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Research Article

Correlation and path coefficient studies of yield and yield associated traits in bread wheat (*Triticum aestivum* L.) Genotypes

Abstract

Sixty four wheat genotypes were tested in 8x8 simple lattice design at Ginchi, West Shewa in 2012/13 cropping season,. The overall objective was to study the to assess the association among yield and yield contributing traits and identify traits those have the most direct and indirect effects on grain yield. Analysis of variance revealed that there was a significant difference among the sixty four genotypes for all the characters studied. Grain yield had positive correlation with grain filling period, number of productive tillers per plant, spike length, number of spikelets per spike, number of kernels per spike, , 1000 kernel weight, biomass yield per plot, hectoliter weight and harvest index at both phenotypic and genotypic levels. Path coefficient analysis showed that biological yield, thousand kernel weight, harvest index and number of kernels per spike showed positive direct effect. Among these characters biological yield, thousand kernel weight, harvest index and number of kernels per spike had positive correlation with grain yield in the process of selection much attention should be given to them as these characters are helpful for indirect selection.

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Introduction

Wheat is a self-pollinating annual plant plays a major role among the few crop species being extensively grown as staple food sources in the world Mollasadeghi et al.[1] It was one of the first cereals to be domesticated, and is thought to have originated in the 'Fertile Crescent' (includes parts of Jordan, Lebanon, Palestine, Syria, Southeastern Turkey, Iraq and Western Iran) around 11,000years ago and it had reached to Ethiopia, India, Great Britain, Ireland and Spain before 5,000years ago Dubcovsky et al.[2] Globally, wheat is the leading source of cereal and vegetable protein in human food, having higher protein content than either maize (corn) or rice, the other major cereals. In terms of total production tonnages used for food, it is currently ahead of rice and maize as the main human food crop, after allowing for maize's more extensive use in animal feeds Mollasadeghi et al.[1] 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.[3] 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 et al.[4] Correlation coefficient is an important statistical method, which can help wheat breeders in selection for higher yields. Some of the researchers indicated the positive correlation between grain yield and yield component traits in wheat such as spikes number per plant and grains number per spike Kashif et al.,[5] straw yield and 1000kernel weight Akbar et al.,[6] biological yield and harvest index.[7]

The grain yield and yield components of wheat are affected very much by the genotype and the environment. Therefore, as new cultivars are being produced by breeding, the breeders study the relationships between yield and its components. To increase the yield, study of direct and indirect effects of yield components provides the basis for its successful breeding programme and hence the problem of yield increase can be more effectively tackled because of performance of yield components and selection for closely related characters[8] Although correlation estimates are helpful in determining the components of complex trait such as yield, they do not provide an exact picture of the relative importance of direct and indirect influences of each of the component characteristics of this trait. So far, little information is generated about character associations between yield and yield contributing characters in these exotic bread wheat genotypes in Ethiopia. Therefore, the objective of this study was to assess the association among yield and yield contributing traits and identify traits those have the most direct and indirect effects on grain yield.

Materials and methods

Description of the study area

The experiment was conducted at Ginchi, West Shewa in 2012/13 cropping season. Ginchi Agricultural Research Sub Center is located at an altitude of 2240meters above sea level, 84kilometers (kms) to the West of Addis Ababa, and at a Latitude and Longitude of 09°03'N and 38°15'E, respectively. It is the center where the cereal crops like Teff, barley and wheat are grown. The maximum and minimum temperatures of the area are 24.72℃ and 8.76℃, respectively, whereasthe mean annual rainfall is 1080.4mm. The major soil types are black (Vertisol) and clay loam with pH of 6.4, which is heavy clay with 0.91-1.32% organic matter (HARC, Soil Analysis and Plant Physiology Team, 2012).

Experimental materials

A total of sixty four bread wheat (*Triticum aestivum L.*) genotypes that include three standard checks and sixty one exotic bread wheat accessions introduced from CIMMYT were included in this study (Table 1). The accessions were obtained kindly from HARC. The three released cultivars Digelu, Alidoro and Meraro were used as a standard checks. They were selected based on their agronomic performances and suitability to the growing conditions.

Table 1 List of genotypes used in the study

Entry	Pedigree	Seed source	Entry	Pedigree	Seed source
1	CIMMYTOB/2	CIMMYT	33	CIMMYTOB/65	CIMMYT
2	CIMMYTOB/7	CIMMYT	34	CIMMYTOB/66	CIMMYT
3	CIMMYTOB/14	CIMMYT	35	CIMMYTOB/67	CIMMYT
4	CIMMYTOB/22	CIMMYT	36	CIMMYTOB/68	CIMMYT
5	CIMMYTOB/23	CIMMYT	37	CIMMYTOB/70	CIMMYT
6	CIMMYTOB/24	CIMMYT	38	CIMMYTOB/71	CIMMYT
7	CIMMYTOB/25	CIMMYT	39	CIMMYTOB/75	CIMMYT
8	CIMMYTOB/27	CIMMYT	40	CIMMYTOB/76	CIMMYT
9	CIMMYTOB/29	CIMMYT	41	CIMMYTOB/77	CIMMYT
10	CIMMYTOB/32	CIMMYT	42	CIMMYTOB/78	CIMMYT
11	CIMMYTOB/33	CIMMYT	43	CIMMYTOB/79	CIMMYT
12	CIMMYTOB/35	CIMMYT	44	CIMMYTOB/80	CIMMYT
13	CIMMYTOB/39	CIMMYT	45	CIMMYTADT/1	CIMMYT
14	CIMMYTOB/40	CIMMYT	46	CIMMYTADT/2	CIMMYT
15	CIMMYTOB/41	CIMMYT	47	CIMMYTADT/3	CIMMYT
16	CIMMYTOB/44	CIMMYT	48	CIMMYTADT/4	CIMMYT
17	CIMMYTOB/45	CIMMYT	49	CIMMYTADT/5	CIMMYT
18	CIMMYTOB/48	CIMMYT	50	CIMMYTADT/6	CIMMYT
19	CIMMYTOB/49	CIMMYT	51	CIMMYTADT/7	CIMMYT
20	CIMMYTOB/50	CIMMYT	52	CIMMYTADT/8	CIMMYT
21	CIMMYTOB/51	CIMMYT	53	CIMMYTADT/9	CIMMYT
22	CIMMYTOB/52	CIMMYT	54	CIMMYTADT/11	CIMMYT
23	CIMMYTOB/53	CIMMYT	55	CIMMYTADT/13	CIMMYT
24	CIMMYTOB/54	CIMMYT	56	CIMMYTADT/15	CIMMYT
25	CIMMYTOB/57	CIMMYT	57	CIMMYTADT/16	CIMMYT
26	CIMMYTOB/58	CIMMYT	58	CIMMYTADT/17	CIMMYT
27	CIMMYTOB/59	CIMMYT	59	CIMMYTADT/19	CIMMYT
28	CIMMYTOB/60	CIMMYT	60	CIMMYTADT/20	CIMMYT
29	CIMMYTOB/61	CIMMYT	61	CIMMYTADT/21	CIMMYT
30	CIMMYTOB/62	CIMMYT	62	ALIDORO	HARC
31	CIMMYTOB/63	CIMMYT	63	MERARO	KARC
32	CIMMYTOB/64	CIMMYT	64	DIGELU	KARC

Experimental design and trial management

The experiment was carried out in 8x8 Simple Lattice Design at random. The genotypes were grown under uniform rain fed conditions. The plot size was six rows of 2.5m length with 0.2m row spacing i.e. 1.2mx2.5m =3m^2 (standard plot size for variety trial). Planting was done by hand drilling on July 06, 2012. Seed rate was 150kg/ha (45g/plot). Recommended fertilizer rate of 100/100kg/ha N/P_2O_5 in the forms of Urea and DAP was applied to each plot in the shallow furrow depths and mixed with soil at the same time during sowing. For data collection, the middle four rows were used (2m^2 area). The central four rows were harvested for grain yield and biomass yield from each plot leaving boarder rows to avoid boarder effects. All other agronomic practices were undertaken uniformly to the entire plot as recommended for wheat production in the area during the growing season to raise a healthy crop.

Description of data collected

The data on the following attributes was collected on the basis of the central four rows in each plot per replication.

i. **Days to 50% heading (DH):** The numbers of days from sowing to 50% of plants have started heading.

ii. **Days to 75% maturity (DM):** The numbers of days from date of sowing to a stage at which 75% of the plants have reached physiological maturity or 75% of the spikes on the plots turned golden yellow color.

iii. **Grain filling period:** The grain filling period in days was computed by subtracting the number of days to heading from the number of days to maturity.

iv. **Thousand Kernels weight (TKW):** The weight (g) of 1000 kernels from randomly sampled seeds per plot measured by using sensitive balance. It was the weight (gm) of 1000 kernel estimated by counting 1000 seeds randomly drawn from the grain yield of each plot.

v. **Grain yield per plot (GYP):** The grain yield per plot was measured in grams using sensitive balance after moisture of the seed is adjusted to 12.5%. Total dry weight of grains harvested from the middle four rows out of six rows was taken as grain yield per plot and expressed as grams per plot.

vi. **Biomass yield per plot (BMYP):** It was recorded by weighing the total above ground yield harvested from the four central rows of each experimental plot at the time of harvest.

vii. **Harvest index (%):** It was estimated by dividing grain yield per plot to biological yield per plot. It is ratio of grain yield to the above ground biomass yield.

viii. **Hectoliter weight (HLW):** It is grain weight of one hectoliter volume random sample of wheat grain for each experimental plot expressed by (kg/ha).

ix. Ten plants were randomly selected from the four central plots for recording the following observations:

x. **Plant height (cm):** The average height (cm) of ten randomly taken plants at the maturity time from the middle four rows of each plot of the replication was measured from the ground level to the top of the spike excluding the awn.

xi. **Number of productive tillers per plant:** The numbers of tillers per plant bearing productive heads were counted at the time of harvest and average was recorded for the ten randomly taken plants from the middle four rows.

xii. **Spike length (cm):** The average spike length of ten randomly taken plants from the base of the main spike to the top of the last spikelet excluding awns was recorded in centimeter from four central rows of each plot.

xiii. **Number of spikelets per spike:** Total numbers of spikelets on main spike of all ten plants from four central rows were counted at the time of maturity and average was recorded.

xiv. **Number of kernels per spike (NKPS):** Total number of grains in the main spike were counted at the time of harvest from ten randomly taken plants and expressed as average and recorded from four central rows of each plot.

Statistical Analysis

Analysis of variance (ANOVA)

The data collected for each quantitative trait were subjected to analysis of variance (ANOVA) for simple lattice design. Analysis of variance was done using Proc lattice and Proc GLM procedures of SAS version 9.2[9] after testing the ANOVA assumptions.

The Mathematical Model for Simple Lattice Design is:

$$Y_{ijr} = \mu + Ar + G_{ij} + B_{ir} + B_{jr} + e_{ijr}$$

Where Y_{ijr}= the value observed for the plot in the r^{th} replication containing the genotype G_{ij}, μ=grand mean, G_{ij}= genotype effect in the i^{th} row & j^{th} column, Ar=replication effect, B_{ir}=i^{th} block effect, B_{jr}=j^{th} block effect, e_{ijr},= the plot residual effect*

Correlation coefficient (r)

Estimation of correlation coefficients (r) was computed using GENRES Statistical Software Package (Pascal Intl Software Solutions, 1994) to study positively and negatively correlated characters with yield and among themselves.

Phenotypic correlation and genotypic correlation was computed by the method described Singh and Chaundry (1985).

$$r_p = \frac{p\text{cov } x.y}{\sqrt{\delta^2 px \,.\delta^2\, py}}$$

$$\mathbf{r_g} = \frac{g\mathbf{covx.y}}{\sqrt{\delta^2\mathbf{gx}.\delta^2\mathbf{gy}}}$$

Where,r_p and r_g are phenotypic and genotypic correlation coefficients, respectively;pcovx.y and g covx.y are phenotypic and genotypic, covariance between variables x and y, respectively; δ2px and δ2gx are phenotypic and genotypic, variances for variable x; and δ2py and δ2gy are phenotypic and genotypic variances for the variable y, respectively. The coefficients of correlation were tested using 'r' tabulated value at n-2 degrees of freedom, at 5% and 1% probability level, where n is the number of treatments (accessions).

Path coefficient analysis

The path coefficient analysis was carried out using GENRES Statistical Software Package to study the direct and indirect contributions of the traits to the associations. A measure of direct and indirect effects of each character on grain yield was estimated using a standardized partial regression coefficient known as path coefficientanalysis, as suggested by Dewey et al.[10] Thus, correlation coefficient of different characters with grain yield was partitioned into direct and indirect effects adopting the following formul

$$r_{iy} = r_{1iP1} + r_{2iP2} + \ldots + r_{IiP}{}^{i} + \ldots + r_{niPn}$$

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

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

$$\left(r_{iy}\right) = \left(Pi\right)\left(r_{ij}\right);\ and\ \left(Pi\right) = \left(r_{ij}\right) - 1\left(r_{1i}P_i\right)$$

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

Citation: Mecha B, Alamerew S, Assefa A, et al. Correlation and path coefficient studies of yield and yield associated traits in bread wheat (*Triticum aestivum* L.) Genotypes. *Adv Plants Agric Res.* 2017;6(5):128–136. DOI: 10.15406/apar.2017.06.00226

Results and discussion

Analysis of variance (ANOVA)

Mean squares of the 13 characters from analysis of variance (ANOVA) are presented in (Table 2). Highly significant differences among genotypes ($P<0.01$) were observed for seven characters (days to heading, number of productive tillers per plant, spike length, number of spikelets per spike, 1000 kernel weight, grain yield plot^{-1} and hectoliter weight or test weight), significant at ($p<0.05$) for the rest six characters; namely, days to 75% maturity, grain filling period, plant height, number of kernels spike^{-1}, biomass yield and harvest index. This result indicating that there is variability among the genotypes studied and would respond positively to selection (Figure 1) (Figure 2).

Table 2 Mean square of the 13 characters from analysis of variance

Characters	Replication (df=1)	Genotype (df=63)	Intra Block Error (df=49)	CV (%)	Efficiency relative to RCBD
Days to 50% heading (days)	8.51	86.99**	9.22	10.62	107.38
Days to 75% maturity (days)	2.53	37.75*	5.42	4.04	100.49
Grain filling period (days)	13.78	47.30*	5.58	10.16	100.72
Plant height (cm)	29.55	248.40*	22.48	11.94	101.24
Number of productive tillers per plant	0.018	0.68**	0.1563	10.58	105.37
Spike length (cm)	0.713	1.0870**	0.1043	8.84	109.36
Number of spikelets per spike	3.3	2.5444**	0.2479	6.87	102.31
Number of kernels per spike	25.92	50.4459*	8.8261	16.2	111.15
1000 kernels weight (g)	0.131328	43.2103**	3.722	12.628	103.52
Biomass yield per plot (g)	22578	160197*	9604	19.5	115.26
Harvest index (%)	18.9036	37.2436*	6.1859	18.09	103.12
Hectoliter weight (kg/hL)	6.707	18.4252**	3.4176	13.75	116.27
Grain yield per plot(g)	1287.78	22864**	4066	2.07	120.9

*=significant at 5% probability level and **=highly significant at 1% probability level
CV, coefficient of variation, RCBD, randomized complete block design

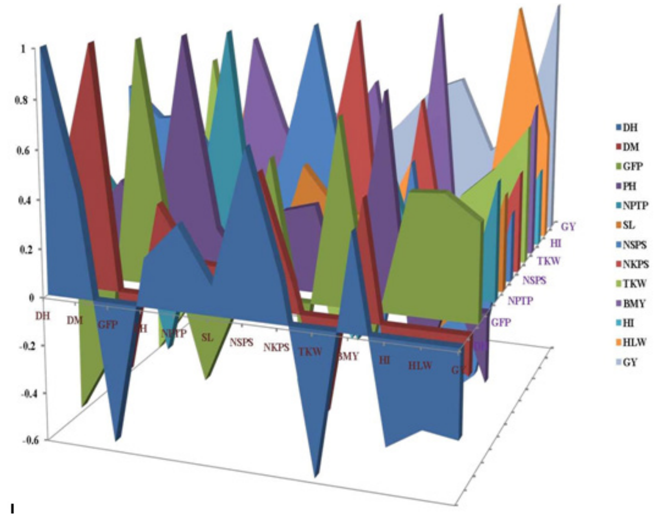

Figure 1 Graphical presentation of phenotypic correlation.

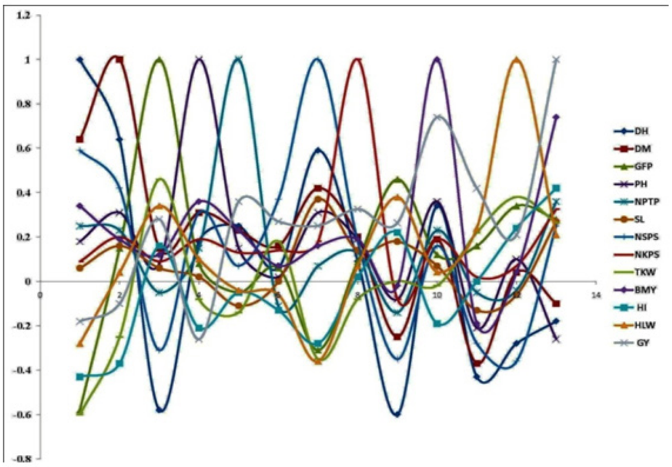

Figure 2 Graphical presentation of genotypic correlation.

Citation: Mecha B, Alamerew S, Assefa A, et al. Correlation and path coefficient studies of yield and yield associated traits in bread wheat (*Triticum aestivum* L.) Genotypes. *Adv Plants Agric Res.* 2017;6(5):128–136. DOI: 10.15406/apar.2017.06.00226

Correlation of grain yield with other traits

Phenotypic (p_r) and genotypic (g_r) correlation between the various characters are presented in Table 3. Grain yield had positive correlation with grain filling period (0.16^{ns}, 0.4**), number of productive tillers per plant (0.36**,0.49**), spike length (0.27*, 0.31*), number of spikelets per spike (0.251*,0.29*), number of kernels per spike (0.326**,0.401**), 1000 kernel weight (0.264*,0.42**), biomass yield per plot (0.74**,0.64**), hectoliter weight (0.21ns, 0.45**) and harvest index (0.42**,0.327**) at both phenotypic and genotypic levels. The works of Virk and Anand (1970) showed that wheat grain yield was positively correlated with spike length, biomass yield per plot and 1000 grain weight. Belay et al.[11] and Aycecik et al.,[12] reported positive correlation of grain yield with number of grains per spike, plant height and 1000 grain weight, which support the present studies. Ahmad et al. (2010), Akcura[13] Ali et al.,[7] and Peymaninia et al.,[14] also reported strong positive correlation and direct effect of total biomass and harvest index on grain yield. Generally, in those characters in which grain yield showed positive and significant correlation, there were component interactions in which a gene conditioning an increase in one character will also influence another character provided other conditions are kept constant (Figure 1) (Figure 2).

Days to heading showed negative association with grain yield plot^{-1} at both phenotypic and genotypic levels (r_p= -0.18, r_g=-0.36). However, the associations were insignificant at phenotypic level. Negative correlation indicated inverse relationship between earliness characters and grain yield that is desirable if stresses such as terminal heat and drought are expected. This is in agreement with the findings Mohammad et al.,[15] Tsegaye et al.,[16] Zafarnaderi et al.[3] and Gelalcha et al.,[17] who reported negative relationship between days to heading and grain yield in their studies in advanced bread wheat lines. Plant height had significant negative association with grain yield (r_p=-0.26*, r_g=-0.284*) at both phenotypic and genotypic levels in agreement with the findings of Mohammad et al. (2005) in ten candidate bread wheat lines. Grain yield displayed negative and insignificant correlation with days to maturity (r_p=-0.1, r_g=-0.16) at phenotypic and genotypic levels. s[18] reported similar negative and insignificant association between days to maturity and grain yield.

Correlation among characters

Phenotypic correlation (r_p). The character, days to heading exerted significant and positive phenotypic correlation with days to maturity (0.64**), number of productive tillers per plant (0.25*), number of spikelets per spike (0.59**) and biomass yield per plot (0.34**). However, the same trait revealed negative and significant correlation with grain filling period (-0.58**), thousand kernels weight (-0.6), harvest index (-0.43**) and hectoliter weight (-0.28*) at phenotypic level. It showed non significant association with the rest of the characters. The works of Iftikhar et al. (2012) support these findings. Significant and positive phenotypic correlation was observed for days to 75% maturity with plant height (0.31*) and number of spikelets per spike (0.42**) whereas positive non-significant phenotypic correlation with biomass yields (0.19^{ns}). Days to maturity had negative and significant phenotypic correlation with thousand kernel weight (-0.25*) and harvest index (-0.37**). However, the trait exhibited insignificant phenotypic associations with the rest characters irrespective of direction.

Grain filling period had highly significant and positive association with thousand kernel weight (0.46**) and hectoliter weight (0.34**) and significant association with grain yield (0.28*); but it showed negative and significant association with number of spikelets per spike (-0.31*) at phenotypic level. This trait revealed insignificant phenotypic association with the rest traits both positive and negative directions. Plant height had significant and positive association with number of spikelets spike^{-1}(0.31*), days to 75% maturity (0.38**) and biomass yield plot^{-1} (0.36**). It showed insignificant phenotypic positive and negative correlations with the rest characters. The findings of Majumder et al.,[18] contradicts the present results reported positive correlation between positive association with number of spikelets spike^{-1} (0.31*), grains per spike, days to maturity, and spike length (cm). The character number of productive tillers per plant showed highly significant and positive association with grain yield per plot (0.36**) and significant and positive correlation with days to 50% heading (0.25*) at phenotypic level. This character showed insignificant positive and negative phenotypic correlations with the rest characters. Earlier reports from Mohammad et al.,[15] Khokhar et al. (2010) and Kumar et al.[19] reported similar results. Spike length revealed highly significant positive association with number of spikelets per spike^{-1} (0.37) and significant association with grain yield per plot (0.27) at phenotypic level. The character showed non-significant positive and negative associations with the rest characters at phenotypic level. Sokoto et al.[20] and Abderrahmane et al.,[21] reported highly significant positive correlation of this character with grain yield. Number of spikelets spike^{-1} exhibited highly significant and positive association with number of days to heading (0.59**) and days to maturity (0.42**) significant and positive association with plant height (0.31*) at phenotypic level. It had negative and significant association with 1000 kernels weight (-0.35**), grain filling period (-0.31*), harvest index (-0.28*) and hectoliter weight (-0.36**) and positive and negative non significant correlation for the rest traits at phenotypic level. Number of kernels spike^{-1} had highly significant and positive association with biomass yield per plot (0.69**) and non-significant positive and negative correlation with the rest characters. Zarei *et al* (2013) reported highly significant and positive association number of kernels spike^{-1} with biomass yield similar results. Thousand kernels weight had highly significant and positive associations with grain filling period (0.46**) and hectoliter weight (0.38**) and it showed negative significant association with days to 50% heading (-0.6**), days to 75% maturity (-0.25*) and number of spikelets per spike (-0.35).

The trait showed positive and negative non-significant phenotypic correlation with all the rest characters. Majumder et al.,[18] found similar results. On the contrary, Khokhar et al. (2010) observed thousand kernels weight had highly significant and negative associations with days to 75% maturity.Biomass yield showed positive and significant correlation with days to heading (0.34**), and plant height (0.36**) and non-significant association with the rest traits at phenotypic level irrespective of direction. The findings of Mohammad et al.[15] contradicted these significant and positive associations of biomass yield with days to heading.

Harvest index exhibited significant negative phenotypic correlation with days to 50% heading (-0.43**), days to maturity (-0.37**) and number of spikelets per spike (-0.28*) but showed insignificant correlations with the rest of all characters in agreement with the results of Sajjad *et al* (2011) and Ashraf et al.[22] Zarei et al. (2013) reported harvest index had positive phenotypic correlation with number of spikelets per spike that contradicted the present result. Harvest index has been recommended as a selection criterion for increasing yield of cereals. Because the high-yielding lines had increased biomass, while maintaining their mean grain weight and harvest index, the source

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and sink were simultaneously increased in these lines. Hectoliter weight exhibited highly significant positive association with grain filling period (0.34**) and thousand kernels weight (0.38**) whereas significant and negative association with days to heading (-0.28*) and number of spikelets spike^{-1} (-0.36**) and insignificant association with the rest characters irrespective of direction at phenotypic level. Demelash *et al* (2013) obtained similar results of highly significant positive correlation of hectoliter weight with thousand grain weights but negatively correlated with days to heading and days to maturity in bread wheat.

Genotypic correlation

The yield components exhibited varying trends of association among themselves. Days to 50% heading exerted significant positive association with days to maturity (0.42**), number of productive tillers per plant (0.35**), number of spikelets per spike (0.35**) and biomass yield per plot (0.4**). However, the trait revealed negative but significant correlation with grain filling period (-0.58), thousand kernel weight (-0.6), harvest index (-0.43) and hectoliter weight (-0.28) at genotypic level. It showed a non-significant positive genotypic correlation with plant height (0.2), spike length (0.12), and number of kernels per spike (0.18).[23] Days to 75% maturity showed significant and positive genotypic correlation with plant height (0.38) and number of spikelets per spike (0. 55). This trait had highly significant and positive correlation with biomass yield (0.49) at genotypic level. Grain filling period had highly significant and positive correlation with thousand kernel weight (0.76), harvest index (0.49), and hectoliter weight (0.5) whereas highly significant and negative association was observed with number of productive tillers plant^{-1} (-0.38) and number of spikelets spike^{-1} (-0.57) at genotypic level. Plant height had highly significant and positive association with number of kernels spike^{-1}(0.36), and biomass yield plot^{-1} (0.84) at genotypic level and showed negative and significant genotypic correlation with harvest index. Number of productive tillers per plant had highly significant and positive genotypic correlation with biomass yield plot^{-1} (0.45**) and insignificant with all other traits irrespective of directions.

Spike length at genotypic level revealed highly significant positive association with number of spikelets per spike^{-1} (0.44**) and significant association with number of kernels spike^{-1}(0.27) and 1000 kernels weight (0.25*). The character revealed insignificant positive and negative associations with the rest characters at genotypic level. Number of spikelets spike^{-1} exhibited significant association with number of kernels spike^{-1} (0.32*) and highly significant association with biomass yield per plot (0.46**) in positive direction at genotypic level. It showed negative highly significant association with 1000 kernels weight (-0.44**), harvest index (-0.54**) and hectoliter weight (-0.42**) at genotypic level. It had positive and negative insignificant correlation for the rest traits at genotypic level irrespective of direction.

Positive significant associations were observed for number of kernels spike^{-1} with plant height (0.36**), spike length (0.27*), number of kernels spike^{-1} (0.32*) and biomass yield per plot (0.69**) at genotypic level. The trait had negative significant association with 1000 kernels weight (-0.25*) at genotypic level and insignificant with the rest characters in positive and negative directions at genotypic level. Thousand kernels weight had strong negative association with days to heading (-0.6**), days to maturity (-0.39**), number of spikelets per spike (-0.44**) and number of kernels per spike (-0.25*) and strong positive association with grain filling period (0.76), harvest index (0.26*) and hectoliter weight (0.39) at genotypic level. Biomass yield plot^{-1} showed positive significant genotypic correlation with days to heading (0.4), days to maturity (0.49), plant height (0.84), number of productive tillers per plant, number of spikelets per spike (0.46) and number of kernels per spike (0.69) and negative significant genotypic correlation with harvest index (-0.59) and non significant association with the rest traits at genotypic level irrespective of direction. Harvest index exhibited significant negative correlation with days to heading (-0.43) days to maturity (-0.44), number of spikelets per spike (-0.54) and biomass yield plot^{-1} (-0.59) at genotypic level whereas it showed significant positive association with grain filling period (0.49**), 1000kernels weight (0.26*) and hectoliter weight (0.31*) at the genotypic level. Hectoliter weight (Test weight) exhibited highly significant positive association with grain filling period (0.50) and thousand kernels weight (0.39) and significant positive association with harvest index (0.31*) at genotypic level. The trait revealed also highly significant negative genotypic correlation with days to heading (-0.34**) and number of spikelets spike^{-1} (-0.42**) while insignificant association with the rests of characters at genotypic level with irrespective of direction.

Path Coefficient Analysis

As correlation does not allow the partitioning of genotypic correlation coefficients into direct and indirect effects, they are further analyzed by path coefficient analysis (Dewy and Lu, 1959) by using grain yield as a dependant variable. The genotypic direct and indirect effects of different characters on grain yield are presented in Table 2. In this study, genotypic path analysis manifested positive direct effect on grain yield for all characters except plant height and hectoliter weight. The highest positive direct effect on grain yield per plot were exhibited by biological yield (1.14**) which had positive and significant correlation with grain yield.

The indirect effect via other characters was negligible or negative. Hence, the genotypic correlation with grain yield was largely due to the direct effect. The direct effect of number of kernels spike^{-1} on grain yield was recorded to be positive with a value of 0.374 that was equivalent to the correlation coefficient it had with grain yield. This suggests the correlation revealed the true relationship and direct selection through this character is effective. The high indirect positive effects of number of kernels per spike revealed via biomass yield (0.37) on grain yield, whereas moderate negative indirect effect via number of productive tillers plant^{-1} (-0.124), thousand kernels weight (-0.162), harvest index (-0.150) and test weight (-0.132) on grain yield. The results revealed that number of kernels per spike may be used as direct selection criteria in any breeding program designed to increase grain yield. The direct effect of 1000 kernels weight and harvest index on grain yield was positive with value of 0.98, suggesting its importance in breeding program for developing wheat genotypes with higher grain yield. The high positive indirect effects of 1000 kernels weight via harvest index (0.562) followed by grain filling period (0.184) exhibited on grain yield. It showed negative indirect effect on grain yield via days to heading and maturity, number of productive tillers per plant, number of spikelets per spike, number of kernels per spike and via hectoliter weight were recorded. These findings were in accordance with those of Iftikhar et al. (2012). The direct effect of harvest index on grain yield was positive and high (0.78) and it showed high positive correlation coefficients. The indirect effects of these traits through other traits were mostly negative. Hence, the correlation coefficients of these traits with grain yield had been largely due to the direct effect.

Hectoliter weight had negative direct effect and positive correlation coefficient. Thus, the positive correlation coefficient was

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largely due to its respective indirect effects. Plant height had negative significant correlation with grain yield (Table 3). Its direct effect on grain yield was also negative and smaller than its correlation value (Table 4) indicating indirect influence of the trait via other component characters. Its high magnitude of indirect effect through biomass yield per plot supports this idea. This result is in agreement with Ahmed et al. (2003), who reported negative correlation and direct effect of plant height with grain yield. Aycicek and Yildirim (2006) also pointed that plant height had negative direct effect on grain yield. Days to heading and days to maturity had positive direct effects on grain yield. Kumar[24] reported similar results in rice cultivars. The correlation coefficient they had with grain yield was negative. This negative relationship between early flowering and maturity accompanied with sufficient grain filling period characters and grain yield is desirable if stresses conditions such as terminal heat and drought are expected during growing season. This suggestion can be justified by earlier report of Gelalcha and Hanchinal (2013) in which correlation between days to flowering and days to maturity with grain yield was negative. The direct effect of days to heading on grain yield, on the other hand, is positive (Table 4). Number of productive tillers per plant was positive strongly correlated with grain yield while the magnitude of the direct effect is also positive and less than that of correlation coefficient indicating importance of other traits via which productive tillers per plant contributed to grain yield (Tables 1) (Table 2). The significantly high magnitude of its indirect effect through total biomass per plot supports this idea. Spike length was positive strongly correlated (0.41) with grain yield while the magnitude of the direct effect (0.204) was also positive and less than that of correlation coefficient indicating importance of other traits via which spike length contributed to grain yield (Tables 1) (Table 2). The indirect positive effects of spike length via showed moderate indirect positive effect through thousand kernels weight (0.169) and biomass yield (0.16) and revealed high negative indirect effect via harvest index (-0.30) on grain yield. Similar findings were reported by Narwal et al. (1999) and Mohsin et al. (2009).

Table 3 Estimates of phenotypic (below diagonal bold) and genotypic (above diagonal not bold) correlation coefficients among yield and yield components in 64 bread wheat genotypes tested at Ginchi (2012/2013)

Character	DH	DM	GFP	PH	NPTP	SL	NSPS	NKPS	TKW	BMY	HI
DH	1	.42**	-.58**	.2ns	.35**	.12ns	.68**	.18ns	-.6**	.40**	-.43**
DM	0.64**	1	-.33**	.38**	.16ns	.15 ns	.55**	.12ns	-.39**	0.49**	-.44**
GFP	-0.58**	.15 ns	1	.11ns	-.38**	-.04ns	-.57**	-.21ns	.76**	-0.14ns	0.49**
PH	0.18 ns	.31*	.08 ns	1	.22ns	.03ns	.32*	.36**	-.09 ns	0.84**	-.39**
NPTP	0.25*	.23 ns	-.05 ns	.15 ns	1	-.11ns	.08 ns	.13 ns	-.23 ns	0.45**	0.004ns
SL	0.06 ns	.16 ns	.06 ns	.02 ns	-.11ns	1.0	.44**	.27*	.25*	0.18ns	-.21ns
NSPS	0.59**	.42**	-.31*	.31*	.07ns	.37**	1	.32*	-.44**	0.46**	-.54**
NKPS	0.09 ns	.20 ns	.09 ns	.19 ns	.13ns	.14 ns	.18 ns	1	-.25*	0.69**	-.16ns
TKW	-0.60**	-.25*	.46**	-.08ns	-.14 ns	.18 ns	-.35**	-.08 ns	1.0	-0.18ns	0.26*
BMY	0.34 **	.19 ns	.12 ns	.36**	.23ns	.07 ns	.16 ns	.19 ns	-.019ns	1	-.59**
HI	-0.43**	-.37**	.16 ns	-.21ns	-.05ns	-.13ns	-.28*	.02 ns	.22 ns	-0.19 ns	1.0
HLW	-0.28*	.04 ns	.34**	.10 ns	-.04ns	-.06ns	-.36**	.07 ns	.38**	.042ns	0.24ns
GY	-0.18 ns	-0.1 ns	.28 *	-.26*	.36 **	.27*	.251*	.326**	.264*	.74**	0.42**

P<0.05=0.25 & P<0.01=0.325 for df=n-2, where n is the number of genotypes, DH, days to heading; DM, days to maturity; GFP, grain filling period; PH, plant height (cm); NPTPP, no. of productive tiller plant-1 and; SL, spike length (cm), NSPS, No. Of spikelets spike-1; NKPS, no. of kernels spike-1; TKW, 1000 kernel weight (g); GY, grain yield plot-1; BMY, biomass yield plot-1; HI, harvest index and HLW, hectoliter weight.

Table 4 Estimate of direct effect (bold face and diagonal) and indirect effects (off diagonal) at genotypic level in 64 bread wheat genotypes tested at Ginchi (2012/13).

Character	**DH**	**DM**	**GFP**	**PH**	**NPTPP**	**SL**	**NSPS**	**NKPS**	**TKW**	**BMY**	**HI**	**HLW**	**Rg**
DH	0.108	0.134	-0.103	0.032	-0.063	-0.016	0.075	0.03	-0.187	0.21	-0.48	0.103	-0.36**
DM	0.22	0.116	-0.182	0.059	-0.029	-0.021	0.058	0.019	-0.11	0.38	-0.36	0.009	-0.16ns
GFP	-0.421	-0.095	0.247	0.016	0.069	0.006	-0.061	-0.035	0.21	-0.31	0.83	-0.152	0.40**
PH	0.103	0.108	0.025	-0.116	-0.039	-0.005	0.035	0.061	-0.024	0.9	-0.77	-0.033	-.284*
NPTPP	0.109	0.045	-0.094	-0.034	0.238	0.015	0.009	0.022	-0.263	0.405	0.008	0.032	0.4.92**
SL	0.059	0.043	0.01	0.005	-0.02	0.204	0.05	0.046	0.169	0.16	-0.3	0.021	0.401**
NSPS	0.354	0.156	-0.14	0.05	-0.015	-0.061	0.102	0.054	-0.12	0.286	-0.41	0.134	0.290*
NKPS	0.092	0.033	0.052	0.057	-0.124	0.038	0.034	0.374	-0.162	0.37	-0.15	-0.132	0.42**
TKW	-0.353	-0.113	0.184	-0.014	-0.262	-0.035	-0.148	-0.14	0.98	-0.033	0.562	-0.112	0.58**
BMY	0.101	0.102	-0.072	0.15	-0.086	-0.008	0.029	0.016	-0.009	1.14	-0.801	-0.008	0.64**

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Table Continued..

Character	DH	DM	GFP	PH	NPTPP	SL	NSPS	NKPS	TKW	BMY	HI	HLW	Rg
HI	-0.185	-0.131	0.144	-0.06	-0.001	0.03	-0.059	-0.004	0.079	-0.23	0.78	-0.096	0.327**
HLW	-0.166	-0.008	0.117	0.016	0.018	0.009	-0.045	0.017	0.1	0.027	0.602	-0.21	0.45**

DH, days to heading; DM, days to maturity; GFP, grain filling period; PH, plant height (cm); NPTPP, no. of productive tiller plant-1 and; SL, spike length (cm), NSPS, No. Of spikelets spike-1; NKPS, no. of kernels spike-1; TKW, 1000 kernel weight (g); GY, grain yield plot-1; BMY, biomass yield plot-1; HI, harvest index and HLW, hectoliter weight.

Number of spikelets per spike had positive direct effect. The indirect effects via other characters were mostly positive and negligible. Therefore, its positive correlation coefficient with grain yield was mainly due to their direct effect. Harvest index had positive direct effect. Its indirect effects through other characters were mostly negative and negligible. Thus, its positive correlation coefficient with grain yield was mainly due to its direct effect. Grain filling period had positive direct effect. The indirect effect of this trait via other traits was mostly negative and negligible. Thus, the correlation coefficient of this trait with grain yield was due to the direct effect. Generally, characters that exerted positive direct effect and positive and significant correlation coefficient with grain yield were known to affect grain yield in the favorable direction and needs much attention during the process of selection cases. Path coefficient analysis for traits like biomass yield per plot, thousand kernels weight, harvest index and number of kernels per spike showed that the highest positive direct effects towards grain yield and strong and positive correlations with grain yield (Tables 8 and 9). The respective indirect effects of these characters via other characters were either negligible or negative. Hence, the correlation coefficient they had with grain yield was largely due to their direct effect. This means that a slight increase in one of the above traits may directly contribute to grain yield and a direct selection through these traits will be effective. These findings led to conclude thousand kernels weight and harvest index as a reliable criterion for getting high yield in bread wheat plants. Ahmad et al. (2010), Akcura (2011), Ali and Shakor (2012) and Peymaninia et al.[14] reported strong positive correlation and direct effect of total biomass, thousand kernels weight and harvest index on grain yield. Fellahi et al.[25] and Gelalcha and Hanchinal (2013) also reported similar results. Our results obtained from 64 bread wheat genotypes, proved that biological yield, 1000 kernels weight, number of kernels per spike and harvest index appeared to be the most important sources affecting grain yield variation under rain fed conditions and consequently may be considered as effective criteria for selecting towards grain yield improvement. The residual effect in path analysis determines how best the component (independent) variables account for the variability of the dependent variable, grain yield per plot (Gelalcha and Hanchinal, 2013). Residual effect in the present study was 0.2705 (Table 4) which means the characters in the path analysis accounted for 72.95% of the variability in grain yield.

Conclusions

Grain yield had positive correlation with grain filling period, number of productive tillers per plant, spike length, number of spikelets per spike, number of kernels per spike, , 1000 kernel weight, biomass yield per plot, hectoliter weight and harvest index at both phenotypic and genotypic levels. By selecting for these traits showing positive and significant correlation with grain yield there is a possibility to increase grain yield of bread wheat.[26–30]

Path coefficient analysis showed that biological yield, thousand kernel weight, harvest index and number of kernels per spike showed positive direct effect. Among these characters biological yield displayed the highest direct effect. Path coefficient analysis based on grain yield as a dependant variable showed that biological yield had the highest positive direct effect. The correlation coefficient with grain yield was also positive and significant. Thousand kernel weight, harvest index and number of kernels per spike also showed positive direct effect. The correlation coefficients were also positive and significant. Since biological yield, thousand kernel weight, harvest index and number of kernels per spike had positive correlation with grain yield in the process of selection much attention should be given to them as these characters are helpful for indirect selection.[31–36]

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Conflict of interest

The author declares no conflict of interest.

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