Estimation of Correlation and Path Analysis of Yield and Yield-Contributing Traits of Bread Wheat (*Triticum aestivum* L.) Genotypes in Southwestern Ethiopia

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ABSTRACT

Forty-nine bread wheat genotypes were tested at Chena, Masha and Shay Bench, southwestern Ethiopia in 2017 and 2018 with the objective of estimating the association among yield and yield-contributing traits and determining the direct and indirect effect of the traits on the grain yield of wheat genotypes using 7x7 simple lattice design. Data were collected for 12 agronomic characters. Grain yield showed significant ($p \leq 0.01$) positive phenotypic correlations with thousand-kernel weight, aboveground biomass, harvest index at the locations except for plant height at Masha. Similarly, grain yield showed significant ($p \leq 0.01$) positive genotypic correlations with 1000-kernel weight, aboveground biomass and harvest index at Masha and Shay Bench and only with aboveground biomass and harvest index at Chena. Likewise, significant ($p \leq 0.01$) positive and negative phenotypic and genotypic correlations between the yield components were observed at all the locations. As per the path analysis, aboveground biomass, 1000-kernel weight and harvest index showed high positive phenotypic direct effect on grain yield at the locations. Similarly, at genotypic level, aboveground biomass, harvest index and 1000-kernel weight showed highly significant direct effect on the grain yield at the locations. Generally, it has been observed the presence of relationships in the tested traits of the genotypes studied. Hence, selection and hybridization on these genotypes based on the trait with high positive correlation coefficient and direct effect on grain yield can be recommended for further yield improvement of bread wheat at respective location.

Keywords*: Direct and indirect effect, grain yield, path analysis, trait association, trait correlation

INTRODUCTION

Bread wheat (*Triticum aestivum* L.) is a hexaploid species with (2n=6x=42) having AABBDD belonging to family *Poaceae* (Yadawad *et al.*, 2015). It is one of the oldest domesticated grain crops for 8000 years which is native to Middle East (Sleper and Poehlman, 2006). It has been the basic staple food of many regions of the world, while it is grown under both irrigated and rain-fed conditions. World wheat production in 2017 was 743.2 million tons with average yield (3.34 t ha^{-1}) accounting for nearly 30% of global cereals (FAO, 2017).

In Ethiopia, wheat has become one of the most important cereal crops ranking 4th in total grain production (3.92 million tons, 15.6%) and 4th in area coverage (1.66 million hectares) next to teff, maize and sorghum (CSA, 2016). Though, bread wheat improvement was started in 1949 and many varieties were released by the national and regional research institutes with different traits of interest including yield and wider agroecological adaptability in the country, there is still a problem in distributing the varieties to all parts of the country on account of accessibilities of the growing areas that limited the testing for the adaptability and yields of the varieties in such areas. Grain yield in wheat is a complex character and is the product of several contributing factors affecting yield directly or indirectly. These factors influence grain production both directly and indirectly and the breeder is naturally interested in investigating the extent and type of association of such traits (Zafarnaderi *et al.*, 2013). Towards a clear understanding of the type of plant traits, correlation and path coefficient analysis are logical steps. Phenotypic and genotypic correlations within varieties are of value to indicate the degree to which various characters are associated with economic productivity (Mudasir and Abdul, 2010).

Correlation coefficient is the measure of the degree for linear association between two variables (Gomez and Gomez, 1984). Knowledge of correlations that exist between important characters may facilitate the interpretation of results obtained and provide the basis for planning more efficient program for future (Johnson *et al.*, 1955). Path coefficient analysis is a reliable statistical technique, which provides means to quantify the interrelationship of different yield components and indicates whether the influence is directly reflected in the yield or takes some other pathways to produce an effect. This technique, therefore, provides a critical examination of specific factors producing a given correlation and can be successfully employed in formulating a selection strategy (Aycicek and Yildirim, 2006).

Although Bench Shako, Kaffa and Sheka Zones are among the potential wheat producing areas in Southern Nations, Nationalities and People's Regional (SNNPR) state, however, no character association studies have been conducted in the study areas. Therefore, such information is essential for the identification of association among traits for further bread wheat improvement particularly, in the area and generally, in the country. In view of this, the current study was carried out to estimate the magnitude of correlation between grain yield and yield-contributing characters, and to partition the correlation coefficients of yield with traits into direct and indirect effects through path analysis.

MATERIALS AND METHODS

Experimental materials

Experimental materials comprised of forty-nine bread wheat genotypes released by different agricultural research centers (Table 1).

Table 1. Bread wheat genotypes used in the study.

S.N	Entry Variety	Source Center	Year of Release
1	Ogolcho	Kulumsa	2012
2	Hoggana	Kulumsa	2011
3	Hulluka	Kulumsa	2012
4	Mekelle-3	Mekelle	2012
5	Mekelle-4	Mekelle	2013
6	Shorima	Kulumsa	2011
7	Mekelle-1	Mekelle	2012
8	Mekelle-2	Mekelle	2011
9	Ga'ambo	Werer	2011
10	Kekeba	Kulumsa	2010
11	Danda'a	Kulumsa	2010
12	Gassay	Adet	2007
13	Alidoro	Holleta	2007
14	Dagelu	Kulumsa	2005
15	Tay	Adet	2005
16	Sofumar	Sinana	1999
17	Mada-Wolabu	Sinana	1999
18	Pavon-76	Kulumsa	1982
19	Jefferson	Kulumsa	2012
20	King Bird	Kulumsa	2014
21	Enkoy	Holeta	1974
22	DERESELGNE	Deberzeit	1974
23	K6290-Bulk	Kulumsa	1977
24	K6290-Bulk	Kulumsa	1980
25	Et-13 A2	Holetta	1981
26	Dashen	Holetta	1984
27	Mitike	Kulumsa	1993
28	Kubsa	Kulumsa	1994
29	Galama	Kulumsa	1995
30	Tusi	Kulumsa	1997
31	Katar	Kulumsa	1998
32	Hawi	Kulumsa	1999
33	Sirbo	Kulumsa	2001
34	Doddota	Kulumsa	2001
35	Bobicho	Kulumsa	2002
36	Meraro	Kulumsa	2005
37	Millinium	Kulumsa	2007
38	Honqolo	Kulumsa	2014
39	Mandoye	Sinana	2014
40	Sanate	Sinana	2014
41	Wane	Kulumsa	2016
42	Bollo	Kulumsa	2009
43	Menze	DaberBeran	2007
44	Dinkinesh	Sinana	2007
45	Kulkulu	Holetta	2009
46	Batu	Holetta	1984
47	KBG-01	Kulumsa	2001
48	Hidase	Kulumsa	2012
49	Biqa	Kulumsa	2014

Table 2. Description of soil, geographic location and climate conditions of testing sites.

Location	Altitude (m.a.s.l)	Average rainfall	Average temp. range	Global positions	
				Latitude	Longitude
Shay Bench	1400-2485	1547.7 mm	22-29°C	$5^0 30^{"}$ - $7^0 00^{"}$N	$34^0 00^{"}$- $36^0 00^{"}$E
Chena	500-3350	1600- 2200 mm	18–21°C	$6^0 24^{'}$ - $7^0 70^{'}$ N	$35^0 69^{'}$- $36^0 78^{"}$ E
Masha	1900-2750	1800-2200 mm	12-29 °C	$7^0 24^{'}$ - $7^0 52^{'}$ N	$35^0 13^{'}$-$35^0 35^{"}$E

Description of the study area

The experiments were conducted in Shay Bench, Chena and Masha woredas (districts) of Bench Shako, Bonga and Sheka zone, respectively (Table 2).

Experimental design and trial management

The experiment was laid down in 7x7 simple lattice design. Each genotype was planted in a plot consisting of six rows each 2.5 m long and 1.2 m wide with spacing of 20 cm between rows. The distances between plots, blocks and replications were 0.5, 0.5 and 1.5 m, respectively. A seed rate of 150 kg ha^{-1} and fertilizer rate of 100 kg ha^{-1} containing NPS were used. Weeding and other agronomic practices were carried out as per recommendations of the respective sites.

Data collection

Ten randomly selected plants from the four central rows of each plot were used for data collection on plant basis and plot basis. Data on plant height, productive tillers per plant, number of kernels per spike, number of spikelets per spike and spike length were collected on plant basis, while days to 50% heading, days to physiological maturity, grain yield, biomass yield and harvest index were used for plot basis.

Statistical analysis

Data recorded were subjected to statistical analysis by using General Linear Model and the statistical package SAS version 9.3 was used for the following statistical procedures (SAS Institute, 2012).

Association of characters

Estimations of genotypic and phenotypic correlation coefficients were done according to the procedure of Dabholkar (1992).

Path coefficient analysis

Direct and indirect effects of the yield-attributing characters on grain yield were calculated based on the method used by Dewey and Lu (1959) as follows:

rij= Pij + Σrikpkj

The residual effect, which determines how best the causal factors account for the variability of the dependent factor yield, was computed using the formula:

1= p^{2}R + Σ p ijrij

where, p^{2}R= residual effect; p ijrij= product of direct effect of any variable and its correlation coefficient with yield.

RESULTS AND DISCUSSION

Association among characters

Estimates of phenotypic and genotypic correlation coefficients between each pair of characters are presented in Table 3, 4 and 5 for Chena, Masha and Shay Bench, respectively and the results showed that magnitudes of genotypic correlation coefficients for most of the characters were higher than their corresponding phenotypic correlation coefficients, except for few cases, which indicate the presence of inherent association among various characters

Correlation of grain yield with other characters

The results at Chena indicated that gain yield had positive and highly significant ($p<0.01$) phenotypic associations with plant height (r= 0.441), biomass yield (r= 0.885) and harvest index (r= 0.523) (Table 3). Grain-filling period (r= 0.322) and thousand-kernel weight (r= 0.323) also exhibited positive and significant ($p<0.05$) phenotypic associations with grain yield. Though low, the number of productive tillers, spike length and number of spikelets per spike had positive and non-significant associations with grain yield at phenotypic level, on the other hand, grain yield showed significant negative correlation with days to heading (r= -0.318). Negative but non-significant correlations were also observed for days to heading, days to maturity and spikelet length with grain yield.

At genotypic level, grain yield had positive and highly significant ($p<0.01$) genotypic correlation with biomass yield (r= 0.722), harvest index (r= 0.532) and also exhibited positive and significant ($p<0.05$) genotypic correlation with plant height (r= 0.321) and thousand-kernel weight (r= 0.296). The positive association of these characters with grain yield might be due to the higher rate of photosynthetic assimilation as biomass increased due to plant height and enhanced photosynthate partitioned to kernels that increased their weight and thereby harvest index. This suggested that improvement of biomass would result in a substantial increment in grain yield that could be used in selection of genotypes for high grain yield under optimum condition.

Similarly, Berhanu *et al.* (2017) and Mesele (2015) reported that total biomass, harvest index, plant height, number of spikes per plant, number of grains per spike are positively correlated with grain yield. In contrast to the present study, Kifle *et al.* (2015) and Girma (2018) reported that grain yield had positive and significant correlation with days to heading and plant height, respectively. The results at Masha indicated that at phenotypic level, grain yield had positive and highly significant ($p<0.01$) associations with plant height (r= 0.457), biomass yield (r= 0.639), harvest index (r= 0.845) and thousand-kernel weight (r= 0.580) (Table 4). The number of kernels per spike (r= 0.295) also exhibited positive and significant ($p<0.05$) phenotypic associations with grain yield. The grain-filling period, spike length and number of spikelets per spike had positive but low associations with grain yield at phenotypic level. On the other hand, grain yield showed non-significant negative phenotypic correlation with days to heading and days to maturity.

The results at Masha indicated that at genotypic level, grain yield had a positive and highly significant ($p<0.01$) correlation with biomass yield (r= 0.607), harvest index (r= 0.828) and thousand-kernel weight (r= 0.513). Grain yield also exhibited positive and significant ($p<0.05$) genotypic correlation with plant height (r= 0.296). Negative but non-significant correlations were observed for days to heading, days to maturity and grain-filling period with grain yield. According to Kearsey and Pooni (1996), the positive correlation of these characters with grain yield resulted from the presence of strong coupling linkage of genes or the characters may be the result of pleiotropic genes that control these characters in the same direction. They further suggested that the presence of such genes effects leads to the improvement of yield as seen in these characters.

The positive and significant association of grain yield with biological yield and harvest index had been reported by several authors (Mesele, 2015; Kifle *et al*., 2016; Berhanu *et al.,* 2017; Obsa *et al.,* 2017). In contrast to the current study results, Singh (2014) and Girma (2018) reported the presence of negative correlation between grain yield and plant height. At Shay Bench, grain yield showed positive and highly significant phenotypic associations with biomass yield (r= 0.876) harvest index (r= 0.772) and thousand-kernel weight (r= 0.792) (Table 5). A positive and non-significant phenotypic association was observed for grain-filling period, spike length, number of spikelets per spike, days to heading and days to maturity with grain yield. At the same location, grain yield showed a non-significant negative phenotypic correlation with the number of tillers per plant.

At genotypic level in Shay Bench, grain yield showed a positive and highly significant (p<0.01) genotypic correlation with biomass yield (r= 0.691), harvest index (r= 0.719) and thousand-kernel weight (r= 0.622). Number of spikelets per spike (r= 0.298) also exhibited positive and significant (p<0.05) genotypic associations with grain yield. A positive and non-significant genotypic association was also observed for grain-filling period, number of tillers per plant, number of spikelets per spike, days to heading, plant height and days to maturity with grain yield. However, the grain yield showed a non-significant negative phenotypic correlation with spike length. A number of authors have reported positive and highly significant correlation of grain yield with biomass weight and harvest index for bread wheat varieties (Obsa, 2014; Almaz, 2017; Ayer *et al*., 2017), which agreed with the present findings. Our results also agreed with the results reported by Adhiena (2015) for grain-filling period and spike length.

e 3. Genotypic (upper diagonal) and phenotypic (lower diagonal) correlation coefficients of the 12
titative traits of bread wheat genotypes at Chena.

Traits	DH	DM	GFP	PH	NT	NGS	NSS	SL	BY	GY	HI	TSW
DH	1	0.92**	0.328*	0.226	-0.52*	0.114	0.319*	0.327*	0.124	-0.129	-0.324*	-0.32*
DM	0.83**	1	0.764**	0.326*	-0.41*	0.159	0.326*	0.243*	0.232	-0.05	-0.334*	-0.32*
GFP	0.33*	0.724**	1	0.335*	-0.193	0.192	0.237	0.315*	0.247	0.189	-0.054	-0.088
PH	0.31*	0.322*	0.394**	1	-0.212	0.298*	0.220	0.152	0.583**	0.321*	0.020	0.068
NT	-0.32*	-0.317*	0.025	-0.122	1	-0.230	-0.336*	-0.214	-0.034	0.212	0.328*	0.409*
NGS	0.13	0.116	0.153	0.309*	-0.028	1	0.721**	0.343*	0.213	0.129	0.011	-0.106
NSS	0.38**	0.393**	0.311*	0.285*	-0.156	0.655**	1	0.635**	0.083	0.052	-0.029	-0.31*
SL	0.28*	0.396**	0.309*	0.293*	-0.052	0.412**	0.651**	1	0.076	-0.029	-0.231	-0.013
BY	0.03	0.105	0.322*	0.561**	-0.025	0.155	0.029	0.067	1	0.722**	-0.230	0.086
GY	-0.31*	-0.016	0.322*	0.427**	0.152	0.136	0.026	-0.033	0.885**	1	0.532**	0.296*
HI	-0.32*	-0.319*	0.054	0.022	0.309*	-0.015	-0.032	-0.112	0.298*	0.532**	1	0.319*
TSW	-0.5**	-0.283*	0.026	0.074	0.291*	-0.134	-0.285*	-0.056	0.120	0.323*	0.293*	1

Generally, at all the locations, grain yield had positive and highly significant correlation with thousand-kernel weight, biomass yield and harvest index at both phenotypic and genotypic levels. Thus, selection of these traits would be effective to increase grain yield. Obsa *et al.* (2017) reported positive correlation of grain yield both at genotype and phenotype levels with 1000-grain weight, harvest index, and biomass yield which support the results of present studies. Similarly, Alemu *et al.* (2016) and Berhanu *et al.* (2017) also reported similar results for the same characters at both genotype and phenotype levels.

The existence of a strong correlation is the indication that these traits are conditioned by the same set of genes, be it in the positive or negative direction (Falconer, 1989). Consequently, selection for one trait can indirectly introduce changes in the other trait in positive or negative direction due to either genetic linkage or presence of pleiotropic gene effect or both (Falconer, 1989).

Table 4. Genotypic (upper diagonal) and phenotypic (lower diagonal) correlation coefficients of the 12 quantitative traits of bread wheat genotypes at Masha.

Traits	DH	DM	GFP	GY	TKW	BMY	HI	NT	PH (cm	NSS	NGS	SL
DH	1	0.92**	-0.564*	-0.031	-0.55**	0.62**	-0.333*	-0.22	0.42**	0.71**	0.354	0.63**
DM	0.838**	1	-0.229	-0.051	-0.443*	0.61**	-0.425*	-0.115	0.414*	0.79**	0.279	0.65**
GFP	-0.51**	-0.145	1	-0.022	0.46**	-0.215	0.157	0.256	-0.239	-0.245	-0.219	-0.233
GY	-0.02	0.02	0.06	1	0.51**	0.61**	0.82**	0.025	0. 296*	0.023	0.236	0.120
TKW	-0.45**	-0.34**	0.41**	0.58**	1	0.06	0.62**	0.233	0.025	-0.337*	-0.233	-0.230
BMY	0.428**	0.52**	-0.125	0.63**	0.130	1	0.234	-0.035	0.63**	0.53**	0.332*	0.53**
HI	-0.43**	-0.43**	0.149	0.85**	0.64**	0.283*	1	0.019	0.116	-0.219	0.017	-0.213
NT	-0.098	-0.068	0.057	0.063	0.293*	-0.086	0.067	1	-0.0063	-0.234	-0.217	-0.33*
PH	0.399**	0.43**	-0.117	0.45**	0.123	0.52**	0.322*	0.008	1	0.42**	0.53**	0.63**
NSS	0.654**	0.79**	-0.069	0.150	-0.294*	0.45**	-0.127	-0.220	0.43**	1	0.53**	0.82**
NGS	0.530**	0.43**	-0.123	0.295*	-0.129	0.39**	0.120	-0.116	0.55**	0.55**	1	0.53**
SL	0.642**	0.54**	-0.327*	0.046	-0.295*	0.38**	-0.18	-0.08	0.58**	0.68**	0.48**	1

Table 5. Genotypic (upper diagonal) and phenotypic (lower diagonal) correlation coefficients of the 12 quantitative traits of bread wheat genotypes at Shay Bench.

** and * indicates highly significant at 1% and 5% probability levels, respectively. DH= days to heading, DM= days to maturity, GFP= grain-filling period, GY= grain yield, TKW= 1000-kernel weight, BMY= aboveground biomass (kg ha^{-1}), HI= harvest index, NT= number of tillers per plant, PH= plant height (cm), NSS= spikelets per spike, NG= number of grains per spike, SL= spike length.

Traits	DH	DM	GFP	NT	GY	BMY	HI	TKW	PH(cm)	NGS	NSS	SL
DH	1	0.642**	0.148	-0.18	0.263	0.283*	0.036	-0.209	0.236	0.263	0.263	0.029
DM	0.564**	1	0.478**	-0.17	0.254	0.257	0.162	0.129	0.297*	0.313*	0.327*	-0.03
GFP	0.248	0.679**	1	-0.25	0.165	0.123	0.129	0.225	0.259	0.238	0.287*	-0.07
NT	-0.293*	-0.285*	-0.292*	1	0.253	0.089	-0.343*	-0.28*	-0.123	-0.158	-0.142	0.121
GY	0.163	0.162	0.105	-0.12	1	0.691**	0.719**	0.622*	0.242	0.114	0.233	-0.02
BMY	0.279*	0.287*	0.072	0.176	0.876**	1	0.084	0.379*	0. 207	0.136	0.175	0.005
HI	0.006	0.021	0.065	-0.21	0.772**	-0.033	1	0.327*	-0.226	-0.057	0.199	-0.15
TKW	-0.132	-0.102	0.189	-0.28*	0.792**	0.321*	0.291*	1	0.256	0.157	0.199	0.054
PH(cm	0.293*	0.416**	0.276*	0.028	0.211	0.280*	-0.044	0.276*	1	0.779**	0.231	0.119
NGS	0.283*	0.348*	0.301*	-0.06	0.111	0.219	-0.045	0.159	0.896**	1	0.249	0.115
NSS	0.356*	0.464**	0.312*	-0.05	0.298*	0.215	0.199	0.055	0.293*	0.185	1	0.116
SL	0.031	-0.056	-0.121	0.216	0.074	0.101	-0.074	-0.038	0.129	0.091	0.276*	1

Path coefficient analysis

Association of characters determined by correlation coefficients may not be sufficient to indicate the contribution of traits to yield. Therefore, it was necessary to understand the relative importance of direct and indirect effects of each trait on yield. Association study with path coefficient analysis gives detailed information on the causal factors as direct and indirect effect through others, on target trait (Adefris *et al*. 2000). Such analysis leads to identification of important component traits useful in indirect selection for complex traits like yield. In this study, the characters which had a significant correlation with grain yield and thought to have direct relationships with grain yield were included in the path analysis (Dewy and Lu, 1959) and both the genotypic and phenotypic correlations were partitioned into direct and indirect effects using seed yield as a dependent variable. The phenotypic and genotypic direct and indirect effects of different characters on seed yield are presented in Table 6, 7 and 8.

Genotypic direct and indirect effects of various characters on grain yield

At Chena, genotypic path analysis showed that biomass weight (0.946) exerted high positive direct effect on grain yield followed by harvest index (0.964) (Table 6). This indicates that slightly increase in any one of the above traits may directly contribute towards grain yield. As biomass weight and harvest index exhibited significant positive correlations with grain yield, these two traits could be used as main components of selection in a breeding program for obtaining higher grain yield. The correlation coefficients of plant height and thousand-kernel weight were positive and their direct effects were negative. Hence, the correlations they had with grain yield were largely due to the indirect effect. The negative direct effect of plant height was in harmony with the results of Ashraf (2014). The estimated value of the residual effects was 0.1256 (Table 10) which indicates that all the traits included in the study explained high percentage of variation in grain yield (87.44%); other factors not included in the study can explain only 13.6%, so, the yield components used were good.

Table 6. Genotypic path coefficients of direct (main diagonal) and indirect (off-diagonal) effects of yield-related traits at Chena.

Traits	PH	BY	HI	TSW	rg
PH	**-0.0904**	0.66849	0.0173	-0.0017	0.321*
BY	-0.2276	**0.94664**	-0.1989	-0.0022	0.722**
HI	-0.0078	-0.2637	**0.86492**	-0.0081	0.523**
TSW	-0.0265	0.09861	0.27591	**-0.0255**	0.296*

Residual effect= 0.1256, PH= plant height, BMW= biomass weight, HI= harvest index, TKW= thousand- kernel weight, rg= genotypic correlation, **= highly significant association at p<0.01.

Table 7. Genotypic path coefficients of direct (main diagonal) and indirect (off-diagonal) effects of yield-related traits at Masha.

Traits	TKW	BMY	HI	PH(cm)	rg
TKW	**-0.060784**	-0.00626	0.712664	-0.00667	0.513**
BMY	0.020902	**0.804362**	0.266395	-0.16972	0.607**
HI	0.103224	-0.02953	**0.83844**	-0.03096	0.828**
PH	0.019776	-0.0551	0.366578	**-0.02686**	0.296*

Residual effect=0.1362, PH= plant height, BMW= biomass weight, HI= harvest index, TKW= thousand-kernel weight, rg= genotypic correlation, **= highly significant association at p<0.01.

Table 8. Genotypic path coefficients of direct (main diagonal) and indirect (off-diagonal) effects of yield-related traits at Shay Bench.

Traits	BMY	HI	TKW	rg
BMY	**0.596776**	0.080301	0.231349	0.691**
HI	0.008129	**0.955963**	0.199607	0.719**
TKW	0.036678	0.3126	**0.610419**	0.622**

Residual effect= 0.1198, BMW= biomass weight, HI= harvest index, TKW= thousand kernel weight, rg= genotypic correlation, **= highly significant association at p<0.01.

At Masha, genotypic path coefficient analysis revealed that aboveground biomass (0.718) and harvest index (0.441) exerted high and favorable direct effects on grain yield (Table 7). The results suggested that selection of genotypes with high biomass yield will lead to improvement of grain yield. Similar results were also reported by Obsa (2014), Adhiena (2015) and Almaz (2017) for the effects of biomass weight and harvest index on grain yield. The estimated value of the residual effects was 0.1362 which indicates that 86.38% of variations were explained by the characters considered in the present study. This might suggest that the yield-related characters other than those considered in the present study might be attributed to the remaining 13.62% variations observed in the study. Generally, both at Masha and Chena, the genotypic correlation coefficients of thousand-kernel weight and plant height were significant and positive with grain yield; however, these characters had low and negligible negative direct effect on grain yield. This implies that the indirect effects of these characters on grain yield through other characters could be the cause for significant and positive correlation. The results of this study were in harmony with that of Adhiena (2015).

At Shay Bench, harvest index (0.70) followed by thousand-kernel weight (0.610) and biomass yield (0.597) exerted the highest positive direct effect on grain yield (Table 11). These findings indicate that slightly increase in any one of the above traits may directly contribute towards grain yield. Thus, selections of these traits would be effective for high grain yield. Similar results were also reported by Berhanu *et al.* (2017) and Girma (2018) for biomass weight and harvest index on grain yield. The estimated value of the residual effects was 0.1198 which indicates that 88.02% of variations were explained by the characters considered in the present study. This might suggest that the yield-related characters other than those considered in the present study might be attributed to the remaining 12.07% variations observed.

Phenotypic path coefficient analysis

The phenotypic direct and indirect effects of some traits on seed yield are given in Table 9, 10 and 11 for Chena, Masha and Shay Bench, respectively. At Chena, phenotypic path coefficient analysis showed that biomass yield (0.718) followed by harvest index (0.441) exerted highest positive direct effect on grain yield. In addition, plant height (0.166) exerted positive and less magnitude of direct effect on grain yield. However, grain-filling period (-0.5883) and days to heading (-0.2629) had negative phenotypic direct effect on grain yield (Table 9). Biomass yield and harvest index exerted highest and positive direct effect on grain yield and they had positive and highly significant phenotypic correlation at Chena. This shows that the correlations they had with grain yield were largely due to the direct effect. Therefore, direct selection for these traits will improve grain yield. Similar results were also reported by Berhanu *et al.* (2017) and Girma (2018) for the effects of biomass weight and harvest index on grain yield.

Days to heading correlated significantly and negatively with grain yield and it exerted negative direct effect and has also negative indirect effects through biomass yield and harvest index. Therefore, the phenotypic correlation of this trait with grain yield was due to both the direct effect and the indirect effect through biomass yield and harvest index. Thus, whenever selection is made for improved grain yield, days to heading accompanied by biomass yield and harvest index should be considered. This is consistent with the findings of Adhiena (2015) which revealed negative correlation of days to heading with grain yield resulting from both the direct and indirect negative effects. Residual effect in this study at phenotypic level was (0.1887) which indicated that 11 traits included in the study explained 81.13% of the variability in grain yield. This further elaborates that the choice of yield-attributing traits in the study was moderately better, even if other traits are also needed to explain grain yield. At Masha, phenotypic path coefficient analysis showed that biomass yield (0.696) followed by harvest index (0.595) and thousand-kernel weight (0.420) exerted highest positive direct effect on grain yield. This justifies the presence of true relationship between these characters and grain yield as depicted by positive and significant correlations of grain yield with harvest index and biological yield, there by direct selection through these characters would result in reasonable effect on grain yield. Our findings get support from those of Alemu *et al.* (2016) and Berhanu *et al.* (2017).

In addition, plant height (0.182) exerted positive and less magnitude of direct effect on grain yield. However, number kernels per spike (-0.262) had negative phenotypic direct effect on grain yield (Table 10). However, number kernels per spike which had negative highly significant correlation exerted strongly negative direct effect phenotypically. As a result, selection of high yielding genotypes with a fewer number of kernels per spike can be suitable for the study area. The residual effect at Masha was 0.1035 (Table 10) showing that 89.65% of the variability in grain yield was explained by the component factors. The remaining 10.35% is explained by other traits not considered in the study. This further clarifies that yield-attributing traits chosen for the study of the bread wheat genotypes were good.

Phenotypic path coefficient analysis at Shay Bench revealed that harvest index (0.813) and biological yield (0.804) exerted high and favorable direct effects on grain yield. This justifies that the presence of true relationship between these characters and grain yield, there by direct selection through these characters would result in reasonable effect on grain yield. Similar results were also reported by Obsa (2014), Adhiena (2015) and Almaz (2017) for the effects of biomass weight and harvest index on grain yield. Residual effects at Shay Bench was 0.1123 which indicates that 11 characters included in the study explained 88.76% of the variability in grain yield. This further elaborates that the choice of yield-attributing characters in the study was quite better, even if other characters are also needed to justify grain yield.

In general, both genotypic and phenotypic path coefficient analysis for grain yield revealed that positive and direct effects were exerted by harvest index and biomass yield at all the locations.

Table 1. Phenotypic path coefficients of direct (main diagonal) and indirect (off-diagonal) effects of yield-related traits at Chena.

Traits	DH	GFP	PH	BY	HI	r_{ph}
DH	**-0.2629**	-0.36023	0.05297	-0.02514	-0.14476	-0.318*
GFP	-0.38492	**-0.5883**	0.065423	0.231312	0.023832	0.322*
PH	-0.37096	-0.42879	**0.166049**	0.402999	0.009709	0.427**
BY	-0.0407	-0.35043	0.093154	**0.718359**	0.131516	0.885**
HI	0.38143	-0.05877	0.003653	0.214071	**0.441328**	0.298*

Residual effect= 0.1887, PH= plant height, GFP= grain-filling period, DH= days to heading, BMW= biomass weight, HI= harvest index, TKW= thousand-kernel weight, r_{ph}= phenotypic correlation, **= highly significant association at $p<0.01$.

Table 2. Phenotypic path coefficients of direct (main diagonal) and indirect (off-diagonal) effects of yield-related traits at Masha.

Traits	BMY	HI	TKW	PH	NGS	r_{ph}
BMY	**0.696776**	0.070301	0.231349	0.121149	-0.04324	0.639**
HI	0.008129	**0.595963**	0.199607	-0.13227	0.018123	0.845**
TKW	0.036678	0.3126	**0.420419**	0.149827	-0.04992	0.580**
PH (cm)	0.026129	-0.21605	0.156267	**0.185261**	-0.24769	0.456**
NGS	0.013161	-0.05449	0.095836	0.455918	**-0.31796**	0.295*

Residual effect= 0.1035, PH= plant height, GFP= grain-filling period, DH= days to heading, BMW= biomass weight, HI= harvest index, TKW= thousand-kernel weight, r_{ph}= phenotypic correlation, ** = highly significant association at $p<0.01$.

Table 11. Phenotypic path coefficients of direct (main diagonal) and indirect (off-diagonal) effects of yield-related traits at Shay Bench.

Traits	TKW	BMY	HI	r_{ph}
TKW	0.160784	-0.06026	0.622664	0.876**
BMY	0.030902	0.804362	0.236395	0.772**
HI	0.093224	-0.01953	0.813844	0.759**

Residual effect= 0.1123, PH= plant height, GFP= grain-filling period, DH=days to heading, BMW= biomass weight, HI= harvest index, TKW= thousand-kernel weight, r_{ph}= phenotypic correlation, **= highly significant association at $p< 0.01$.

CONCLUSION

Correlation results of the study indicated that grain yield had positive and highly significant correlation with thousand-kernel weight, biomass yield and harvest index at both phenotypic and genotypic levels at all the locations. This suggests that grain yield potential can be effectively improved by obtaining maximum expression of these characters. The significant and positive association between grain yield and its components at genotypic and phenotypic levels showed that these characters contributed positively towards yield and therefore emphasis should be given on these traits when selecting for high grain yield.

Phenotypic path coefficient analysis on grain yield showed that harvest index, biomass yield, days to heading and grain-filling period exerted highest positive direct effect. However, days to maturity exerted highest and negative direct effect on grain yield. This suggests that longer days to maturity disfavor grain yield. The biomass yield exerted a positive and moderate indirect effect on grain yield through plant height, days to maturity and days to heading, whereas the indirect effects via harvest index were also negatively strong.

In general, both genotypic and phenotypic path coefficient analysis on grain yield revealed that positive and direct effects were exerted by harvest index and biomass yield at all the locations. Therefore, selection for high mean values of harvest index and biomass yield could be considered as the simultaneous selection criteria for genotypes for high gain yield.

To sum up, the presence of considerable variability among the tested wheat genotypes in the study confirmed possibility to increase wheat productivity in target area. Hence, due attention should be given to yield performance of bread wheat genotypes to exploit genetic potential of the crop via selection or hybridization.

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