# Correlations and Path Analysis of Some Quantitative and Qualitative Characters in Durum Wheat (*Triticum Turgidum* L.) Accessions in Western Oromia, Ethiopia

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## ABSTRACT

Durum wheat is the second most important triticum species next to bread wheat. Ethiopia is one of the centers of diversity for durum wheat. The present study was to determine the interrelationship and direct and indirect effects of yield component traits on grain yield of Ethiopian landraces durum wheat for further breeding activities of yield improvement. Out, 97 durum wheat accessions along with 3 improved varieties were evaluated in 10 x 10 simple lattice design during 2018 main cropping season at Mata Sub site of Haro Sabu Agricultural Research Center. Analysis of variance revealed highly significant differences among accessions for all traits. More than 36% of accessions were superior in mean grain yield than the standard checks. Grain yield exhibited positive and significant correlation both at genotypic and phenotypic level with most of the characters such as plant height (rp = 0.22, rg = 0.25), harvest index (rp=0.79, rg = 0.78), biological yield (rp = 0.31, rg = 0.30), number of kernels per spike (rp = 0.17, rg = 0.21), spike length, (rp = 0.36, rg = 0.39), and hectoliter weight (kg hl$^{-1}$) (rp = 0.44, rg = 0.45). The association between yield, and yield related characters through phenotypic genotypic path coefficients revealed that biological yield, spike length, harvest index and plant height exerted highest positive direct effect on grain yield. This suggests that simultaneous improvement in these characters might be possible.

KEYWORDS: correlation, direct and indirect effects, durum wheat and path analysis

## INTRODUCTION

Durum wheat (*Triticum durum* L.) is a member of the Gramineae family, which belongs to the Triticeae tribe. It is an allotetraploid (two genomes: AABB) with 28 chromosomes (2n = 4x =28). (Colomba and Gregorini, 2011).Durum wheat is one of the important cereal crops in many countries in the world (Maniee *et al*., 2009; Kahrizi *et al*., 2010a, b; Mohammadi *et al*., 2010). Durum wheat global acreage is estimated at 17 million hectares (ha) and the most important growing areas are situated in the North America, North and East Africa and South West Asia (Maccaferri *et al*., 2014).However, in Ethiopia, it ranked 3rd after maize and rice in production tons per hectare (CSA, 2017/2018).The national average yield is still 2.74 tons ha$^{-1}$which is far less than potential yields of 8 to 10 tha$^{-1}$ (CSA, 2017/2018).

There are two types of wheat grown in Ethiopia and both of them are produced under rainfed conditions: durum (pasta and macaroni) wheat, accounting for 40% of production, and bread wheat, accounting for the remaining 60% (Bergh *et al*., 2012).It is traditionally grown by small-scale farmers on the heavy black clay soils (Vertisols) of the high lands at altitude ranging between 1800 and 2800 meters above sea levels (masl) and rainfall distribution varying from 600 to more than 1200 mm per annum (Hailu, 1991). According to Tesfaye (1986), close to 85 % of the cultivated durum wheat in Ethiopia are landraces. In crop plants, the most of the agronomic characters are quantitative in nature. Yield is one that character that results due to the actions and interactions of various component characters (Grafius, 1960). The genetic architecture of yield can be resolved better by studying its component characters. This enables the plant breeder to breed for high yielding genotypes with desired combinations of traits (Khan and Dar, 2010). Correlation analysis is used as effective tool to determine the relationship among different traits in genetic diverse population for enhancement of crop improvement process (Kandel *et al*., 2018b; Dhami *et al*., 2018; Kharel *et al*., 2018). The correlations are very important in plant breeding because of its reflection in dependence degree between two or more traits. Correlation analysis shows

the intensity of dependence (correlation) between studied traits. In wheat, many breeders try to explain the relations between grain yield and agronomic and morphological traits by using simple correlation coefficients. Path analysis provides a measure of relative importance of each independent variable to prediction of changes in the dependent one. A path coefficient is a standardized partial regression coefficient and as such measures the direct effect of one trait upon other and permits the separation of correlation coefficient into direct and indirect effects (Dewey and Lu, 1959; Phougat et al., 2017). Path coefficients show direct influence of independent variable upon dependent variable (Lidansky, 1988).

In agriculture, path coefficient analysis has been used by plant breeders to assist in identifying traits that are useful as selection criteria to improve crop yield (Dewey and Lu, 1959; Milligan et al., 1990; Ahmed et al., 2003; Bhujel et al., 2018; Kandel et al., 2018a). Quantitative characters like as grain yield is a complex character influenced directly or indirectly by several genes present in the plant (Bhutta et al., 2005) that making difficult for direct selection. In most breeding programs, the strategy is based on simultaneous selection for several traits and therefore the knowledge on the genetic association between traits is very useful for the establishment of selection criteria. The objective of this study was to establish the interrelationship and direct and indirect effects of some yield components among themselves and with grain yield in durum wheat accessions.

## MATERIALS AND METHODS
### Study Area
The experiment was conducted during the main cropping season of 2018 at Mata research sub-site of Haro-Sabu Agricultural Research Center (HSARC), Sayo district of Kellem Wollega Zone. Mata research sub-site is located at 652km West of Addis Ababa.It is located between 8º10'00''N to 8º50'00''N and 34º39'30''E to 34º59'30''E (Figure 1) with an elevation of 2025 meters above sea level.
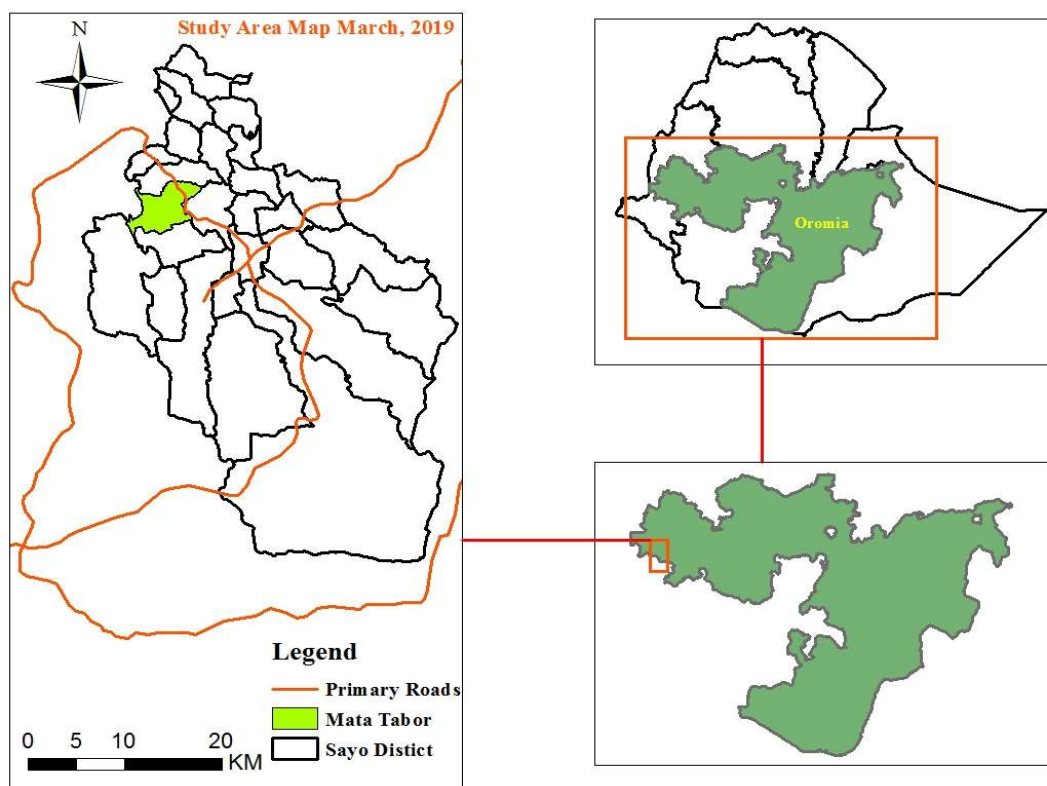


Figure1: Map of the study area.

Soil types of the study area classified as 90% loam, 6% sand and 4% clay soil type. Mean annual rainfall of the area is 1219.15 mm and the minimum and maximum annual temperatures are16.21 and 27.77°C, respectively with the relative humidity of 67.5% Source: (Sayo district Agriculturen and Natural Resource office, Dembi Dollo, unpublished)

### Breeding materials and experimental design
Materials of this study consisted of 100 genotypes of durum wheat, of which 97 landraces (accessions) and three released varieties as standard checks (Bekalcha, Dire and Obsa) obtained from Sinana Agricultural Research Center were used for this study provided by Ethiopia Biodiversity Institute (EBI) (Table 1) Materials were sown in the first week of August 2018 in Mata sub site in 10 x 10 simple lattice design with two replications. Seed was drilled on 20 cm rowspacing, 1m row length and 1 m spacing between each block.Seed rate of 150 kg ha^{-1} and.combination of UREA and NPS fertilizers were applied at the recommendation rate of 100 kg ha^{-1}. UREA was applied in split form (half at planting and the rest half was applied at tiller initiation 35 days after emergence. Other crop management practices were undertaken as per the recommendation.

**Table1: List of durum wheat accessions collected from different regions of Ethiopia.**

| Entry code | Acc. No | Genus name | species name | Region | Latitude | Longitude | Altitude |
|---|---|---|---|---|---|---|---|
| 1 | 7375 | *Triticum* | *dicoccum* | Oromia | 07-07-00-N | 40-43-00-E | 1710 |
| 2 | 5582 | *Triticum* | *dicoccum* | Oromia | 08-57-00-N | 37-52-00-E | 2280 |
| 3 | 7710 | *Triticum* | *dicoccum* | Oromia | 07-08-00-N | 40-43-00-E | 1980 |
| 4 | 238891 | *Triticum* | *dicoccum* | Oromia | 07-01-30-N | 40-21-07-E | 2200 |
| 5 | 7207 | *Triticum* | *dicoccum* | Oromia | 07-01-40-N | 40-23-55-E | 1990 |
| 6 | 5181 | *Triticum* | *dicoccum* | Oromia | 07-01-20-N | 40-19-46-E | 1900 |
| 7 | 242782 | *Triticum* | *sp* | Amara | 11-05-00-N | 37-52-00-E | 2400 |
| 8 | 242793 | *Triticum* | *sp* | Amara | 10-18-00-N | 38-12-00-E | 2460 |
| 9 | 7532 | *Triticum* | *sp* | Amara | 10-18-00-N | 38-12-00-E | 2460 |
| 10 | 7056 | *Triticum* | *sp* | Oromia | 09-00-00-N | 38-07-00-E | 2350 |
| 11 | 7880 | *Triticum* | *sp* | Oromia | 07-17-00-N | 38-36-00-E | 2030 |
| 12 | 242781 | *Triticum* | *sp* | Oromia | 07-44-00-N | 39-34-00-E | 2140 |
| 13 | 5182 | *Triticum* | *sp* | Oromia | 08-24-00-N | 39-52-00-E | 2040 |
| 14 | 5171 | *Triticum* | *sp* | Amara | 10-34-00-N | 38-14-00-E | 2390 |
| 15 | 222393 | *Triticum* | *sp* | Oromia | 08-49-00-N | 38-54-00-E | 2400 |
| 16 | 7649 | *Triticum* | *sp* | Amara | 10-26-00-N | 38-20-00-E | 2460 |
| 17 | 5216 | *Triticum* | *sp* | Oromia | 08-12-00-N | 39-34-00-E | 2150 |
| 18 | 5020 | *Triticum* | *sp* | Oromia | 08-24-00-N | 39-52-00-E | 2040 |
| 19 | 6102 | *Triticum* | *sp* | Oromia | 07-46-00-N | 39-47-00-E | 2440 |
| 20 | 242790 | *Triticum* | *sp* | Oromia | 07-41-00-N | 40-13-00-E | 2395 |
| 21 | 5184 | *Triticum* | *sp* | Oromia | 07-45-00-N | 39-40-00-E | 2400 |
| 22 | 5515 | *Triticum* | *sp* | Oromia | 07-44-00-N | 39-53-00-E | 2430 |
| 23 | 5528 | *Triticum* | *sp* | Amara | 10-18-00-N | 38-12-00-E | 2460 |
| 24 | 7084 | *Triticum* | *sp* | Amara | 10-14-00-N | 38-01-00-E | 2440 |
| 25 | 7683 | *Triticum* | *sp* | Oromia | 07-39-00-N | 39-46-00-E | 2430 |
| 26 | 242785 | *Triticum* | *sp* | Oromia | 07-50-00-N | 39-38-00-E | 2410 |
| 27 | 7343 | *Triticum* | *sp* | Amara | 10-18-00-N | 38-12-00-E | 2460 |
| 28 | 7832 | *Triticum* | *sp* | Amara | 11-21-00-N | 39-18-00-E | 2300 |
| 29 | 6983 | *Triticum* | *sp* | Amara | 10-28-00-N | 38-17-00-E | 2430 |
| 30 | 5472 | *Triticum* | *sp* | Amara | 10-28-00-N | 38-18-00-E | 2410 |
| 31 | 5354 | *Triticum* | *sp* | Oromia | 08-53-00-N | 37-51-00-E | 2310 |
| 32 | 5729 | *Triticum* | *sp* | Amara | 11-06-00-N | 39-45-00-E | 1790 |
| 33 | 7647 | *Triticum* | *sp* | Amara | 11-05-00-N | 37-42-00-E | 2470 |
| 34 | 6988 | *Triticum* | *sp* | Oromia | 09-14-00-N | 41-09-00-E | 2260 |
| 35 | 5583 | *Triticum* | *sp* | Oromia | 08-54-00-N | 38-54-00-E | 2300 |
| 36 | 7020 | *Triticum* | *sp* | Oromia | 09-00-00-N | 39-07-00-E | 2330 |
| 37 | 239694 | *Triticum* | *sp* | Oromia | 38-54-00-N | 38-54-00-E | 2300 |
| 38 | 5183 | *Triticum* | *sp* | Oromia | 08-47-00-N | 39-15-00-E | 2300 |
| 39 | 5556 | *Triticum* | *sp* | Oromia | 09-47-00-N | 39-16-00-E | 2200 |
| 40 | 5175 | *Triticum* | *sp* | Oromia | 08-52-00-N | 39-01-00-E | 2133 |
| 41 | 5373 | *Triticum* | *sp* | Oromia | 38-54-00-N | 38-54-00-E | 2300 |
| 42 | 6968 | *Triticum* | *sp* | Oromia | 09-24-00-N | 38-47-00-E | 2160 |
| 43 | 7664 | *Triticum* | *sp* | Oromia | 09-01-00-N | 39-15-00-E | 2300 |
| 44 | 7218 | *Triticum* | *sp* | Oromia | 09-00-00-N | 39-07-00-E | 2330 |
| 45 | 5043 | *Triticum* | *sp* | Amara | 08-50-00-N | 39-19-00-E | 2260 |
| 46 | 6978 | *Triticum* | *sp* | Amara | 08-50-00-N | 39-19-00-E | 2260 |
| 47 | 7009 | *Triticum* | *sp* | Oromia | 08-51-00-N | 38-30-00-E | 2333 |
| 48 | 5174 | *Triticum* | *sp* | Oromia | 08-59-00-N | 38-52-00-E | 2300 |
| 49 | 7709 | *Triticum* | *sp* | Oromia | 09-01-00-N | 39-03-00-E | 2450 |
| 50 | 230678 | *Triticum* | *sp* | Oromia | 08-51-00-N | 38-52-00-E | 2300 |

| Entry code | Acc. No | Genus name | species name | Region | Latitude | Longitude | Altitude |
|---|---|---|---|---|---|---|---|
| 51 | 242789 | *Triticum* | *sp* | Oromia | 08-54-00-N | 39-01-00-E | 2350 |
| 52 | 242792 | *Triticum* | *sp* | Oromia | 08-59-00-N | 38-52-00-E | 2300 |
| 53 | 5214 | *Triticum* | *sp* | Oromia | 08-58-00-N | 39-00-00-E | 2420 |
| 54 | 5428 | *Triticum* | *sp* | Oromia | 08-47-00-N | 39-15-00-E | 2300 |
| 55 | 7801 | *Triticum* | *sp* | Oromia | 09-01-00-N | 39-15-00-E | 2300 |
| 56 | 242791 | *Triticum* | *sp* | Oromia | 09-01-00-N | 39-15-00-E | 2300 |
| 57 | 5491 | *Triticum* | *sp* | Oromia | 08-59-00-N | 38-52-00-E | 2300 |
| 58 | 5510 | *Triticum* | *sp* | Oromia | 08-54-00-N | 39-05-00-E | 2200 |

| 59 | 7015 | Triticum | sp | Oromia | 08-49-00-N | 39-00-00-E | 1915 |
| 60 | 242784 | Triticum | sp | Oromia | 08-45-00-N | 39-08-00-E | 2350 |
| 61 | 5635 | Triticum | sp | Tigray | 14-10-00-N | 38-42-00-E | 2367 |
| 62 | 5609 | Triticum | sp | Oromia | 08-48-00-N | 38-54-00-E | 2080 |
| 63 | 5666 | Triticum | sp | Tigray | 14-07-00-N | 38-29-00-E | 2487 |
| 64 | 5572 | Triticum | sp | Oromia | 08-45-00-N | 39-13-00-E | 2070 |
| 65 | 5504 | Triticum | sp | Oromia | 08-45-00-N | 39-15-00-E | 2120 |
| 66 | 5197 | Triticum | sp | Oromia | 08-45-00-N | 39-13-00-E | 2160 |
| 67 | 7827 | Triticum | sp | Oromia | 08-47-00-N | 39-15-00-E | 2300 |
| 68 | 242786 | Triticum | sp | Oromia | 08-45-00-N | 39-15-00-E | 2120 |
| 69 | 5653 | Triticum | sp | Oromia | 08-45-00-N | 39-08-00-E | 2340 |
| 70 | 5534 | Triticum | sp | Oromia | 08-45-00-N | 39-15-00-E | 2120 |
| 71 | 242783 | Triticum | sp | Oromia | 09-47-00-N | 39-46-00-E | 2300 |
| 72 | 226897 | Triticum | sp | Oromia | 09-47-00-N | 39-46-00-E | 2300 |
| 73 | 5168 | Triticum | sp | Oromia | 09-47-00-N | 39-16-00-E | 2200 |
| 74 | 5179 | Triticum | sp | Oromia | 09-47-00-N | 39-16-00-E | 2300 |
| 75 | 7825 | Triticum | sp | Oromia | 09-47-00-N | 39-16-00-E | 2300 |
| 76 | 5198 | Triticum | sp | Amara | 08-50-00-N | 39-19-00-E | 2260 |
| 77 | 8072 | Triticum | sp | Amara | 08-50-00-N | 39-19-00-E | 2260 |
| 78 | 242779 | Triticum | sp | Amara | 08-50-00-N | 39-19-00-E | 2260 |
| 79 | 5492 | Triticum | sp | Amara | 08-50-00-N | 39-19-00-E | 2260 |
| 80 | 243733 | Triticum | sp | SNNP | 09-29-00-N | 38-30-00-E | 2333 |
| 81 | 5638 | Triticum | sp | Oromia | 08-51-00-N | 38-30-00-E | 2330 |
| 82 | 242780 | Triticum | sp | Amara | 08-50-00-N | 39-19-00-E | 2260 |
| 83 | 5597 | Triticum | sp | Amara | 12-38-00-N | 37-28-00-E | 2100 |
| 84 | 5044 | Triticum | sp | Oromia | 09-47-00-N | 39-46-00-E | 2300 |
| 85 | 5152 | Triticum | sp | Oromia | 08-47-00-N | 39-46-00-E | 2300 |
| 86 | 5554 | Triticum | sp | Amara | 10-34-00-N | 37-29-00-E | 2145 |
| 87 | 7018 | Triticum | sp | Amara | 11-00-00-N | 36-54-00-E | 2489 |
| 88 | 5669 | Triticum | sp | Oromia | 07-12-00-N | 38-35-00-E | 1773 |
| 89 | 7828 | Triticum | sp | Oromia | 08-50-00-N | 38-22-00-E | 1773 |
| 90 | 5367 | Triticum | sp | Oromia | 08-54-00-N | 39-01-00-E | 2350 |
| 91 | 5344 | Triticum | sp | Amara | 12-19-00-N | 37-33-00-E | 2145 |
| 92 | 5434 | Triticum | sp | Oromia | 08-47-00-N | 39-15-00-E | 2300 |
| 93 | 5166 | Triticum | sp | Oromia | 08-51-00-N | 38-30-00-E | 2333 |
| 94 | 5149 | Triticum | sp | Oromia | 08-16-00-N | 38-52-00-E | 1791 |
| 95 | 5169 | Triticum | sp | Oromia | 08-59-00-N | 38-52-00-E | 2300 |
| 96 | 5441 | Triticum | turgidum | Oromia | 07-47-00-N | 39-39-00-E | 2415 |
| 97 | 5557 | Triticum | polonicum | Oromia | 08-58-00-N | 37-36-00-E | 2430 |
| 98 | Bekalcha | Triticum | Improved variety | Sinana ARC | | | |
| 99 | Dire | Triticum | Improved variety | Sinana ARC | | | |
| 100 | obsa | Triticum | Improved variety | Sinana ARC | | | |

**Source: Ethiopian Biodiversity Institute (EBI) and Sinana ARC**

## Method of data collection
Ten plants were selected randomly before heading from each row and tagged with thread and all the necessary plant based (measurable quantitative traits) average data were collected from these ten sampled plants.

**Plant-based data:**- number of kernels per spike, plant height, spike length, spike weight per plant and number of spikelets per spike

**Plot based data:**- days to heading, days to maturity, days to grain filling period, = thousand seed weight, grain yield, biological yield and harvest index

## Statistical analysis
ANOVA of the tested genotypes was conducted for the simple lattice for the quantitative and qualitative data. Associations between all possible pairs of quantitative traits were evaluated for their significance using SAS software version 9.2 (SAS, 2008). Phenotypic and genotypic correlations between yield and yield related traits were estimated using the method described by Miller *et al*. (1958) and Kashiani and Saleh (2010) from the corresponding variance and covariance components as follows:

Phenotypic correlation coefficient:
$$rpxy = \frac{pcov\,x.y}{\sqrt{\delta^2 px * \delta^2 py}}$$

Genotypic correlation coefficient:
$$rgxy = \frac{gcov\,x.y}{\sqrt{\delta^2 gx * \delta^2 gy}}$$

Where, rpxy= Phenotypic correlation coefficient between characters X and Y, rgxy= genotypic correlation coefficients between characters X and Y, pcovx.y and gcovx.y are phenotypic and genotypic covariance between variables x and y, respectively, $\sigma^2 p$ =Phenotypic Variance between characters X and Y, $\sigma^2 g$ =Genotypic Variance between characters X and Y. The calculated phenotypic correlation value was tested for its significance using t-test according to Sharma (1998):

$$t = \frac{r_p}{SE\ (r_p)}$$

Where, rp = Phenotypic correlation; SE (rp) = Standard error of phenotypic correlation obtained using in the following procedure (Sharma, 1998).

$$SE\ (r_p) = \sqrt{\frac{(1 - r^2_p)}{(n - 2)}}$$

Where, n is the number of genotypes tested, and rp is phenotypic correlation coefficient. The coefficients of correlations at genotypic levels were tested for their significance using the formula described by Robertson (1959) as indicated below:

$$t = \frac{r_{gxy}}{SEr_{gxy}}$$

The calculated "t" value was compared with the tabulated "t" value at (n-2) degree of freedom at 5% and 1% level of significance.Where, n = number of genotypes:

$$SEr_{gxy} = \sqrt{\frac{1 - r^2_{gxy}}{2Hx.Hy}}$$

Where, $H^2x$ = Heritability of trait x and $H^2 y$ = Heritability of trait y.

### Path coefficient analysis
Path coefficient analysis was computed by Dewey and Lu (1959) using the phenotypic and genotypic correlation coefficients as:rij = Pij + Σrik * Pkj Where, rij = mutual association between the independent character i (yield-related trait) and dependent character, j (grain yield) as measured by the genotypic correlation coefficients; Pij = components of direct effects of the independent character (i) on the dependent character (j) as measured by the path coefficients; and

Σrikpkj = summation of components of indirect effects of a given independent character (i) on a given dependent character (j) via all other independent characters (k). The residual factor (PR), was calculated as:

$$P_R = \sqrt{(1 - \sum pijrij)}$$

Where, i=any trait in the model, j=dependent variable (grain yield) and r=correlation coefficient between any trait i and the dependent variable j. Residual (R) is the square root of non-determination; the magnitude of PR indicates how best the causal factors account for the variability of the dependent factor (Singh and Chaudhary,1999).

### RESULTS AND DISCUSSION
#### Analysis of variance
The analysis of variance revealed that there were highly significant differences (p<0.01) among the accessions with respect to grain yield, yield related traits and quality parameters (Table 2). Significant differences were recorded for parameters like Days to heading, days to maturity, grain filling period, plant height, biological yield, grain yield, harvest index, spike weight, thousand kernel weight (TKW), number of kernels per spike, number of spikelets per spike, spike length, gluten (%), moisture (%), protein (%), hectoliter weight and Water absorption (%) exhibited highly significant difference (p<0.01) among accessions.

The result of relative efficiency of the design revealed that, for most characters' more than 71%, simple lattice design was more efficient than randomized complete block design (Table 2). However, for traits like biological yield tons per hectare, percent gluten, percent moisture and hectoliter weight (kg hl⁻¹), the error variance of the blocks within replications were smaller than to the intra block error. The significant differences of the parameters indicated that, there is considerable amount of genetic variation among the studied landraces (Table 2). This variation would offer scope of selection for development of desirable genotypes which, could also be attributed to the diverse composition of the populations evolved through time.Several researchers reported significant differences among bread and durum wheat genotypes studied (Kifle *et al.*, 2016; Kumar *et al.*, 2016; Wolde *et al.*, 2016; Birhanu *et al.*, 2016). Similarly, significant differences were reported for major traits in bread wheat (Kalimullah *et al.*, 2012; Shashikala, 2006; Naik *et al.*, 2015; Rahman *et al.*, 2016)

**Table2: Mean squares, degrees of freedom and some of statistical parameters of all studied traits of durum wheat landraces evaluated in 2018 season using simple lattice design. for 20 traits in 100 Accessions**

| Traits | Treatments | Replications | Blocks within Replications | IntraBlock Error | Grand Mean | CV% | Mean± SE | LSD 5% | Eff | R² (%) |
|---|---|---|---|---|---|---|---|---|---|---|
| | DF=99 | DF=1 | DF=18 | DF=81 | | | | | | |
| DH | 18.41** | 1.28 | 0.99 | 0.85 | 68.77 | 1.34 | 68.77(±)0.92 | 1.86 | 100.38 | 97 |
| DM | 33.58** | 0.05 | 0.77 | 1.14 | 103.57 | 1.03 | 103.57(±)1.07 | 2.06 | 94.12 | 97 |
| GFP | 52.75** | 1.81 | 1.78 | 1.55 | 34.8 | 3.83 | 34.80(±)1.33 | 2.61 | 108.69 | 97 |
| PH | 366.00** | 9.25 | 58.76 | 58.76 | 87.54 | 8.76 | 87.54(±)7.67 | 15.21 | 100 | 90 |
| BY | 9.29** | 1.83** | 0.02 | 0.03 | 8.6 | 1.88 | 8.60(±)0.16 | 0.32 | 96.61 | 100 |
| GY | 1.10** | 0.02 | 0.05 | 0.04 | 1.57 | 11.93 | 1.57(±)0.19 | 0.38 | 101.69 | 97 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| HI | 147.33** | 1.78 | 6.45 | 5.37 | 18.88 | 12.27 | 18.88(±)2.32 | 4.68 | 100.6 | 97 |
| SWT | 0.44** | 4.81** | 0.01 | 0.01 | 1.39 | 7.25 | 1.39(±)0.10 | 0.20 | 101.14 | 98 |
| TKW | 206.23** | 18.91* | 6.95* | 3.87 | 32.43 | 6.07 | 32.43(±)1.97 | 4.18 | 105.92 | 99 |
| NKPS | 102.31** | 2461.91** | 0.02 | 0.02 | 42.61 | 0.29 | 42.61(±)0.12 | 0.25 | 101.29 | 100 |
| NSPS | 40.51** | 2119.01** | 0.81 | 0.51 | 30.4 | 2.36 | 30.40(±)0.72 | 1.50 | 103.63 | 99 |
| SL | 9.39** | 109.52** | 0.22 | 0.21 | 7.61 | 5.99 | 7.61(±)1.46 | 0.91 | 100.04 | 99 |
| GLT | 16.77** | 33.29** | 0.49 | 0.6 | 31.72 | 2.44 | 31.72 (±)0.77 | 1.53 | 96.67 | 97.6 |
| MTR | 0.30** | 17.36** | 0.04 | 0.07 | 10.56 | 2.49 | 10.56 (±)0.26 | 0.52 | 92.26 | 90.2 |
| PRT | 7.95** | 11.43** | 0.04 | 0.03 | 16.61 | 1.04 | 16.61(±)0.17 | 0.34 | 100.52 | 99.7 |
| HLW | 76.80** | 9.54** | 0.05 | 0.03 | 69.43 | 0.23 | 69.42(±)0.16 | 0.32 | 105.44 | 100 |
| WAB | 25.99** | 42.30** | 0.26 | 0.38 | 16.38 | 3.74 | 16.38 (±) 0.61 | 1.22 | 94.29 | 99 |

Key: *and ** indicates significance at 0.05 and 0.01 probability levels, respectively. CV (%) = coefficient of variation, DF= degree of freedom Eff. = efficiency of lattice design relative to randomized complete block design and $R^2$= r- square, SE= standard error; LSD=least significant difference, BY= biological yield tons ha-,[1] DH= days to heading, DM= days to maturity, GLT= gluten (%), GFP = grain filling period, GY = grain yield tons ha-,[1], HI = harvest index (%), HLW= hectoliter weight (kg hl-[1]), MTR= moisture (%),NKPS= number of kernels per spike, NSPS=number of spikelets per spike,PH = plant height(cm), PRT= protein (%),SL= spike length(cm), SW = spike weight(g), , TKW = thousand kernels weight(g), and WAB=water obsorption (%)

**Genotypic and phenotypic correlation of grain yield with other traits**
In the present study, the predictable values of phenotypic and genotypic correlation coefficients between all pairs of characters are presented in (Table 3). The analyses showed, genotypic correlation coefficient values were greater for most of the characters than their corresponding phenotypic correlation coefficient values, indicating inherent association of the characters so, that selection for the correlated characters could give a better yield.

**Phenotypic correlations**
Grain yield per plant showed positive and high significant (p<0.01) correlation with spike length (rp = 0.359), hectoliter weight (rp = 0.443), biological yield (rp = 0.297), and harvest index (rp = 0.790) (Table 3).It appears that phenotypic selection of phenotypically high values of these characters' result in increasing yield potential. The studies made by Kifle *et al*. (2016), Kole (2006) and Anwar *et al*. (2009) showed that grain yield per plant had positive and significant correlations with spike length, biological yield, harvest index, number of kernels per spike and plant height both at genotypic and phenotypic levels. At phenotypic level, grain yield per plant was positively and significantly associated with biological yield and harvest index (Amardeep *et al*., 2017). Moreover, grain yield showed negative and high significant phenotypic correlation with percent of protein (rp = -0.548) (Table 3) Similarly, Blanco *et al*. (2010) reported negative and significant correlation between days to heading and lodging.

**Genotypic correlations**
Grain yield showed positive and highly significant correlation with spike length (rg = 0.389), hectoliter weight (rg = 0.450), biological yield (rg = 0.300), and harvest index (rg = 0.784). Similarly, grain yield had positive and highly significant genotypic correlation with 1000-kernel weight and biological yield in all environments (Azeb *et al*., 2016) and with biological yield and plant height at the genotypic level (Amardeep *et al*., 2017). However, lodging (rg = -0.509) and percent of protein (rg = -0.563) had negatively high significant correlation with grain yield (Table 3) which was also similarly reported by Negash *et al*. (2019). Azeb *et al*. (2016) also reported negative and highly significant genotypic correlation of grain yield with days to heading and days to maturity. This might be due to the presence of common genetic elements that controlled the characters in the same and/or in different direction. The observed significant positive correlation could be either due to the strong coupling linkage between the genes or was the result of pleiotropic genes that controlled these characters in the same direction (Kearsey and Pooni, 1996). The yield components exhibited varying trends of association among themselves. In contrast to the current result, Singh (2014) reported the presence of negative correlation between grain yield and plant height. The work of Surma *et al*. (2012) showed positive and significant correlation of grain yield with thousand kernel weight, hectoliter weight and starch content.

Therefore, positive correlation coefficients of grain yield with most of the traits implied that, improving one or more of these traits could result in high grain yield (Yagdi and Sozen, 2009). Further more, plant height had positive significant association with number of kernels per spike, number of spikelets per spike, spike length, and hectoliter weight. Spike length had positive and highly significant correlation with biological yield, and harvest index. The correlation of hectoliter weight,with plant height, number of kernels per spike, number of spikelets per spike, harvest index and spike length was positive and significant.number of kernels per spike had positive and significant correlation with grain yield, hectoliter weight, plant height and biological yield (Table 3). The positive significant associations between grain yield and plant height because of these tall genotypes generally excelled in their capacity to support kernel growth by stem reserve mobilization (Blum *et al*., 1989). Therefore, selection for tall plants tends to increase grain yield per plant.

**Table3. Phenotypic (rp) and genotypic (rg) correlation coefficients of studied traits of durum wheat accessions evaluated in 2018 season**

| Traits | GY | DH | DM | GFP | PH | BY | HI | SWT | TKW | NKPS | NSPS | SL | GLT | MTR | PRT | HLW | WAB |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| GY | rg | -0.019 | 0.111 | 0.098 | 0.267* | 0.300** | 0.784** | 0.082 | -0.094 | 0.208* | 0.091 | 0.389** | -0.231* | -0.080 | -0.563** | 0.450** | 0.003 |
|  | rp | -0.007 | 0.106 | 0.086 | 0.217* | 0.297** | 0.790** | 0.069 | -0.09 | 0.175* | 0.080 | 0.359** | -0.221* | -0.057 | -0.548** | 0.443** | 0.004 |
| DH | rg | 1 | -0.055 | 0.631** | -0.030 | -0.022 | 0.001 | -0.025 | -0.008 | -0.103 | -0.019 | -0.148 | 0.092 | 0.051 | 0.127 | -0.070 | 0.132 |
|  | rp |  | -0.049 | 0.630** | -0.026 | -0.023 | 0.011 | -0.015 | -0.003 | -0.080 | 0.007 | -0.144* | 0.088 | 0.025 | 0.120 | -0.068 | 0.122 |
| DM | rg |  | 1 | 0.809** | -0.044 | 0.050 | 0.113 | 0.054 | 0.063 | -0.020 | 0.002 | 0.109 | -0.022 | -0.050 | -0.067 | 0.100 | 0.295** |
|  | rp |  |  | 0.806** | -0.034 | 0.047 | 0.108 | 0.045 | 0.062 | -0.020 | -0.016 | 0.103 | -0.016 | -0.056 | -0.067 | 0.099 | 0.284** |
| GFP | rg |  |  | 1 | -0.017 | 0.052 | 0.088 | 0.056 | 0.054 | 0.045 | 0.013 | 0.171 | -0.071 | -0.070 | -0.127 | 0.118 | 0.151 |
|  | rp |  |  |  | -0.010 | 0.050 | 0.077 | 0.044 | 0.050 | 0.032 | -0.017 | 0.166* | -0.064 | -0.058 | -0.123 | 0.117 | 0.148 |
| PH | rg |  |  |  | 1 | 0.339* | -0.015 | 0.041 | 0.033 | 0.253* | 0.214* | 0.356* | -0.069 | -0.020 | -0.249* | 0.221* | 0.094 |
|  | rp |  |  |  |  | 0.310** | -0.021 | 0.034 | 0.025 | 0.216* | 0.158* | 0.317** | -0.058 | -0.022 | -0.234* | 0.206* | 0.081 |
| BY | rg |  |  |  |  | 1 | -0.300* | 0.052 | -0.140 | 0.294* | 0.279* | 0.501** | -0.204* | -0.060 | -0.254* | 0.408** | 0.102 |
|  | rp |  |  |  |  |  | -0.293** | 0.036 | -0.140* | 0.247* | 0.236* | 0.484** | -0.193* | -0.018 | -0.246* | 0.408** | 0.106 |
| HI | rg |  |  |  |  |  | 1 | 0.040 | -0.028 | 0.009 | -0.062 | 0.034 | -0.180 | -0.020 | -0.438** | 0.212* | -0.031 |
|  | rp |  |  |  |  |  |  | 0.031 | -0.026 | 0.001 | -0.050 | 0.027 | -0.172* | -0.015 | -0.426** | 0.209* | -0.030 |
| SWT | rg |  |  |  |  |  |  | 1 | 0.119 | -0.124 | 0.099 | 0.222* | -0.050 | -0.017 | -0.042 | 0.061 | 0.001 |
|  | rp |  |  |  |  |  |  |  | 0.118 | 0.027 | 0.131 | 0.102 | -0.086 | -0.179* | -0.072 | 0.048 | -0.036 |
| TKW | rg |  |  |  |  |  |  |  | 1 | -0.089 | -0.119 | -0.081 | -0.100 | 0.136 | 0.091 | -0.075 | 0.010 |
|  | rp |  |  |  |  |  |  |  |  | -0.07 | -0.093 | -0.083 | -0.102 | 0.089 | 0.086 | -0.075 | 0.007 |
| NKPS | rg |  |  |  |  |  |  |  |  | 1 | 0.507** | 0.152 | -0.223* | -0.030 | -0.253* | 0.231* | -0.029 |
|  | rp |  |  |  |  |  |  |  |  |  | 0.453** | -0.002 | -0.250* | -0.254* | -0.272** | 0.194* | 0.004 |
| NSPS | rg |  |  |  |  |  |  |  |  |  | 1 | 0.145 | -0.248* | 0.002 | -0.299* | 0.256* | -0.034 |
|  | rp |  |  |  |  |  |  |  |  |  |  | 0.073 | -0.227* | -0.053 | -0.265* | 0.215* | 0.122 |
| SL | rg |  |  |  |  |  |  |  |  |  |  | 1 | -0.085 | -0.110 | -0.217* | 0.340* | 0.193 |
|  | rp |  |  |  |  |  |  |  |  |  |  |  | -0.037 | 0.097 | -0.169* | 0.330** | 0.284** |
| GLT | rg |  |  |  |  |  |  |  |  |  |  |  | 1 | -0.384** | 0.554** | -0.395** | -0.071 |
|  | rp |  |  |  |  |  |  |  |  |  |  |  |  | -0.216* | 0.551** | -0.382** | -0.030 |
| MTR | rg |  |  |  |  |  |  |  |  |  |  |  |  | 1 | 0.045 | -0.046 | 0.141 |
|  | rp |  |  |  |  |  |  |  |  |  |  |  |  |  | 0.096 | -0.020 | 0.151 |
| PRT | rg |  |  |  |  |  |  |  |  |  |  |  |  |  | 1 | -0.602** | -0.013 |
|  | rp |  |  |  |  |  |  |  |  |  |  |  |  |  |  | -0.594** | -0.036 |
| HLW | rg |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 1 | -0.004 |
|  | rp |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 0.007 |
| WAB | | | | | | | | | | | | | | | | | 1 |

Key : BY= biological yield tons ha-,[1] DH= days to heading, DM= days to maturity, GLT= gluten (%), GFP = grain filling period, GY = grain yield tons ha-,[1], HI = harvest index (%), HLW= hectoliter weight (kg hl[-1]), MTR= moisture (%),NKPS= number of kernels per spike, NSPS=number of spikelets per spike,PH = plant height(cm), PRT= protein (%),SL= spike length(cm), SW = spike weight(g), TKW = thousand kernels weight(g), and WAB=water obsorption (%)

## Path coefficient analysis
Both phenotypic and genotypic correlations were analyzed by path coefficient analysis technique to identify the important yield attributes by estimating the direct effects of traits contributing to grain yield and separating the direct from the indirect effects through other related traits by partitioning the correlation coefficient and finding out the relative importance of different characters as selection criteria. This analysis was conducted using grain yield as dependent variable and all other traits studied as independent (causal) variables. In this study, grain yield was the result of plant height, biological yield, harvest index, number of kernels per spike and spike length (Tables 4 and 5).

## Genotypic path coefficient
Harvest index had positive tend significant correlation coefficient and it showed the highest positive direct effect (0.93) on grain yield. Harvest index has also showed large indirect effects Plant height, biological yield, number of kernels per spike, spike length, gluten and hectoliter weight than other characters included in the analysis showing its high contribution for abetter partitioning of the photosynthetic products into the grain. The direct effect of biological yield followed by spike

length, Plant height, number of kernels per spike, hectoliter weight, and gluten on grain yield was positive with significant correlation and so exerted positive direct effect (Table 4).

Biological yield, Harvest index, Plant height and spike length revealed positive direct effect and had positive genetic correlation explaining the existence of real relation between the characters and yield indicating that, indirect selection of yield via this characteristic is effective. Similarly, Negash *et al*. (2019) reported positive direct effect of the biological yield on grain yield in Ethiopian barley landraces. Azeb *et al*. (2016) indicated that biological yield exerted maximum positive direct effect on grain yield across locations. ). The studies made by Kifle *et al*. (2016), Kole (2006) and Anwar *et al.* (2009) showed that grain yield per plant had positive and significant correlations with spike length, biological yield, harvest index, number of kernels per spike and plant height both at genotypic and phenotypic levels. Protein exerted negative direct effects on grain yield also negative and highly significant association at genotypic levels. The indirect effects of protein with other characters were mostly negatives and negligible. Singh and Chaundhary (1985) suggested that an indirect effect seemed to be the cause of correlation and hence, these indirect causal factors (traits) should be considered simultaneously for selection (Table 4).Besides to significant, Plant height, biological yield, harvest index, number of kernels per spike, spike length, gluten and hectoliter weight exhibited positive direct effects on grain yield indicating that, increasing in those traits could possibly to increase grain yield. The genotypic residual value (0.04) showed that, the characters under study accounted for 96 % of the variability with grain yield components (Table 4).

**Table4: Estimates of direct (bold diagonal) and indirect effect (off-diagonal) at genotypic level of 8 traits on grain yield of 100 durum wheat accessions**

| Traits | PH | BY | HI | NKPS | SL | GLT | PRT | HLW | rg |
|---|---|---|---|---|---|---|---|---|---|
| PH | 0.05 | 0.12 | -0.01 | 0.01 | 0.01 | 0.00 | 0.01 | 0.01 | 0.27* |
| BY | 0.01 | 0.52 | -0.20 | 0.01 | 0.02 | -0.01 | 0.01 | 0.01 | 0.46* |
| HI | 0.00 | -0.11 | 0.93 | 0.00 | 0.00 | -0.01 | 0.01 | 0.01 | 0.78** |
| NKPS | 0.01 | 0.10 | 0.01 | 0.05 | 0.01 | -0.01 | 0.01 | 0.01 | 0.21* |
| SL | 0.01 | 0.18 | 0.02 | 0.01 | 0.08 | 0.00 | 0.01 | 0.01 | 0.39** |
| GLT | 0.00 | -0.07 | -0.12 | -0.01 | 0.00 | 0.05 | -0.01 | -0.01 | -0.23* |
| PRT | -0.01 | -0.09 | -0.29 | -0.01 | -0.01 | 0.03 | -0.03 | -0.02 | -0.56** |
| HLW | 0.01 | 0.14 | 0.14 | 0.01 | 0.01 | -0.02 | 0.02 | 0.04 | 0.45** |

Key: BY = biological yield tons ha-$^1$, GLT= gluten (%), rg =genotypic correlations, HI = harvest index (%), HLW= hectoliter weight (kg hl-$^1$), KNPS=kernel number per spike, PH=plant height, PRT =protein (%), residual effect = 0.04 is unexplained, 0.96 is explained and SL=spike length

**Phenotypic path coefficient analysis**
Harvest index and biological yield showed positive and significant correlation (r = 0. 79) and (r = 0.30) with grain yield and they had the highest direct effect (0.94) and (0.53) on grain yield respectively. The existence of negligible and positive indirect effect of harvest index and biological yield with most of the other characters determines that, the correlation of these traits with grain yield were found to be due to the direct effect (Table 5). Plant height, spike length, number of kernels per spike, gluten and hectoliter weight have positive and negligible direct effect on grain yield and the phenotypic correlation they had with grain yield were positive. The indirect effect of harvest index through Plant height, spike length, number of kernels per spike, gluten and hectoliter and biological yield counter balanced the direct effect harvest index on grain yield. The indirect effect of biological yield through harvest index (-0.20) counter balanced the direct effect of biological yield on grain yield (0.53). The residual value (0.05) showed the characters under the study accounted 95% of the variability in grain yield (Table 5).

**Table5: Estimates of direct (bold diagonal) and indirect effect (off-diagonal) at phenotypic level of 8 traits on grain yield of 100 durum wheat accessions**

| Traits | PH | BY | HI | NKPS | SL | GLT | PRT | HLW | rp |
|---|---|---|---|---|---|---|---|---|---|
| PH | 0.05 | 0.12 | 0.00 | 0.01 | 0.01 | 0.00 | 0.01 | 0.01 | 0.22* |
| By | 0.01 | 0.53 | -0.20 | 0.01 | 0.02 | 0.00 | 0.01 | 0.01 | 0.30** |
| HI | 0.00 | -0.11 | 0.94 | 0.00 | 0.00 | 0.00 | 0.01 | 0.01 | 0.79** |
| NKPS | 0.01 | 0.10 | 0.00 | 0.05 | 0.00 | 0.00 | 0.01 | 0.01 | 0.17* |
| SL | 0.01 | 0.19 | 0.02 | 0.00 | 0.07 | 0.00 | 0.00 | 0.01 | 0.36** |
| GLT | 0.00 | -0.07 | -0.10 | -0.01 | 0.00 | 0.06 | 0.00 | -0.01 | -0.22* |
| PRT | -0.01 | -0.10 | -0.30 | -0.01 | 0.00 | 0.03 | -0.03 | -0.02 | -0.55** |
| HLW | 0.01 | 0.16 | 0.15 | 0.01 | 0.01 | 0.00 | 0.02 | 0.03 | 0.44** |

Key: BY = biological yield tons ha-1, GLT= gluten (%), HI = harvest index (%) , HLW= hectoliter weight (kg hl-$^1$), KNPS=kernel number per spike, PH=plant height, PRT =protein (%), rp = phenotypic correlations residual effect = 0.05 is unexplained, 0.95 is explained and SL=spike length

## Conclusions

Study of relationship between yield and yield contributing characters in durum wheat through genotypic and phenotypic correlations suggests that grain yield (t ha-1) had shown significant and highly significant (P<0.05 and P<0.01) and positive phenotypic and genotypic correlation with thousand Plant height, biological yield, harvest index, number of kernels per spike, spike length, gluten and hectoliter weight had positive. Thus implies that the genetic influence on these traits was similar and grain yield could be improved directly by improving these traits. Grain yield had positive but not significant correlation at genotypic and phenotypic level with number of spikelet per spike, spike weight and water obsorption.

Generally, significant differences of the characters showed that, there is substantial amount of genetic variation among the studied materials and is a strong correlation between most of the studied desirable characters that can afford basic information for further breeding activities for crop improvement.

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