Original Research Article

ASSOCIATIONS ANALYSIS OF TRAITS OF DURUM WHEAT (*Triticum turgidum* L.) LANDRACES IN BALE HIGHLANDS, ETHIOPIA

ABSTRACT

Durum wheat is one of the most important cereal crops in Ethiopia. The national average productivity and quality of durum wheat is low due to lack of improved varieties and different biotic and abiotic constraints prevailing in the country these calls for development of improved durum wheat varieties. Knowledge on extent of trait association of important characters and their interrelationship is a prerequisite for the development of high yielding and quality durum wheat variety. The present study was carried out to assess the extent of character association among yield and yield related traits in selected durum wheat landraces. Forty nine durum wheat accessions were studied for 20 traits at Sinana and Selka locations using 7x7 simple lattice design in 2018/19. Grain yield showed significant positive correlations with biological yield, harvest index, number of spikelets/spike, kernels/spike and productive tillers per plant both at genotypic and phenotypic levels, indicating that the possibility of simultaneously improving these traits through selection. Path coefficient analysis revealed that, biomass and harvest index had high effect on yield indicating that this trait could be considered as important trait in durum wheat yield improvement program.

Key words: Genotypic; Phenotypic; Correlation; Path analysis

1. INTRODUCTION

Wheat is the leading grain crop of the temperate climate of the world. It is used mainly for human consumption and support nearly 35% of the world population (Mohammadi-joo *et al*., 2015), providing 20% of the total food calories. In Ethiopia, wheat covers about 1.7 million hectares of land, accounting for 14.5% of the total grain crops area, with an annual production of 4.5 million tons, contributing about 17.8% of the total grain production (CSA, 2018). Durum wheat (*Triticum turgidum* L.) is among the most cultivated crops in the Mediterranean basin, where approximately 75% of the world's durum wheat area is still grown, which contributes to 50% of the worldwide production (Graziani *et al*., 2014). Globally its acreage is estimated at 17 million hectares and the most important growing areas are situated in the Mediterranean Basin, North America, North and East Africa and South West Asia (Bonjean *et al*., 2011). Out of these regions, durum wheat is the oldest traditional crop produced in Ethiopia. Farmers' varieties which, are often referred to as 'landraces', are characterized by significant phenotypic variability (Mengistu *et al*., 2016). The *abyssinicum* subspecies is morphologically very different; with un-compact spikes and small dark seeds that contains huge important traits (Mengistu *et al*., 2015). This has greatly resulted in improvement of local varieties on yield, quality and other associated traits. However, the relationship that exists amongst the traits is greatly influenced by genetic constitution and the environment and it needs clarification under existing conditions through exploration of genotypic and phenotypic correlations.

Correlation coefficient analysis helps to determine the nature and degree of relationship between any two measurable characters (Fellahi *et al.,* 2013). Such correlations can be either negative or positive. Most of the time in wheat grain yield is positively and significantly correlated with its components such as with thousand kernels weight, spike length, number of spikelets per spike and kernels per spike (Firew *et al*., 2012). In plant breeding program, direct selection for yield as such could not be effective (Ashfaq *et al*., 2014). Grain number and grain weight are the main components affecting grain yield and are negatively correlated to each other (Gonzalez-Ribot *et al*., 2017). Under optimum conditions, all the yield components such as spike length, number of spikelets per spike, grain filling period, harvest index and biomass have considerable contribution to grain yield, implying that selection for any of the yield components could significantly improve the yield (Tattaris *et al*., 2016). Also path coefficient analysis measures the direct influence of one variable upon the other and permits separation of correlation coefficients into components of direct and indirect effects which provides actual information on contribution of characters and thus forms the real basis of selection for the yield improvement (Khan and Dar, 2010). In the present study, only characters that had significant relationship with grain yield were included in the path coefficient analysis as suggested by Dewey and Lu, (1959). Thus, the current study was planned to investigate durum wheat traits association for different important agronomic and quality traits in Ethiopian durum wheat landraces which were recently collected.

Objective

- to estimate association among traits and determine direct and indirect effects of traits on yield, yield related and quality parameters.

2. MATERIALS AND METHODS

2.1. Description of the Study Areas

The field experiment was conducted at two locations in Southeastern Ethiopia namely, at Sinana with geographical coordinate units of 07°07' N, 40°10'E and Selka with geographical coordinate units of 07°04'28''N, 040°12'18''E during 2018/19 main cropping season. Both experimental sites are characterized by pellic vertisol with a slightly acidic soil and its PH ranges from 6.3 to 6.8 (SARC, 2006). Altitude 2400 m and 2509 m above sea level for both locations representing the potential durum wheat production area in the zone. Sinana Agricultural Research Center (SARC) is located 463 km South-East of Addis Ababa in the highlands of Bale Zone, South-Eastern Oromia and at a distance of 33km in East of Robe town, the capital city of the Zone. Selka site is on the way to Sinana Agricultural Research Center (SARC) 7km away from the SARC. Both areas are characterized by bi-modal rainfall pattern and receive annual total rainfall ranging from 750 to 1400mm. The main season receives 270 to 842mm rainfall, while the short season receives from 250 to 562mm rainfall annually. Mean annual minimum and maximum temperatures are 9.6 and 20.7^{o}C, respectively. The experiment at both locations was conducted during the main cropping season 'which extends from August to December.

2.2. Experimental Materials

The experimental materials comprised of 49 durum wheat germ-plasm including three (checks) released durum wheat varieties from Sinana Agricultural Research Center viz. Bulala, Dire and Obsa and. These landraces were developed in to pure lines by SARC from collections introduced from Institute of Biodiversity and Conservation (IBC). The details of durum wheat accessions along with checks used in this study are summarized in the following Table (Table 1).

Table 1. Names and origin of 49 durum wheat germ-plasm used in the experiment.

S/N	Name	Form	Origin	Woreda	Locality
1	Acc 5152	Landrace	SNNP	Hula	Hagere
2	Acc 5373	Landrace	Oromia	Ada'a	Filtino
3	Acc 243733	Landrace	Amahra	Gonda	7.8km
4	Acc 242791	Landrace	Oromia	Gimbic	
5	Acc 5457,	Landrace	Oromia	Ejere	
6	Acc 242787	Landrace	Oromia	Gimbic	
7	Acc 5344	Landrace	Oromia	Akaki	Bole
8	Acc 7576	Landrace	Amhara	Were	Kata on
9	Acc 7010,	Landrace	B/Gumz	Wenber	
10	Acc 5760	Landrace	Oromia	Mana	10km SE
11	Acc 7580	Landrace	Amahra	Jama	Gibat on
12	Dire	Improved	Oromia	Sinana	SARC
13	Acc 243401,	Landrace	Oromia	Gasara	Jile
14	Acc 5472	Landrace	Amahra	Minjar	Yenigus
15	Acc 230678	Landrace	Oromia	Ginir	01Kabele
16	Bulala	Improved	Oromia	Sinana	SARC
17	Acc 6988	Landrace	Oromia	Merti	Ofa 6Km
18	Acc 5473,	Landrace	Amhara	Farta	
19	Acc 5149	Landrace	Oromia	Alem	Tefki
20	Acc 222393	Landrace	Oromia	A/Robe	-
21	Acc 7295,	Landrace	Amhara	Debre	
22	Acc 6978	Landrace	Amahra	Enarj	Embeyem
23	Acc 8072	Landrace	Oromia	Ginir	Ginir
24	Acc 5020	Landrace	Oromia	Ada'a	SE slope
25	Acc 5342,	Landrace	Amhara	Macha	
26	Acc 5586,	Landrace	Oromia	Gedo	
27	Acc 5428	Landrace	Oromia	Tiyo	Asela
28	Acc 6933	Landrace	Oromia	Agarfa	Agarfa
29	Obsa	Improved	Oromia	Sinana	SARC
30	Acc 242780	Landrace	Oromia	Lome	25km
31	Acc 2211,	Landrace	Oromia	Meta	
32	Acc 226879	Landrace	Oromia	Meta	--
33	Acc 5141,	Landrace	Tigray	Endam	
34	Acc 7665	Landrace	Amahra	Enema	Sherar
35	Acc 5354	Landrace	Oromia	Alem	Tefki
36	Acc 7673	Landrace	Amahra	Enema	Yerez
37	Acc 5198	Landrace	Amhara	Dembe	Denbech
38	Acc 243706,	Landrace	Oromia	Mulo	
39	Acc 5510	Landrace	Oromia	Bereh	Kakisa
40	Acc 242783	Landrace	Oromia	Lome	1km
41	Acc 242782	Landrace	Oromia	Lome	1km
42	Acc 226694	Landrace	Oromia	--	--
43	Acc 235051	Landrace	Amhara	Legam	110km
44	Acc 7210	Landrace	Oromia	Ambo	Asgori
45	Acc 7647	Landrace	Amahra	Hulet	Mota
46	Acc 6974	Landrace	Amahra	Enema	22km
47	Acc 5591	Landrace	Oromia	Akaki	sheno
48	Acc 242790	Landrace	Oromia	Gimbic	Gimbic
49	Acc 243403,	Landrace	Oromia	Gsara	Engoye

Acc = Accession, SNNP= South Nation and Nationalities and People, SARC= Sinana Agricultural Research Center

2.3. Experimental Design and Trial Management

The experiment was laid out in 7x7 simple lattice design with two replications having plot size of four rows of 20cm spacing and 2.5m length. Seed and fertilizer rate 150 kg/ha and 69/46 N/P_2O_5 were applied. UREA (N) was applied in split application where 1/3rd was applied at planting and the remaining 2/3rd was applied at tillering stage and all agronomic practices were followed uniformly according to the recommendation for the area. Planting was done by hand drilling; weed was controlled by using hand weeding and as well as by using herbicide called Pallas 45OD at the recommended rate and time of application.

2.4. Data Collection

All agronomic, yield and yield related traits and quality traits both on plant and plot basis were recorded from the two middle rows of experimental unit. Plant-based data were collected from randomly selected and representative ten plants in the plot while, the plot-based data were collected from the whole harvestable plot. Plant height (PLH) (cm), Spike length (SPL) (cm), Number of spikelets/spike (SPS), Productive tillers/plant (PTL), Number of grains/spike (KPS), Days to heading (DH), Days to physiological maturity (DM), Grain Filling Period (GFP), Grain yield (GY) (kg ha^{-1}), Biomass Yield (BM) (kg ha^{-1}), Harvest Index (HI) (%), Thousand kernel weight (TKW) (g), Vitreousness (VTR) (%), Hectoliter weight (HLW) (kg/L), Grain protein content (GPT) (%), Grain gluten content (GGL) (%), Zeleny Index (ZI) (ml), Wet gluten content (WGL) (%), Sodium dodecyl sulfate (SDS) sedimentation (ml) and Ash content (ASC) (%).

2.5. Data Analysis

Phenotypic correlation coefficient estimates were computed by calculating first variance and covariance at phenotypic and environmental levels. The simple correlation coefficients were computed to determine the degree of association of yield with yield attributes and quality traits. These simple correlation coefficients were then partitioned to genotypic and phenotypic components. Phenotypic and genotypic correlations between yield, yield related and quality related traits were estimated using the method described by Al-Jibouri *et al.* (1958) and tested for statistical significance against the correlation table values at 5 and 1% levels of significance.

The coefficients of correlations at phenotypic level were tested for their significance by comparing the values of correlation coefficient with tabulated r-value at g-2 degree of freedom. However, the coefficient of correlations at genotypic level were tested for their significance using the formula described by Robertson (1959) indicated below.

$$\text{Phenotye Correlatio n } (r_{pxy}) = \frac{\text{phenotypic covariance of x and y}}{\sqrt{\sigma^2 px \times \sigma^2 py}}$$

$$\text{Genotype Correlation } (r_{gxy}) = \frac{\text{genotypic covariance of x and y}}{\sqrt{\sigma^2 gx \times \sigma^2 gy}}$$

Where: r_{gxy} = genetic correlation coefficient between traits x and y, r_{pxy} = phenotypic correlation coefficient between traits x and y, σ^2_p of X = Phenotypic variance for trait X, σ^2_P Y = Phenotypic variance for trait Y, σ^2_g X = Genotypic variance for trait X and, σ^2_g Y = Genotypic variance for trait

Also a measure of direct and indirect effects of each character on grain yield is estimated using a standardized partial regression coefficient known as path coefficient analysis, as suggested by Dewey and Lu (1959). The residual effect, which determines how best the causal factors account for the variability of the dependent factor yield, was calculated.

$$r_{ij} = p_{ij} + \sum r_{ik} p_{kj}$$

Where: r_{ij} = is mutual association between independent variable ith and dependent variable jth as measured by phenotypic and genotypic correlation coefficient, P_{ij} = direct effects of the independent character ith on the dependent variable jth as measured by the genotypic and phenotypic path coefficients, and $\Sigma r_{ik} p_{kj}$ = Summation of components of indirect effects of a given independent character ith on a given dependent character jth via all other independent characters kth.

3. RESULTS AND DISCUSSIONS

3.1. Association of Studied Traits

3.1.1. Correlation of grain yield with yield components

Since all of the studied traits showed homogeneous error of variance and qualified for pooled analysis, based on the results of analysis of variance, the phenotypic (r_p) and genotypic (r_g) correlation estimates among the various characters were computed for the combined data and are presented in Table 2. Grain yield showed significant and positive phenotypic and genotypic correlations with traits such as BM, HI, SPS, KPS and PTL but, TKW and GFP were positively correlated only at phenotype level. The positive correlation coefficient of grain yield with traits implies that, improving one or more of the traits could result in high grain yield improvement. On the contrary, PLH and DH had showed significant and negative relationship with grain yield at genotypic level while; DH, PLH and SDS-sedimentation had showed significant and negative correlation with grain yield at phenotypic level (Table 2). Also as SDS increases, it decreases grain yield since SDS and protein content are positively correlated with each other and inversely correlated with grain yield or, the nitrogen moves into the filling kernels to form protein during early grain development. If yields are low because the kernels do not fill properly, the grain is high in protein. If the grain fills normally and yields and test weights are high, grain protein is frequently lower because it is diluted by other materials Edwards (2010). The negative correlation of grain yield with DH indicated that, breeding for early varieties would improve yield particularly under moisture stress condition to escape the low moisture stress that prevail during the growth of the crop. It is evident that, some earliest and shortest genotypes had high GY, which could be due to their ability to maintain a high number of PTL and a relatively high TKW. Barnard *et al.* (2002) reported that the negative correlation which often exists between quality and yield is a further constraint in durum wheat breeding. Fischer (2011) also reported negative correlation of wheat grain yield with that of PLH. Similarly, Mansouri *et al.* (2018) reported grain yield was positively correlated with KPS, HI and BM. Again Dawit *et al.* (2012) reported for HI, PTL and TKW also, Mohammad *et al.* (2012) and Graziani *et al.* (2014) reported for SPS, KPS, TKW and HI. Dawit *et al*. (2012) reported negative association of SDS and DH with GY.

Generally, grain yield is the most complex trait and it is influenced by many factors (known and unknown) that determine the yield. Therefore, understanding of the inheritance and interrelationship of grain yield with that of characters influencing grain yield is highly important for formulating selection program for the improvement of this important and ultimate trait. The genotypic correlation coefficient values for most of the characters were higher in magnitude than the corresponding phenotypic values showing the existence of inherent association among the traits. Totally, it was observed that 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.

3.1.2. Phenotypic and genotypic correlations among traits other than yield

Correlation coefficients among other than yield traits are presented in Table 2. BM had positive and significant genotype and phenotype interrelated with DM, SPS, KPS and PTL but, negative and significant interrelated with HI both at phenotype and genotype levels. These results suggested aboveground biomass as an indirect selection criterion to improve grain yield, along with DM, SPS, KPS and PTL. The same result was also reported by Yonas *et al.* (2016) who reported positive and significant association of BM with DM both at phenotype and genotype level. Also, Mansouri *et al.* (2018) reported the positive interrelated of BM with SPS and negatively interrelated with HI.

Plant height had showed positive and significant phenotype and genotype correlation with DH and SPL. PLH positive and significant correlated with DM only at phenotype level however, it was negatively and significant correlated with GFP, HI, KPS and HLW both at genotypic and phenotypic level while, PLH significant and negatively correlated with ZI, VTR, TKW, PTL and ASC only at phenotypic level. Similar, Royo, *et al.* (2007) reported that PLH is usually negatively correlated with HI.

Days to heading showed positive and significant genotypic and phenotypic correlation with DM, PLH, SPL, SDS and ASC content however, it had exhibited positive correlation with protein content only at genotypic level. On the other hand, this trait had showed negative and significant genotypic and phenotypic correlation with GFP, HI and TKW. It was significant and negative correlation with WGL and KPS only at phenotypic level.

Days to maturity had also showed positive and significant genotypic and phenotypic correlation with DH, BM, GFP, ZI, GGL and SDS however, PLH and TKW were positively correlated with DM only at phenotypic level. On the other hand, DM were negatively and significant correlated with HI both at genotypic and phenotypic level (Table 2). Similar results were also reported by Mohammed *et al.* (2011) and Firew *et al.* (2012).

Spike length is one of the major yield components that showed positive and significant correlated with DH, PLH, GPC and GGL content at genotypic and phenotypic level however; it had exhibited positively correlated with ZI only at phenotypic level. It showed negative and significant genotypic correlation with kernels/spike. Similarly, number of SPS had showed positive and significant correlated with BM, KPS and PTL both at genotypic and phenotypic level.

Kernels/spike which is the most important yield component and it had exhibited positive and significant correlated with GFP, BM, SPS and PTL both at genotypic and phenotypic correlation level whereas, TKW was showed positive and significantly correlated with KPS only at phenotypic level. It was negative and significantly correlated with PLH both at genotypic and phenotypic levels. Also, it exhibited negative and significantly correlated with SPL only at genotypic level while, with DH only at phenotypic level. Productive tillers/plant also positively and significant correlated with BM, HLW, SPS and KPS both at genotypic and phenotypic level but, HI and ZI were only correlated at phenotypic level with it. PLH was the only trait which showed negative and significant phenotypic correlation with productive tillers/plants (Table 2). Similar results were also reported by Kumar *et al*. (2013) positive correlation of kernels/spike with spike length.

Thousand kernel weight was showed positive and significant genotypic correlated with GFP whereas; it was positive and significant correlation with DM, GFP, KPS and HLW at phenotypic level. However, it was negatively and significantly correlated with DH and ASC both phenotypic and genotypic level. It also showed negative and significant correlation with PLH only at phenotypic level (Table 2). Protein content positively and significantly correlated with SPL, ZI and GGL both at genotypic and phenotypic levels however, it correlated with DH only at genotypic level and with WGL only at phenotypic level. Similarly, Yagdi (2004) reported a positive correlation between protein and gluten.

Grain gluten was positively and significantly correlated with DM, SPL, PTL, ZI and WGL, both at genotypic and phenotypic levels (Table 2). As strong gluten durum semolina is required for production of pasta, the estimation of gluten strength is usually an important selection criterion in a breeding programme. To determine gluten strength in wheat, one of the cheapest and easiest is the SDS sedimentation test (Clarke *et al*., 1993). SDS sedimentation had showed positive and significant correlation with DH and DM both at genotypic and phenotypic levels while, it was negatively and significantly correlated with HI only at phenotypic level. A positive and significant correlation of gluten content and zeleny index was also reported by Irani (2000).

Test weight had showed positive and significantly correlated with GFP, PTL and WGL both at genotypic and phenotypic levels but with ZI it correlated only at genotypic level and TKW only at phenotypic level. It was significantly and negatively correlated with PLH both at genotypic and phenotypic levels. Also vitreousness was positive and significantly correlated with ZI and ASC both at genotypic and phenotypic level while, it was significant and negatively correlated with PLH only at phenotypic level (Table 2).

Zeleny index is also another durum wheat quality trait that, was positively and significant correlated with DM, GGL, WGL, HLW, VTR and with GPC at genotypic level whereas; it was positively and significant phenotypic correlation with DM, GFP, SPS, PTL, VTR, GPC, GGL, WGL and with ASC. However, it was significantly and negatively correlated with PLH only at phenotypic level while, with HI only at genotypic level. Ash content positive and significant correlated with DH and VTR both at genotypic and phenotypic levels however, with ZI correlated only at phenotypic level. It was significant and negative correlated with TKW and WGL at genotypic level whereas, with TKW, PLH and GFP at phenotypic level (Table 2). Most of the genotypic correlation coefficient values of most studied characters were higher in magnitude than the corresponding phenotypic values showing the existence of inherent association among the traits. Generally considering these results, characters association are important criteria because they could be easily measured and they may directly or indirectly correlate with GY and quality traits.

Table 2. Genotypic below and phenotypic above diagonal correlation coefficients for the twenty characters combined over locations, 2018/19.

Traits	DH	DM	PLH	GFP	BM	HI	SPL	SPS	KPS	PTL
DH		0.386**	0.465**	-0.45**	0.124	-0.350**	0.273**	0.043	-0.194*	-0.027
DM	0.468*		0.176*	0.650**	0.239*	-0.300**	0.123	0.097	0.09	0.118
PLH	0.516*	0.156		-0.210*	0.042	-0.290**	0.262*	0.025	-0.299**	-0.178*
GFP	-0.430*	0.596**	-0.309*		0.130	-0.010	-0.105	0.059	0.247*	0.136
BM	0.132	0.305*	0.012	0.192		-0.660**	-0.002	0.212*	0.232*	0.153*
HI	-0.503*	-0.335*	-0.379*	0.114	-0.459*		-0.028	0.053	0.092	0.142*
SPL	0.308*	0.163	0.376*	-0.113	0.096	-0.132		0.038	-0.106	0.122
SPS	-0.046	0.104	-0.135	0.148	0.429*	0.127	-0.059		0.452**	0.300**
KPS	-0.252	0.091	-0.429*	0.322*	0.362*	0.156	-0.300*	0.530**		0.284**
PTL	-0.016	0.204	-0.216	0.223	0.325*	0.209	0.077	0.528**	0.395*	
TKW	-0.316*	0.237	-0.129	0.529**	0.012	0.23	-0.078	-0.038	0.192	0.159
HLW	-0.183	0.202	-0.388*	0.373*	0.085	0.107	0.16	0.215	0.17	0.442*
VTR	0.044	0.175	-0.177	0.139	0.046	0.039	-0.211	0.034	0.124	-0.062
GPC	0.282*	0.271	0.213	0.021	0.044	-0.365*	0.517**	-0.090	-0.217	0.042
ZI	0.260	0.422*	-0.002	0.195	0.153	-0.289*	0.173	0.144	0.064	0.211
GGL	0.222	0.339*	0.148	0.145	0.035	-0.216	0.440*	-0.047	-0.121	0.086
WGL	-0.251	-0.183	-0.052	0.041	-0.164	0.126	0.116	0.09	-0.02	0.068
ASC	0.377*	0.099	-0.109	-0.241	-0.005	-0.04	-0.243	-0.004	0.026	-0.075
SDS	0.456*	0.489*	0.098	0.086	0.159	-0.287*	-0.102	0.189	0.047	0.158
GY	-0.345*	-0.033	-0.328*	0.28	0.668**	0.330*	-0.049	0.552**	0.521**	0.490*

Table 2: Combined Correlation continued

Traits	TKW	HLW	VTR	GPC	ZI	GGL	WGL	ASC	SDS	GY
DH	-0.27**	-0.09	-0.02	0.13	0.03	0.13	-0.20*	0.19*	0.32**	-0.30**
DM	0.15*	0.13	0.112	0.11	0.19*	0.24*	-0.028	0.01	0.31**	-0.11
PLH	-0.15*	-0.23*	-0.15*	0.07	-0.16*	0.02	-0.118	-0.14*	0.12	-0.32**
GFP	0.37**	0.21*	0.13	0.01	0.16*	0.12	0.14*	-0.15*	0.04	0.14*
BM	-0.01	0.07	0.01	-0.01	0.03	-0.02	-0.10	-0.01	0.06	0.41**
HI	0.16*	-0.01	0.04	-0.06	0.08	-0.03	0.10	0.03	-0.20*	0.37**
SPL	-0.12	0.08	-0.13	0.34**	0.18*	0.37**	0.09	-0.12	-0.04	-0.02
SPS	-0.01	0.08	0.03	-0.04	0.06	-0.02	-0.01	-0.02	0.13	0.35**
KPS	0.14*	0.13	0.08	-0.11	0.12	-0.05	0.03	0.03	-0.01	0.42**
PTL	0.08	0.18*	-0.01	0.05	0.23*	0.10	0.13	0.01	0.02	0.35**
TKW		0.28**	-0.08	-0.08	0.12	0.03	0.09	-0.30**	-0.11	0.19*
HLW	0.25		-0.02	0.01	0.05	0.02	0.17*	-0.12	0.01	0.06
VTR	-0.09	-0.03		-0.02	0.26**	0.03	0.05	0.20*	0.01	0.04
GPC	-0.08	0.16	-0.08		0.53**	0.65**	0.20*	0.01	0.11	-0.08
ZI	0.14	0.29*	0.36*	0.69**		0.63**	0.35**	0.17*	0.08	0.11
GGL	0.09	0.16	0.03	0.86**	0.75**		0.39**	-0.10	0.11	-0.06
WGL	0.15	0.34*	-0.01	0.27	0.35*	0.42*		-0.11	-0.03	-0.01
ASC	-0.35*	-0.09	0.28*	-0.11	0.04	-0.25	-0.32*		0.04	-0.01
SDS	-0.13	0.06	0.06	0.22	0.25	0.17	-0.08	0.15		-0.18*
GY	0.19	0.13	0.06	-0.25	-0.08	-0.14	-0.05	-0.07	-0.12	

Where; *and **, $p \leq 0.05$ and 0.01 level of significances, DH = Days to heading, DM= Days to mature, PLH= Plant height, GFP= Grain filling period, BM= Biomass, GY= Grain yield, HI= Harvest Index, SPL= Spike length, SPS= Spike pe/spike, KPS= Number of kernel/spike, PTL=Productive tiller, KW= Thousand kernel weight, HLW= Hecto liter weight, VTR= Vitreousness, PC= Protein content, ZI= Zeleny Index, GGL= Grain gluten, WGL=Wet gluten, ASC=Ash content, SDS= Sodium Dodecyl Sulphate

3.2. Path Coefficient Analysis

3.2.1. Genotypic direct and indirect effects of various characters on grain yield

Results of path coefficient analysis were classified as suggested by Lenka and Mishra (1973), who classified them as 0.00 to 0.09 as negligible association effects, 0.10 to 0.19 as low, 0.20 to 0.29 as moderate, 0.30 to 0.99 as high and $\geq$1.0 as very high. Genotypic path coefficient analysis combined over the two locations revealed that, biomass (1.017) and harvest index (0.744) had the highest direct effect on grain yield (Table 3). These traits were showed positive and highly significant correlation coefficient with grain yield. All of the indirect effects *via* other traits were positive but, low or negligible. Therefore, the genotypic correlation with grain yield was due to their direct effects. The effects of number of SPS (0.02) and KPS (0.002) were positive and significant correlation coefficient with grain yield. However, the direct effect they had on grain yield was negligible. Therefore the correlation coefficient they had with grain yield were mainly because of the indirect effect *via* biomass (Table 2). Similarly, Mansouri *et al.* (2018) and Yonas *et al*. (2016) reported high direct of BM and HI on grain yield. Again, Yonas *et al*. (2016) reported the indirect effects of KPS and number of SPS *via* other traits on grain yield.

However, days to heading had negative direct effect (-0.102) and the genotypic correlation it had with GY was also negative and significant (-0.345). The indirect effect *via* other trait was positive and higher values than direct effect so; the effect was *via* indirect effect. Therefore the correlation coefficient it had with grain yield was mainly because of the indirect effect *via* BM. Similarly, plant height showed negative direct effect (-0.003) and it had negative correlation with GY. The indirect effect *via* other trait was higher than the negative direct effect. Therefore the effect on GY was because of the indirect effect via BM (Table 3). Also PTL had negative direct effect (-0.010) but, its direct effect was negative and negligible. Therefore the effect it had on GY was indirectly via BM. The negative direct effects on GY indicate that selection for these traits will not be rewarding for yield improvement. Generally, positive direct effect and positive and significant correlation coefficient with grain yield had true association and their importance in improving of grain yield. Khan *et al.* (2013) and Dawit *et al*. (2012) reported large indirect effects of days to heading and plant height on grain yield.

The residual effect (0.03) which indicates that characters, which were included in the path analysis, explained about 97% of the total variation in grain yield in which the number of characters chosen for the study were appropriate for yield improvement in durum wheat, even though there are still unexploited variation remaining.

Table 3. Genotypic path analyses direct (bold & diagonal) and indirect (off diagonal) effects of six traits on grain yield tested over locations 2018/19.

	EFFECTS							
Variable	DH	PLH	BM	HI	SPS	KPS	PTL	r_g
DH	**-0.102**	-0.002	0.134	-0.374	-0.001	-0.001	0.000	-0.345*
PLH	-0.053	**-0.003**	0.012	-0.282	-0.003	-0.001	0.002	-0.328*
BM	-0.014	0.000	**1.017**	-0.342	0.009	0.001	-0.003	0.668**
HI	0.052	0.001	-0.467	**0.744**	0.003	0.000	-0.002	0.330*
SPS	0.005	0.000	0.436	0.094	**0.020**	0.001	-0.005	0.552**
KPS	0.026	0.001	0.368	0.116	0.011	**0.002**	-0.004	0.521**
PTL	0.002	0.001	0.331	0.156	0.011	0.001	**-0.010**	0.490*

Residual = 0.03

Where; * and **, p< 0.05 and 0.01 level of significances, DH = Days to heading, PLH = Plant height, BM = Biomass, HI = Harvest index, SPS = Number of spike per spike, KPS= Number of kernel per spike, PTL = Productive tillers, r_g = genotypic correlation coefficient of trait with grain yield.

3.2.2. Phenotypic direct and indirect effects of various characters on grain yield

Phenotypic path coefficient analysis for combined over the two locations data revealed that biological yield (1.104) followed by harvest index (1.049) had the highest direct effect on grain yield and their indirect effect via other traits were negligible (Table 4). Therefore, the correlation coefficient they had with grain yield was largely due to their direct effect. SPS (0.058), KPS (0.025), PTL (0.007) and TKW (0.023) had positive but, their direct effects on GY were minimum or negligible. Therefore, the effects of SPS, PTL and KPS on grain yield were via BM while; the effects of TKW on grain yield was via HI (Table 4). However, DH (-0.073), PLH (-0.023), GFP (-0.048) and SDS-sedimentation (-0.019) had negative direct effect and the genotypic correlation they had with grain yield was also negative and significant. Some of their indirect effects on grain yield *via* other traits were positive for all of them. Therefore, the effect they had on grain yield was mainly because of indirect effects via BM yield (Table 4).

Similarly, Ali and Shakor (2012) and Mohammed et *al.* (2011) reported the direct effect of biomass and harvest index is exerted on grain yield expression. The result of thousands grain weight is in contradiction to the results of Dawit *et al.* (2012) who reported the negative direct effect of TKW on grain yield. Similar results of the negative direct effect of DH on grain yield was reported by Dawit *et al.* (2012). The SDS negative phenotypic direct effect on GY is in contradiction with the results of Yonas *et al.* (2016) who reported the positive direct effect of SDS -sedimentation on GY. Residual effect was (0.09) indicates that characters, showing that about 91% of the variability in the GY of durum wheat was contributed by the characters studied in path analysis. Generally, BM and HI influenced GY directly. Therefore, these traits should be included in selection for grain yield improvement of durum wheat.

Table 4. Phenotypic path analyses direct (bold & diagonal) and indirect (off diagonal) effects of eight traits on grain yield tested over locations 2018/19.

	EFFECTS									
Traits	DH	PLH	GFP	BM	HI	SPS	KPS	PTL	TKW	SDS	r_p
DH	**-0.073**	-0.011	0.021	0.137	-0.368	0.003	-0.005	0.000	-0.006	-0.006	-0.30**
PLH	-0.034	**-0.023**	0.010	0.046	-0.308	0.001	-0.008	-0.001	-0.004	-0.002	-0.32**
GFP	0.032	0.005	**-0.047**	0.144	-0.009	0.003	0.006	0.001	0.008	-0.001	0.14*
BM	-0.009	-0.001	-0.006	**1.104**	-0.690	0.012	0.006	0.001	0.000	-0.001	0.41**
HI	0.025	0.007	0.000	-0.726	**1.049**	0.003	0.002	0.001	0.004	0.004	0.37**
SPS	-0.003	-0.001	-0.003	0.234	0.056	**0.058**	0.011	0.002	-0.002	-0.003	0.35**
KPS	0.014	0.007	-0.012	0.256	0.097	0.026	**0.025**	0.002	0.003	0.000	0.42**
PTL	0.002	0.004	-0.006	0.169	0.149	0.017	0.007	**0.007**	0.002	0.000	0.35**
TKW	0.020	0.004	-0.018	-0.002	0.170	-0.005	0.004	0.001	**0.023**	0.002	0.19*
SDS	-0.023	-0.003	-0.002	0.074	-0.214	0.008	0.000	0.000	-0.003	**-0.019**	-0.18*

Residual = 0.09

Where; * and **, $p < 0.05$ and 0.01 level of significances, DH = Days to heading, PLH = Plant height, GFP = Grain filling period, BM = biomass, HI = Harvest index, SPS = Number of spike per spike, KPS = Number of kernel per spike, PTL= Productive tiller, TKW = Thousand kernel weight, SDS = Sodium Dodecyl Sulphate, r_p = phenotypic correlation coefficient of trait with grain yield.

4. SUMMARY AND CONCLUSION

Durum wheat is commercial crop and the demand for this crop is increasing from time to time because of the emerging agro-processing industries particularly for past and macaroni processing. Thus, developing durum wheat varieties with high yield, quality and stress tolerant/resistance traits is crucial in Ethiopia nowadays. Alternatively, landraces have often been considered a key resource for contemporary agriculture and thus have been used in plant breeding programs to enlarge the genetic diversity of modern genetic pools. Availability of genetic diversity in crop improvement is a pre-requisite for developing crop varieties with desirable traits. Including durum wheat, Ethiopia is the center of diversity for many plant species. So the existing durum wheat genetic potential is a big resource and should be properly utilized for the improvement durum wheat in future breeding programs by providing a basis for selection of superior parental combinations and predictions of progeny performance. In view of this, the present study was conducted using 49 durum wheat genotypes at Sinana and Selka areas under field condition during the 2018/19 growing season with the objectives of assessing the genetic variability and quality for 20 traits.

Grain yield had significant and positive phenotypic and genotypic correlation with harvest index, biomass, days to heading, plant height, harvest index, spikelets per spike, kernels per spike, SDS-sedimentation and productive tillers per plant. By selecting for these traits that reveal positive and significant correlation with grain yield, there is possibility of increasing grain yield. Path coefficient analysis based on grain yield as a dependent variable showed that, biomass and harvest index had the highest direct effects on grain yield while, spikelets per spike, productive tillers per plant and kernels per spike had positive indirect effect on yield both at phenotypic and genotypic levels. Generally these traits had positive and significant association with grain yield so, much attention should be given to them in selection as these traits are helpful for indirect selection to improve yield.

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