

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 ($r_p = 0.22$, $r_g = 0.25$), harvest index ($r_p = 0.79$, $r_g = 0.78$), biological yield ($r_p = 0.31$, $r_g = 0.30$), number of kernels per spike ($r_p = 0.17$, $r_g = 0.21$), spike length, ($r_p = 0.36$, $r_g = 0.39$), and hectoliter weight ($kg\ hl^{-1}$) ($r_p = 0.44$, $r_g = 0.45$). 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

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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; Dhama *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 8°10'00"N to 8°50'00"N and 34°39'30"E to 34°59'30"E (Figure 1) with an elevation of 2025 meters above sea level.

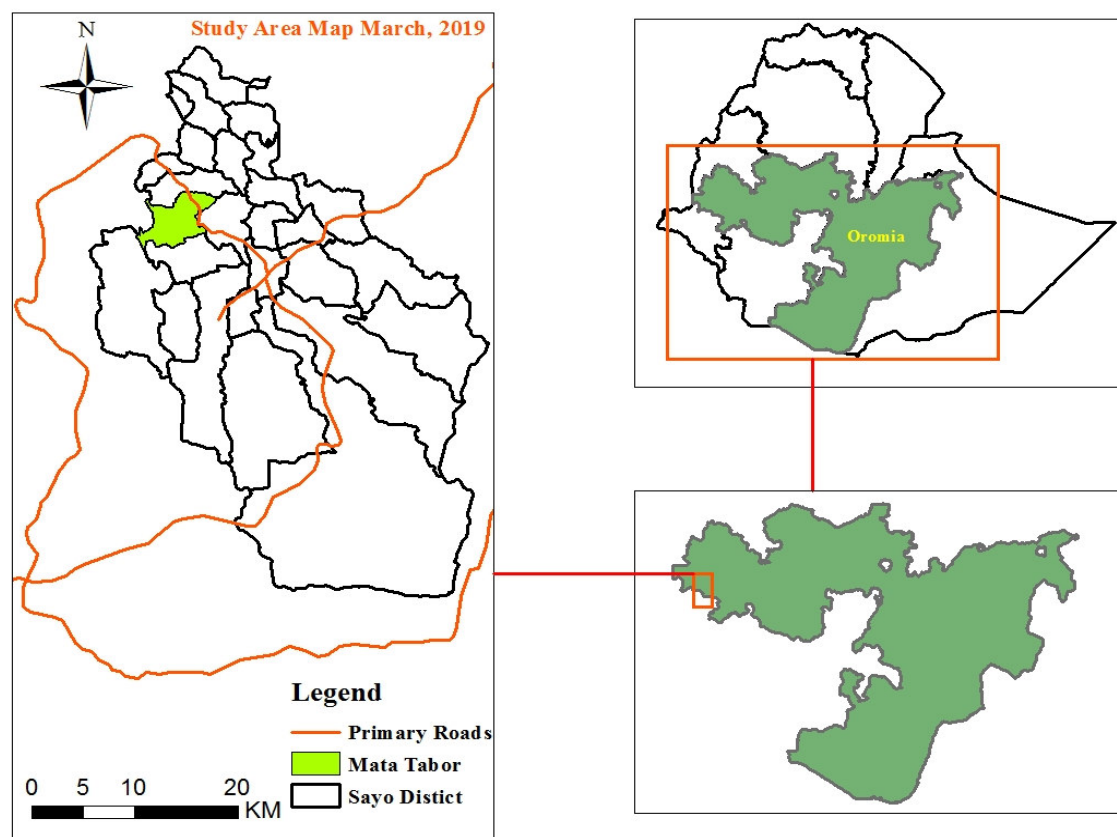


Figure 1: Map of the study area.

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 are 16.21 and 27.77°C, respectively with the relative humidity of 67.5%. Source: (Sayo district Agriculture 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

Table 1: 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	<i>Triticum</i>	<i>dicoccum</i>	Oromia	07-07-00-N	40-43-00-E	1710
2	5582	<i>Triticum</i>	<i>dicoccum</i>	Oromia	08-57-00-N	37-52-00-E	2280
3	7710	<i>Triticum</i>	<i>dicoccum</i>	Oromia	07-08-00-N	40-43-00-E	1980
4	238891	<i>Triticum</i>	<i>dicoccum</i>	Oromia	07-01-30-N	40-21-07-E	2200
5	7207	<i>Triticum</i>	<i>dicoccum</i>	Oromia	07-01-40-N	40-23-55-E	1990
6	5181	<i>Triticum</i>	<i>dicoccum</i>	Oromia	07-01-20-N	40-19-46-E	1900
7	242782	<i>Triticum</i>	<i>sp</i>	Amara	11-05-00-N	37-52-00-E	2400
8	242793	<i>Triticum</i>	<i>sp</i>	Amara	10-18-00-N	38-12-00-E	2460
9	7532	<i>Triticum</i>	<i>sp</i>	Amara	10-18-00-N	38-12-00-E	2460
10	7056	<i>Triticum</i>	<i>sp</i>	Oromia	09-00-00-N	38-07-00-E	2350
11	7880	<i>Triticum</i>	<i>sp</i>	Oromia	07-17-00-N	38-36-00-E	2030
12	242781	<i>Triticum</i>	<i>sp</i>	Oromia	07-44-00-N	39-34-00-E	2140
13	5182	<i>Triticum</i>	<i>sp</i>	Oromia	08-24-00-N	39-52-00-E	2040
14	5171	<i>Triticum</i>	<i>sp</i>	Amara	10-34-00-N	38-14-00-E	2390
15	222393	<i>Triticum</i>	<i>sp</i>	Oromia	08-49-00-N	38-54-00-E	2400
16	7649	<i>Triticum</i>	<i>sp</i>	Amara	10-26-00-N	38-20-00-E	2460
17	5216	<i>Triticum</i>	<i>sp</i>	Oromia	08-12-00-N	39-34-00-E	2150
18	5020	<i>Triticum</i>	<i>sp</i>	Oromia	08-24-00-N	39-52-00-E	2040
19	6102	<i>Triticum</i>	<i>sp</i>	Oromia	07-46-00-N	39-47-00-E	2440
20	242790	<i>Triticum</i>	<i>sp</i>	Oromia	07-41-00-N	40-13-00-E	2395
21	5184	<i>Triticum</i>	<i>sp</i>	Oromia	07-45-00-N	39-40-00-E	2400
22	5515	<i>Triticum</i>	<i>sp</i>	Oromia	07-44-00-N	39-53-00-E	2430
23	5528	<i>Triticum</i>	<i>sp</i>	Amara	10-18-00-N	38-12-00-E	2460
24	7084	<i>Triticum</i>	<i>sp</i>	Amara	10-14-00-N	38-01-00-E	2440
25	7683	<i>Triticum</i>	<i>sp</i>	Oromia	07-39-00-N	39-46-00-E	2430
26	242785	<i>Triticum</i>	<i>sp</i>	Oromia	07-50-00-N	39-38-00-E	2410
27	7343	<i>Triticum</i>	<i>sp</i>	Amara	10-18-00-N	38-12-00-E	2460
28	7832	<i>Triticum</i>	<i>sp</i>	Amara	11-21-00-N	39-18-00-E	2300
29	6983	<i>Triticum</i>	<i>sp</i>	Amara	10-28-00-N	38-17-00-E	2430
30	5472	<i>Triticum</i>	<i>sp</i>	Amara	10-28-00-N	38-18-00-E	2410
31	5354	<i>Triticum</i>	<i>sp</i>	Oromia	08-53-00-N	37-51-00-E	2310
32	5729	<i>Triticum</i>	<i>sp</i>	Amara	11-06-00-N	39-45-00-E	1790
33	7647	<i>Triticum</i>	<i>sp</i>	Amara	11-05-00-N	37-42-00-E	2470
34	6988	<i>Triticum</i>	<i>sp</i>	Oromia	09-14-00-N	41-09-00-E	2260
35	5583	<i>Triticum</i>	<i>sp</i>	Oromia	08-54-00-N	38-54-00-E	2300
36	7020	<i>Triticum</i>	<i>sp</i>	Oromia	09-00-00-N	39-07-00-E	2330
37	239694	<i>Triticum</i>	<i>sp</i>	Oromia	38-54-00-N	38-54-00-E	2300
38	5183	<i>Triticum</i>	<i>sp</i>	Oromia	08-47-00-N	39-15-00-E	2300
39	5556	<i>Triticum</i>	<i>sp</i>	Oromia	09-47-00-N	39-16-00-E	2200
40	5175	<i>Triticum</i>	<i>sp</i>	Oromia	08-52-00-N	39-01-00-E	2133
41	5373	<i>Triticum</i>	<i>sp</i>	Oromia	38-54-00-N	38-54-00-E	2300
42	6968	<i>Triticum</i>	<i>sp</i>	Oromia	09-24-00-N	38-47-00-E	2160
43	7664	<i>Triticum</i>	<i>sp</i>	Oromia	09-01-00-N	39-15-00-E	2300
44	7218	<i>Triticum</i>	<i>sp</i>	Oromia	09-00-00-N	39-07-00-E	2330
45	5043	<i>Triticum</i>	<i>sp</i>	Amara	08-50-00-N	39-19-00-E	2260
46	6978	<i>Triticum</i>	<i>sp</i>	Amara	08-50-00-N	39-19-00-E	2260
47	7009	<i>Triticum</i>	<i>sp</i>	Oromia	08-51-00-N	38-30-00-E	2333
48	5174	<i>Triticum</i>	<i>sp</i>	Oromia	08-59-00-N	38-52-00-E	2300
49	7709	<i>Triticum</i>	<i>sp</i>	Oromia	09-01-00-N	39-03-00-E	2450
50	230678	<i>Triticum</i>	<i>sp</i>	Oromia	08-51-00-N	38-52-00-E	2300
51	242789	<i>Triticum</i>	<i>sp</i>	Oromia	08-54-00-N	39-01-00-E	2350
52	242792	<i>Triticum</i>	<i>sp</i>	Oromia	08-59-00-N	38-52-00-E	2300
53	5214	<i>Triticum</i>	<i>sp</i>	Oromia	08-58-00-N	39-00-00-E	2420
54	5428	<i>Triticum</i>	<i>sp</i>	Oromia	08-47-00-N	39-15-00-E	2300
55	7801	<i>Triticum</i>	<i>sp</i>	Oromia	09-01-00-N	39-15-00-E	2300
56	242791	<i>Triticum</i>	<i>sp</i>	Oromia	09-01-00-N	39-15-00-E	2300

Entry code	Acc. No	Genus name	species name	Region	Latitude	Longitude	Altitude
57	5491	<i>Triticum</i>	<i>sp</i>	Oromia	08-59-00-N	38-52-00-E	2300
58	5510	<i>Triticum</i>	<i>sp</i>	Oromia	08-54-00-N	39-05-00-E	2200
59	7015	<i>Triticum</i>	<i>sp</i>	Oromia	08-49-00-N	39-00-00-E	1915
60	242784	<i>Triticum</i>	<i>sp</i>	Oromia	08-45-00-N	39-08-00-E	2350
61	5635	<i>Triticum</i>	<i>sp</i>	Tigray	14-10-00-N	38-42-00-E	2367
62	5609	<i>Triticum</i>	<i>sp</i>	Oromia	08-48-00-N	38-54-00-E	2080
63	5666	<i>Triticum</i>	<i>sp</i>	Tigray	14-07-00-N	38-29-00-E	2487
64	5572	<i>Triticum</i>	<i>sp</i>	Oromia	08-45-00-N	39-13-00-E	2070
65	5504	<i>Triticum</i>	<i>sp</i>	Oromia	08-45-00-N	39-15-00-E	2120
66	5197	<i>Triticum</i>	<i>sp</i>	Oromia	08-45-00-N	39-13-00-E	2160
67	7827	<i>Triticum</i>	<i>sp</i>	Oromia	08-47-00-N	39-15-00-E	2300
68	242786	<i>Triticum</i>	<i>sp</i>	Oromia	08-45-00-N	39-15-00-E	2120
69	5653	<i>Triticum</i>	<i>sp</i>	Oromia	08-45-00-N	39-08-00-E	2340
70	5534	<i>Triticum</i>	<i>sp</i>	Oromia	08-45-00-N	39-15-00-E	2120
71	242783	<i>Triticum</i>	<i>sp</i>	Oromia	09-47-00-N	39-46-00-E	2300
72	226897	<i>Triticum</i>	<i>sp</i>	Oromia	09-47-00-N	39-46-00-E	2300
73	5168	<i>Triticum</i>	<i>sp</i>	Oromia	09-47-00-N	39-16-00-E	2200
74	5179	<i>Triticum</i>	<i>sp</i>	Oromia	09-47-00-N	39-16-00-E	2300
75	7825	<i>Triticum</i>	<i>sp</i>	Oromia	09-47-00-N	39-16-00-E	2300
76	5198	<i>Triticum</i>	<i>sp</i>	Amara	08-50-00-N	39-19-00-E	2260
77	8072	<i>Triticum</i>	<i>sp</i>	Amara	08-50-00-N	39-19-00-E	2260
78	242779	<i>Triticum</i>	<i>sp</i>	Amara	08-50-00-N	39-19-00-E	2260
79	5492	<i>Triticum</i>	<i>sp</i>	Amara	08-50-00-N	39-19-00-E	2260
80	243733	<i>Triticum</i>	<i>sp</i>	SNNP	09-29-00-N	38-30-00-E	2333
81	5638	<i>Triticum</i>	<i>sp</i>	Oromia	08-51-00-N	38-30-00-E	2330
82	242780	<i>Triticum</i>	<i>sp</i>	Amara	08-50-00-N	39-19-00-E	2260
83	5597	<i>Triticum</i>	<i>sp</i>	Amara	12-38-00-N	37-28-00-E	2100
84	5044	<i>Triticum</i>	<i>sp</i>	Oromia	09-47-00-N	39-46-00-E	2300
85	5152	<i>Triticum</i>	<i>sp</i>	Oromia	08-47-00-N	39-46-00-E	2300
86	5554	<i>Triticum</i>	<i>sp</i>	Amara	10-34-00-N	37-29-00-E	2145
87	7018	<i>Triticum</i>	<i>sp</i>	Amara	11-00-00-N	36-54-00-E	2489
88	5669	<i>Triticum</i>	<i>sp</i>	Oromia	07-12-00-N	38-35-00-E	1773
89	7828	<i>Triticum</i>	<i>sp</i>	Oromia	08-50-00-N	38-22-00-E	1773
90	5367	<i>Triticum</i>	<i>sp</i>	Oromia	08-54-00-N	39-01-00-E	2350
91	5344	<i>Triticum</i>	<i>sp</i>	Amara	12-19-00-N	37-33-00-E	2145
92	5434	<i>Triticum</i>	<i>sp</i>	Oromia	08-47-00-N	39-15-00-E	2300
93	5166	<i>Triticum</i>	<i>sp</i>	Oromia	08-51-00-N	38-30-00-E	2333
94	5149	<i>Triticum</i>	<i>sp</i>	Oromia	08-16-00-N	38-52-00-E	1791
95	5169	<i>Triticum</i>	<i>sp</i>	Oromia	08-59-00-N	38-52-00-E	2300
96	5441	<i>Triticum</i>	<i>turgidum</i>	Oromia	07-47-00-N	39-39-00-E	2415
97	5557	<i>Triticum</i>	<i>polonicum</i>	Oromia	08-58-00-N	37-36-00-E	2430
98	Bekalcha	<i>Triticum</i>	Improved variety	Sinana ARC			
99	Dire	<i>Triticum</i>	Improved variety	Sinana ARC			
100	obsa	<i>Triticum</i>	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:

$$r_{pxy} = \frac{pcov\ x.y}{\sqrt{\delta^2_{px} * \delta^2_{py}}}$$

Genotypic correlation coefficient:

$$r_{gxy} = \frac{gcov\ x.y}{\sqrt{\delta^2_{gx} * \delta^2_{gy}}}$$

Where, r_{pxy} = Phenotypic correlation coefficient between characters X and Y, r_{gxy} = genotypic correlation coefficients between characters X and Y, $pcov_{x.y}$ and $gcov_{x.y}$ are phenotypic and genotypic covariance between variables x and y, respectively, σ^2_p = Phenotypic Variance between characters X and Y, σ^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, r_p = Phenotypic correlation; $SE(r_p)$ = Standard error of phenotypic correlation obtained using in the following procedure (Sharma, 1998).

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

Where, n is the number of genotypes tested, and r_p 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:

$$SEr_{gxy} = \sqrt{\frac{1 - r_{gxy}^2}{2H_x.H_y}}$$

Where, H^2_x = 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: $r_{ij} = P_{ij} + \sum r_{ik} * P_{kj}$ Where, r_{ij} = mutual association between the independent character i (yield-related trait) and dependent character, j (grain yield) as measured by the genotypic correlation coefficients; P_{ij} = components of direct effects of the independent character (i) on the dependent character (j) as measured by the path coefficients; and

$\sum r_{ik}P_{kj}$ = 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:

$$P_R = \sqrt{(1 - \sum p_{ij}r_{ij})}$$

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)

Table 2: 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 DF=99	Replications DF=1	Blockswithin Replications DF=18	IntraBlock Error DF=81	Grand Mean	CV%	Mean± SE	LSD 5%	Eff	R ² (%)
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 R²= 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 absorption (%)

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 ($r_p = 0.359$), hectoliter weight ($r_p = 0.443$), biological yield ($r_p = 0.297$), and harvest index ($r_p = 0.790$) (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 ($r_p = -0.548$) (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 ($r_g = 0.389$), hectoliter weight ($r_g = 0.450$), biological yield ($r_g = 0.300$), and harvest index ($r_g = 0.784$). 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 ($r_g = -0.509$) and percent of protein ($r_g = -0.563$) 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.

Table 3. Phenotypic (r_p) and genotypic (r_g) 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	1															
	rp	-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
DH	rg		1														
	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
DM	rg			1													
	rp	-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	
DM	rg				1												
	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	
GFP	rg					1											
	rp	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**		
GFP	rg						1										
	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**		
PH	rg							1									
	rp	-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			
PH	rg								1								
	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			
BY	rg									1							
	rp	0.339*	-0.015	0.041	0.033	0.253*	0.214*	0.356*	-0.069	-0.020	-0.249*	0.221*	0.094				
BY	rg										1						
	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				
HI	rg											1					
	rp	-0.300*	0.052	-0.140	0.294*	0.279*	0.501**	-0.204*	-0.060	-0.254*	0.408**	0.102					
HI	rg												1				
	rp	-0.293**	0.036	-0.140*	0.247*	0.236*	0.484**	-0.193*	-0.018	-0.246*	0.408**	0.106					
SWT	rg													1			
	rp	0.040	-0.028	0.009	-0.062	0.034	-0.180	-0.020	-0.438**	0.212*	-0.031						
SWT	rg														1		
	rp	0.031	-0.026	0.001	-0.050	0.027	-0.172*	-0.015	-0.426**	0.209*	-0.030						
TKW	rg															1	
	rp	0.119	-0.124	0.099	0.222*	-0.050	-0.017	-0.042	0.061	0.001							
TKW	rg																1
	rp	0.118	0.027	0.131	0.102	-0.086	-0.179*	-0.072	0.048	-0.036							
NKPS	rg																
	rp	-0.07	-0.093	-0.102	-0.083	-0.102	-0.100	0.136	0.091	-0.075	0.010						
NSPS	rg																
	rp	0.453**	-0.002	-0.250*	-0.254*	-0.272**	0.194*	0.004									
SL	rg																
	rp	0.453**	-0.002	-0.250*	-0.254*	-0.272**	0.194*	0.004									
GLT	rg																
	rp	0.145	-0.248*	0.002	-0.299*	0.256*	-0.034										
GLT	rg																
	rp	0.073	-0.227*	-0.053	-0.265*	0.215*	0.122										
MTR	rg																
	rp	0.453**	-0.002	-0.250*	-0.254*	-0.272**	0.194*	0.004									
SL	rg																
	rp	0.073	-0.227*	-0.053	-0.265*	0.215*	0.122										
GLT	rg																
	rp	0.073	-0.227*	-0.053	-0.265*	0.215*	0.122										
MTR	rg																
	rp	0.073	-0.227*	-0.053	-0.265*	0.215*	0.122										
PRT	rg																
	rp	0.073	-0.227*	-0.053	-0.265*	0.215*	0.122										
HLW	rg																
	rp	0.073	-0.227*	-0.053	-0.265*	0.215*	0.122										
WAB	rg																
	rp	0.073	-0.227*	-0.053	-0.265*	0.215*	0.122										

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 absorption (%)

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 and 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 a better 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).

Table 4: 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).

Table 5: 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 absorption.

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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