0.96\*\*), hectoliter weight (-0.34\*\*), spike length (-0.329\*\*), number of spikelet's spike<sup>-1</sup>(-0.99\*\*) and number of grains per plant (-0.77\*\*) at genotypic level indicating that selection for the improvement of yield based up on these characters will not be effective. Harvest index showed positive significant association with 1000 kernel weight (0.71\*\*), biomass yield hectare<sup>-1</sup>(0.96\*\*), hectoliter weight plot<sup>-1</sup> (0.55\*\*) and number of productive tillers plant<sup>-1</sup> (0.26\*) but it showed significant negative genotypic correlation with number of spikelet's spike<sup>-1</sup> (-0.25\*) and non-significant with the rest traits irrespective of directions. Hectoliter weight at genotypic level revealed highly significant positive association with 1000 kernels weight (0.84\*\*), harvest index (0.55\*\*) number of productive tillers plant<sup>-1</sup>(0.40\*\*) and grain yield (0.55\*\*). Therefore, selection for improvement based on these characters will be effective. On the other hand the trait showed negative significant association with days to 75% maturity (-0.29\*), spike length (-0.28\*), number of spikelet's spike<sup>-1</sup>

<sup>1</sup>(-0.27\*) and number of grains plant<sup>-1</sup>(-0.27\*) at genotypic level indicating these characters will not be taken as a selection criteria for yield improvement. The character revealed non-significant positive and negative associations with the rest characters at this level. Plant height exhibited highly significant positive association with biomass yield hectare<sup>-1</sup> (0.32\*\*) and days to 75% maturity (0.35\*\*), but it showed highly significant negative association with spike length (-0.42\*\*). The trait exhibited non-significant negative and positive genotypic correlation with the rest traits.

Spike length had a significant negative association with biomass yield hectare<sup>-1</sup> (-0.329\*\*), plant height (-0.42\*\*) and hectoliter weight (-0.28\*) at genotypic level while it showed non-significant association at genotypic level with the rest traits irrespective of the directions. Number of productive tillers plant<sup>-1</sup> at genotypic level showed highly significant positive correlation with days to 50% heading (0.47\*\*), days to 75% maturity (0.31\*\*), hectoliter weight plot<sup>1</sup>(0.40\*\*) and number of grains plant<sup>-1</sup> (0.31\*\*). It also had positive and significant correlation for grain yield hectare<sup>-1</sup>(0.24\*) and harvest index (0.26\*\*). This indicates these traits can be used as selection criteria for yield improvement.

Negative associations were observed for number of spikelet's per spike with days to 50% heading (-0.31\*\*), biomass yield hectare<sup>-1</sup>(-0.99\*\*) days to 75% maturity (-0.24\*), 1000 kernel weight plot<sup>-1</sup> (-0.26\*), harvest index (-0.25\*) and hectoliter weight (-0.27\*) at genotypic level. The trait had non-significant positive and negative association with the rest characters. Number of grains plant<sup>-1</sup> had strong positive genotypic correlation with days to 50% heading (0.43\*\*) and number of productive tillers plant<sup>-1</sup> (0.31\*\*) whereas it had significant and negative correlation with grain filling period (-0.42\*\*), biomass yield hectare<sup>-1</sup> (-0.77\*\*) and hectoliter weightplot<sup>-1</sup>(-0.27\*) at genotypic level. The trait exhibited non-significant genotypic correlation for the rest traits irrespective of the directions. Grain yield hectare<sup>-1</sup> at genotypic level showed positive correlation with all the traits studied except for number of spikelet's spike<sup>-1</sup>(-0.19). The trait exhibited highly significant positive association with 1000 kernel weight (0.78\*\*), biomass yield (0.29\*) harvest index (0.96\*\*), hectoliter weight (0.55\*\*) and number of productive tillersplant<sup>-1</sup>(0.24\*) at genotypic level indicating these traits could be the selection criteria for yield improvement.

**Table 4:** Estimates of direct effect (the underlined bold face and diagonal) and indirect effect (off diagonal) at genotypic level in 64 bread wheat genotypes tested at Kulumsa (2014/15)

Character	HD	MD	GFP	TKW	BY	HI	HLW	PH	SL	NPT	NSPS	NGP	r <sub>e</sub>
HD	<u><b>-1.893</b></u>	0.939	0.932	0.005	-0.010	0.152	-0.058	0.039	-0.008	-0.028	-0.008	0.017	0.08
MD	-1.4953	<u><b>1.189</b></u>	0.3188	0.012	-0.009	0.101	-0.078	0.076	-0.004	-0.018	-0.006	0.008	0.09
GFP	1.521	-0.327	<u><b>-1.160</b></u>	0.002	0.003	-0.084	0.013	0.030	0.006	0.0197	0.005	-0.017	0.01
TKW	0.069	-0.096	0.013	<u><b>-0.142</b></u>	-0.042	0.744	0.225	0.023	-0.015	-0.0003	-0.007	0.005	0.78**
BY	-1.035	0.615	0.149	-0.315	<u><b>-0.019</b></u>	2.076	1.695	-0.437	-0.225	0.087	-0.026	0.273	0.29*
HI	-0.272	0.113	0.092	-0.099	-0.037	<u><b>1.057</b></u>	0.148	-0.019	0.004	-0.016	-0.007	-0.002	0.96**
HLW	0.407	-0.346	-0.055	-0.119	-0.121	0.584	<u><b>0.268</b></u>	-0.006	-0.019	-0.024	-0.007	-0.011	0.55**
PH	-0.339	0.417	-0.159	-0.015	0.038	-0.093	-0.007	<u><b>0.218</b></u>	-0.028	-0.001	0.002	-0.006	0.03
SL	0.219	-0.064	-0.109	0.030	0.063	0.065	-0.075	-0.090	<u><b>0.068</b></u>	-0.006	0.002	-0.002	0.10
NPT	-0.882	0.363	0.382	-0.001	0.028	0.274	0.107	0.002	0.007	<u><b>-0.059</b></u>	0.004	0.013	0.24*
NSPS	0.579	-0.288	-0.236	0.036	0.019	-0.266	-0.073	0.019	0.005	-0.009	<u><b>0.026</b></u>	0.040	-0.19
NGP	-0.803	0.223	0.491	-0.017	0.129	-0.043	-0.072	-0.475	0.027	0.252	-0.181	<u><b>0.041</b></u>	0.11

Residual = 0.2147

HD= Days to heading, MD= Days to maturity, GFP= Grain filling period, TKW=1000 kernel weight (g), BY= Biomass yield plot<sup>-1</sup> HI = Harvest index, HLW= Hectoliter weight, PH= Plant height (cm), SL= Spike length (cm), NPT= No. of productive tiller plant<sup>-1</sup>, NSPS = No. of spikelet's spike<sup>-1</sup>, NGP= No. of grains spike<sup>-1</sup>.

The high positive correlation between different traits shows the possibility of simultaneous improvement of these multiple traits. Significant negative correlations between two traits might pose problem during selection for higher values of both traits and care should be taken, Asaye Demelash *et al.* (2013). In general, the estimates of genotypic correlation coefficients were higher for most of the characters than phenotypic correlation coefficient, indicating a strong inherent association among various characters.

### 3.4. Path Coefficient Analysis

Path coefficient analysis proved an effective mean of separating direct and indirect causes of association and permits critical evaluation of specific forces acting to produce a given correlation and measure the relative importance of each causal factor. As correlation does not allow the partitioning of genotypic correlation coefficients into direct and indirect effects, they are further analyzed by path coefficient analysis (Dewey and Lu, 1959) by using grain yield as a dependent variable. The genotypic direct and indirect effects of different characters on grain yield are presented in Table 4. The highest positive direct effect on grain yield per plot was exhibited by days to 75% maturity (1.189) which had positive correlation with grain yield followed by harvest index (1.057\*\*) indicating the true relationship between these traits as good contributors to grain yield. On the other hand, highest negative direct effect on grain yield hectare<sup>-1</sup> was exhibited by days to 50% heading (-1.893) followed by grain filling period (-1.160), but non-significant.

#### 3.4.1. Direct effects

Maximum positive direct effect was exhibited by days to 75% maturity (1.189) followed by harvest index

(1.057). This suggests the correlation revealed true relationship and direct selection through these characters is effective. Kumar (2011) reported similar results in rice cultivars. Hectoliter weight (0.268), spike length (0.068), number of grains plant<sup>-1</sup> (0.041) and number of spikelet's spike<sup>-1</sup> (0.026) had positive direct effects and positive correlation coefficients, except for number of spikelet's spike<sup>-1</sup> and number of grains per plant which had non-significant negative correlation with grain yield. The indirect effects of these traits through other traits were mostly negative. Hence, the correlation coefficients of these traits with grain yield had been largely due to the direct effect. Number of productive tillers plant<sup>-1</sup> had negative direct effect and positive correlation coefficient. Thus, the positive correlation coefficient was largely due to its respective indirect effects. Days to 50% heading (-1.893) and grain filling period (-1.160) exhibited negative direct effect with negligible correlation. Selection this trait will not be improving grain yield of bread wheat advanced lines. Therefore, direct selection of these characters is ineffective. Plant height had positive correlation with grain yield, but non-significant (Table 3). The direct effect of plant height on grain yield was also positive and greater than its correlation value (Table 4) indicating its indirect effect through days to 50% heading (-0.339), grain filling period (-0.159), 1000 kernel weight (-0.015), harvest index (-0.093), hectoliter weight (-0.007), spike length (-0.028) and number of grains plant<sup>-1</sup> (-0.006) counter balanced its direct effect (0.218) on grain yield and reduced the correlation coefficient to (+0.03). This result is in agreement with the findings of RAKESH CHOUDHARY; BABU LAL JAT *et.al* (2012) who reported positive correlation and direct effect of plant height with grain yield.

#### 3.4.2. Indirect effects

Maximum and positive indirect effect was exhibited by biomass yield through harvest index (2.076) followed by biomass yield through hectoliter weight (1.695) and grain filling period through days to 50 percent heading (1.521). The indirect effect of days to 50% heading through days to 75% maturity (0.939), grain filling period (0.932), 1000 kernel weight (0.005), harvest index (0.152), plant height (0.039) and number grains plant<sup>-1</sup>(0.017) counter balanced the negative direct effect of number of days to 50% heading on grain yield (-1.893) and reduced the correlation coefficient to +0.08 (Tables 3 and 4). Similarly, the indirect effect of grain filling period through days to 50% heading (1.521), 1000 kernel weight (0.002), biomass yield per hectare (0.003), hectoliter weight (0.013), plant height (0.030), spike length (0.006), number of productive tillers plant<sup>-1</sup> (0.0197) and number of spikelet's spike<sup>-1</sup> (0.005) counter balanced the negative direct effect of grain filling period on grain yield per hectare (-1.160) and reduced the correlation coefficient to +0.01 (Table 3 and 4). Moreover, the positive direct effects of 1000 kernel weight through days to 50% heading (0.069), grain filling period (0.013), harvest index (0.744), hectoliter weight (0.225), plant height (0.023) and number of grains per plant (0.005) counter balanced the negative direct effect of 1000 kernel weight on grain yield (-0.142) and reduced its genotypic correlation to +0.78 (Table 3). Similar results were obtained by Ali *et al.*, (2008) and Mollasadeghi and Shahyari (2011).

The negative direct effect of biomass yield per hectare on grain yield per hectare (-0.019) was counter balanced mainly by its positive indirect effects through harvest index (2.076) and hectoliter weight plot<sup>-1</sup> (1.695) and reduced its genotypic correlation to +2.29. Harvest index exhibited moderate negative indirect effect on grain yield through days to 50% heading (-0.272) followed by biomass yield (-0.099) and grain filling period (0.092). Hectoliter weight showed maximum positive indirect effect on grain yield through harvest index (0.584) and days to 50% heading (0.407). The negative indirect effect of plant height on grain yield per plot through traits like days to heading (-0.339), grain filling period (-0.159), 1000 kernel weight (-0.015), harvest index (-0.093) and spike length (-0.028) counter balanced the positive direct effect of plant height on grain yield (0.218) and reduced its correlation to +0.03 at genotypic level.

Spike length at genotypic level showed moderate indirect positive effect on grain yield through days to 50% heading (0.219), harvest index (0.065) and biomass yield (0.063). Similarly, it exhibited moderate negative indirect effect on grain yield via grain filling period (-0.109) plant height (-0.090) and hectoliter weight (-0.075). In this study the direct effect of spike length on grain yield was positive (0.068), but this effect was counter balanced by its negative indirect effects through grain filling period (-0.109), plant height (-0.090), hectoliter weight plot<sup>-1</sup> (-0.075) and days to 75% maturity (-0.064) and reduced the genotypic correlation of spike length to +0.10. This indicates the positive relationship between spike length and grain yield non-significant. Number of productive tillers plant<sup>-1</sup> showed negative direct effect on grain yield (-0.059). But the indirect effect of number of productive tillers plant<sup>-1</sup> through grain filling period (0.382), days to 75% maturity (0.363), harvest index (0.274), hectoliter weight plot<sup>-1</sup> (0.107), biomass yield hectare<sup>-1</sup> and number of grains plant<sup>-1</sup>(0.013) mainly counter balanced its negative direct effect and reduced the genotypic correlation coefficient to +0.24 which shows significant positive correlation of the trait with grain yield. Number of spikelet's spike<sup>-1</sup> at genotypic level revealed high positive indirect effect via days to 50% heading (0.579) on grain yield plot<sup>-1</sup> and moderate negative indirect effect via days to 75% maturity (-0.288) followed by harvest index (-0.266) and grain filling period (-0.236) on grain yield per plot.

#### 4. CONCLUSION

The estimates of genotypic correlation coefficient were higher for most of the characters than phenotypic correlation coefficient, indicating a strong inherent association among various characters. Grain yield per plot showed highly significant positive correlation at phenotypic level with 1000 kernel weight, harvest index and hectoliter weight while grain filling period, spike length, number of productive tillers and number of spikelet's per spike had negative, non-significant correlation with grain yield. The grain yield showed significant positive correlation with 1000 kernel weight, biomass yield, harvest index, hectoliter weight and number of productive tillers at genotypic level. By selecting for those traits showing positive and significant correlation with grain yield there is a possibility to increase grain yield of bread wheat. Therefore, selection for the improvement of the grain yield based upon these characters will be effective.

Hectoliter weight showed highly significant and positive association with grain yield per plot (0.46\*\*) and 1000 kernel weight (0.51\*\*). Days to 50% heading exerted highly significant and positive association with days to maturity (0.79\*\*), biomass yield per plot (0.55\*\*), number of productive tillers per plant (0.47\*\*) and number of grains per plant (0.43\*\*) at genotypic level. Thousand kernel weight had a highly significant and negative association with biomass yield (-0.322\*\*), but it exhibited highly significant positive association with harvest index (0.71\*\*), hectoliter weight (0.84\*\*) and grain yield (0.78\*\*) indicating that selection for the improvement of the grain yield based upon these characters will be effective. Biomass yield plot<sup>-1</sup> had highly significant and positive association with days to 50% heading (0.55\*\*), days to 75% maturity (0.52\*\*), plant height (0.32\*\*) and number of productive tillers per plant (0.45\*\*). It had highly significant negative association with 1000 kernel weight (-0.322\*\*), harvest index (-0.96\*\*), hectoliter weight (-0.34\*\*), spike length (-0.329\*\*), number of spikelet's spike<sup>-1</sup> (-0.99\*\*) and number of grains per plant (-0.77\*\*) at genotypic level indicating that selection for the improvement of yield based up on these characters will not be effective. Harvest index showed positive significant association with 1000 kernel weight (0.71\*\*), biomass yield hectare<sup>-1</sup> (0.96\*\*), hectoliter weight plot<sup>-1</sup> (0.55\*\*) and number of productive tillers plant<sup>-1</sup> (0.26\*). Hectoliter weight at genotypic level revealed highly significant positive association with 1000 kernels weight (0.84\*\*), harvest index (0.55\*\*) number of productive tillers plant<sup>-1</sup> (0.40\*\*) and grain yield (0.55\*\*). Therefore, selection for improvement based on these characters will be effective.

Path coefficient analysis, based on grain yield as a dependent variable, showed that days to 75% maturity, harvest index, hectoliter weight, plant height, spike length, number of spikelet's per spike and number of grains per plant had positive direct effect. Whereas, days to 50% heading, grain filling period, 1000 kernel weight, number of productive tillers and biomass yield showed negative direct effect. But the negative direct effect of these traits on grain yield was counter balanced by the cumulative indirect effects of other traits so that their genotypic correlation became positive. Since they had positive correlation with grain yield, much attention should be given to days to 75% maturity, harvest index and hectoliter weight as these characters are helpful for direct selection. Maximum positive direct effect was exhibited by days to 75% maturity (1.189) followed by harvest index (1.057). This suggests the correlation revealed true relationship and direct selection through these characters is effective. Maximum and positive indirect effect was exhibited by biomass yield through harvest index (2.076) followed by biomass yield through hectoliter weight (1.695) and grain filling period through days to 50 percent heading (1.521). The indirect effect of days to 50% heading through days to 75% maturity (0.939), grain filling period (0.932), 1000 kernel weight (0.005), harvest index (0.152), plant height (0.039) and number grains plant<sup>-1</sup> (0.017) counter balanced the negative direct effect of number of days to 50% heading on grain yield (-1.893) and reduced the correlation coefficient to +0.08. Similarly, the indirect effect of grain filling period through days to 50% heading (1.521), 1000 kernel weight (0.002), biomass yield per hectare (0.003), hectoliter weight (0.013), plant height (0.030), spike length (0.006), number of productive tillers plant<sup>-1</sup> (0.0197) and number of spikelet's spike<sup>-1</sup> (0.005) counter balanced the negative direct effect of grain filling period on grain yield per hectare (-1.160) and reduced the correlation coefficient to +0.01.

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