

Path Coefficient and Correlation Studies of Yield and Yield Associated Traits in Bread Wheat (*Triticum aestivum* L.) Germplasm

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Abstract: The overall objective was to estimate the extent of association between pairs of characters at genotypic and phenotypic levels and thereby compare the direct and indirect effects of the characters. Sixty four germplasm of bread wheat (*Triticum aestivum* L.) with four standard checks were tested in an augmented design. Among the characters, grain yield showed positive and significant correlation with grain filling, productive tiller, spike length, spikelet spike⁻¹, kernel spike⁻¹, 1000 grain weight, biomass yield and harvest index at both levels. In path coefficient analysis harvest index and biomass yield revealed that direct and indirect effect on yield. These two characters can be considered for selection. Based on these results we could not reach to the final conclusion. But the findings can be used as a bench mark for further study. Therefore, it needs additional study over several years and multi locations.

Key words: Correlation • Path coefficient analysis • Direct effect • Indirect effects

INTRODUCTION

Bread wheat (*Triticum aestivum* L. emThell. 2n=6x=42), a self-pollinating annual plant, is the largest cereal crop extensively grown as a staple food source in the world [1]. It is one of the most important export and strategic cereal crop in the world and in Ethiopia in terms of production and utilization [2]. It has been described as the 'King of cereals' because of the largest hectare it occupies, high productivity and the observable position it holds in the international food grain trade [3]. The Food and Agriculture Organization of the United Nations (FAO) gracefully project the world wide acclaim sticking with wheat as human food and the International Maize and Wheat Improvement Center (CMMYT) has chosen a wheat spike symbol in their logo with the description "Let there be bread. Wheat is also a major source of energy, protein and dietary fiber in human nutrition [4].

A knowledge of correlations that exists between important characters may facilitate the interpretation of result obtained and provide the basis for planning more efficient program for future [5]. Correlation coefficient is the measure of the degree for linear association between

two variables [6]. Correlated characters is important for three basic reasons. First, in connection with the genetic causes of correlation through the pleiotropic action of genes. Second in connection with the changes brought about by selection. Third, in connection with the effect of natural selection on the relationship of metric character with its fitness, which is the primary agent, that determines the genetic properties of that character in a natural population [7].

Inadequate knowledge of interrelationships among various traits and the practice of unilateral selection for agronomic traits frequently end up with less than optimum result in plant breeding [8]. The practical utility of selecting for a given character as a means of improving another depends on the extent to which improvement in major characters is facilitated by selection for the indicators. Such improvement depends not only on the genotypic correlation but also on phenotypic correlation [5]. For selection based on yield component to be effective in increasing yield, [9] stated that the components should fulfill the following: they should be highly heritable, the component should be genotypically independent or genotypic correlation among the

component should be positive and the component should be physiologically related in a positive manner. Simple correlation coefficients are helpful to show the relationship of characters with grain yield and correlation levels of each other but, they do not provide an exact picture of the relative importance of direct and indirect influences of each of the component characters towards this trait [8].

Correlation coefficients measure the absolute value of correlation between variables in a given body of data. Correlation does not say anything about the cause and effect of relationship. [10] designed the method for path analysis for the purpose of interpretation of a system of correlation coefficients in terms of path causation.

As path analysis is based on the assumption that all the variation is due to additive gene action, this analysis has all the limitations of any linear model method in a non-linear world [11]. Information on the extent and nature of interrelationship among characters help in formulating efficient scheme of multiple trait selection, as it provides means of direct and indirect selection of component characters. Therefore, this study was mainly conducted with the objectives of estimate the extent of association between pairs of characters at genotypic and phenotypic levels and thereby compares the direct and indirect effects of the characters.

MATERIALS AND METHODS

Description of the Study Area: The germplasm were tested at Kulumissa Agricultural Research Center (KARC) during 2013/2014 cropping season. KARC is located 8° degree to 8° degree 02 northern latitude and 39° degree 07' to 39° degree 10' eastern longitude. It has an altitude of 2200 m.a.s.l. with annual average rainfall of 850mm. The annual average temperature of the study area is 16.65°C with maximum and minimum temperature of 22.8°C and 10.5°C respectively. With the soil type classified as clay loam soil with a pH of 6.

Experimental Materials: The experimental materials were 64 germplasm of bread wheat (*Triticum aestivum* L.) including four standard checks (*Danda'a*, *Huluka*, *Shorima* and *Kakaba*). They were selected based on their agronomic performances and suitability to the growing conditions in the study area.

Experimental Design and Trial Management: The experiment was carried out in an Augmented Design (AD)

comprising of four blocks, where each block contains 16 test entries and 4 checks (randomly allocated) with the total of 20 germplasms in each blocks. The germplasm were grown under rain fed conditions. Each germplasm was sown in two rows of 1.25 meter long and 20 cm apart, with seed rate of 7.5g, 150 kg h⁻¹. Weeds were controlled manually. Planting was done by hand drilling. Recommended fertilizer @ 100 kg N ha⁻¹ and 100kg P₂O₅ ha⁻¹ in the forms of Urea and DAP was were respectively applied to each plot in the shallow furrow depths and mixed with soil at the same time during sowing.

Agronomic Data Collected: The following data were recorded for seven quantitative characters on plot basis:

Days to 50% Heading (DH): The number of days from planting up to heading.

Days to 75% Maturity (DM): The number of days from planting up to physiological maturity.

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.

Thousand Seed Weight (TSW): Weight of 1000 seeds randomly taken from each plot in gram.

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 two rows was taken as grain yield per plot and expressed as kg ha⁻¹.

Biomass Yield per Plot (BMYP): It was recorded by weighing the total above ground yield harvested from the two rows of each experimental plot at the time of harvest.

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.

$$HI \% = \frac{\text{Grain yield per plot}}{\text{Biomass yield per plot}} \times 100$$

Agronomic Data Collected: The following data were recorded for seven quantitative characters on plant basis:

Plant Height (PH): The distance between the ground level to the tip of the terminal spikelet in cm of the mother ten plants.

Number of Fertile Tiller per Plant (NFTP): The actual count of the fertile numbers of tillers of ten plants (spike bearing) per plant.

Spike Length (SL): Distance from the base of the spike to the tip of the highest spikelet of ten plants (excluding own) in cm.

Number of Spikelet's per Spike: Total numbers of spikelet's on main spike of all ten plants from two rows were counted at the time of maturity and average was recorded.

Number of Kernel per Spike (NKS): The actual count of the number of kernel per spike of all ten plants.

Statistical Analysis: The data were subjected to analysis of variance using the SPAD software developed by IASRI New Delhi, India [12], cluster analysis and principal component analysis Version 9.2 [13]. Phenotypic and genotypic correlation [13]. And path coefficient analysis GENRES Statistical Software or Package [14].

Analysis of Variance (ANOVA): The analysis of variance (ANOVA) was carried out to dissect total variability of the entries into sources attributable to genotype and error using the SPAD software developed by IASRI, New Delhi, India [12]. The statistical model for the augmented design was, $y_{ij} = \mu + g_i + c_j + \beta_j + \epsilon_{ij}$ [12]. Where: y_{ij} is the observation of treatment i in j th block μ is the general mean, g is the effect of test treatment, c_j is the effect of control treatments in j th block, β_j is the block effects, (ϵ) is the error.

Correlation Coefficient (R): Estimation of correlation coefficients (r) was computed using Statistical Analysis System Version 9.2 [13]. To study positively and negatively correlated characters with yield and among themselves. Genotypic (r_g) and phenotypic (r_p) coefficient of correlation were tested for statistical significance against the correlation table values at 5 and 1% levels of significance.

Path Coefficient Analysis: The path coefficient analysis was carried out using GENRES Statistical Software Package [14] 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 coefficient analysis, as suggested by [15]. Thus, correlation coefficient of different characters with grain yield was partitioned into direct and indirect effects adopting the following formula. $r_{iy} = r_{1iP1} + r_{2iP2} + \dots + r_{liPi} + \dots + r_{niPn}$ where r_{iy} is correlation of i th character with grain yield; r_{liPi} 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 n th character on grain yield. Direct effect of different component characters on grain yield were obtained by solving the following equations: $(r_{iy}) = (P_i)$ (r_{ij}) ; and $(P_i) = (r_{ij}) - 1 (r_{liPi})$ where, (P_i) is matrix of direct effect; (r^{ij}) is matrix of correlation coefficients among all the n th component characters; (r^{iv}) is matrix of correlation of all component characters with grain yield; (r_{liPi}) is indirect effect of i th character on seed yield through first character.

RESULTS AND DISCUSSION

Analysis of Variance (ANOVA): Mean squares of the 12 characters from analysis of variance (ANOVA) are presented in Table 1. Significant differences were observed among treatments for all characters studied. Among tests, significant differences were observed for all characters except number of spikelet per spike. Among test versus control all the character showed significant difference for 68 bread wheat germplasm. This indicating the presence of variability, which can be exploited through selection for further breeding programs. Similarly, works of [16] reported that grains per spike number of tillers per plant, 1000 grain weight, spike density and grain yield per plant showed significant differences between forty one bread wheat genotypes were studied. [17] reported significant differences among 169 genotypes for 11 morphological traits such as days to 50% heading, days to 75% maturity, plant height, spike length, number of tillers plant⁻¹, number of spikelet spike⁻¹, 1000 grain weight and grain yield per plot.

Range and Mean Values: The mean performances of the sixty four germplasm and four standard checks for 12 characters are presented in Table 2. The mean values for days to 50% heading ranged from 47.75 (*Huluka*) to 87.18 (226153), days to 75% maturity ranged from 99.5(208204)

Table 1: Analysis of variance (Mean squares) for the 12 characters of 68 bread wheat germplasm

Character	Block (adj) (df=3)	Error (df=)	Trt (adj) (df=67)	Among-controls (df=3)	Among-test (df=63)	Test v Control (df=1)	CV (%)
Days to 50% heading (DH)	10.22	4.84	110.78**	17.72ns	49.99**	4219.5**	3.42
Days to 75% maturity (DM)	1.16	4.22	152.48**	676.5ns	93.76**	2273.7**	1.77
Grain filling period (GF)	7.89	4.61	63.66**	13.56ns	62.83**	266.45**	4.68
Plant height (cm)	5.59	5.52	418.21**	221.8	204.76**	14456.8**	1.99
No. of productive tillers	0.24	0.32	2.12**	0.10	1.44*	50.96**	12.27
Spike length (cm)	3.50	0.34	7.65**	0.07	4.39**	235.93**	5.57
Number of spikelet's spike ⁻¹	2.08	0.88	6.95**	1.10	3.00*	273.8**	4.80
Number of kernels spike ⁻¹	8.40	6.09	322.14**	58.25	73.25**	1679.6**	6.22
Thousand kernels weight (g)	2.16	0.51	91.84**	21.19	14.48**	5051.1**	4.89
Grain yield plot ⁻¹ (kg/h)	1488.91	28643.8	3117652.8**	31044.9	1570742.6**	109832814.6**	6.16
Biomass yield plot ⁻¹ (kg/h)	141272.9	94100.6	23697859.7**	1613822.9	9676011.6**	973326400.3**	1.64
Harvest index (%)	0.16	0.55	82.71**	1.8	79.16**	549.04**	4.99

DF =Degrees of freedom, ns = non significant*=significant at 5% probability level and **=highly significant at 1% probabilitylevelCV= Coefficient of Variation.

Table 2: Estimate of ranges, mean, phenotypic (PV) and genotypic (GV) coefficient of variation, broad sense heritability and genetic advance as percent of mean for 12 characters of 68 bread wheat germplasm tested at KARC

Character	Mean	Range		σ^2_p	σ^2_g	PCV (%)	GCV (%)	H^2_{BS} (%)	GA(k=2.063)	GAM(k=2.063)
		Min	Max							
Days to heading (DH)	64.21	47.75	87.18	110.7	105.9	16.3	16.0	95.6	14.5	22.6
Days to maturity (DM)	115.58	99.5	136.75	152.4	148.2	10.6	10.5	97.2	15.8	13.7
Grain filling period (GF)	45.92	29.81	70.56	63.6	59.04	17.3	16.7	92.7	12.5	27.4
Plant height (PH)	117.96	82.09	155.43	418.2	412.6	17.3	17.2	98.6	20.4	17.3
Fertile productive tillers (FTPP)	4.66	1.73	6.98	2.12	1.8	31.2	28.7	84.9	5.2	112.8
Spikelet per spike (Sps)	19.62	13.33	23.8	6.9	6.06	13.4	12.5	87.2	7.1	36.3
Spike length (Sl)	10.60	5.89	14.59	7.65	7.31	26.00	25.5	95.5	7.4	70.4
Kernel per spike (KPS)	39.68	18.26	74.35	322.14	316.04	45.2	44.7	98.1	19.1	48.2
Thousand grain weight (TGW)	14.70	3.69	32.26	91.8	91.3	65.1	65.00	99.4	14.00	95.4
Biomass yield ha ⁻¹ (BMY, kg ha ⁻¹)	18618.25	8004.37	26107.5	23697860	23603759	26.14	26.09	99.6	31.6	16.9
Harvest index (HI)	14.65	6.65	24.25	82.71	82.17	62.06	61.8	99.4	13.6	93.2
Grain yield (GY, kg ha ⁻¹)	2744.4	533.37	6335.87	3117653	3089009	64.3	64.04	99.08	19.02	69.3

σ^2_p =Phenotypic variation, σ^2_g =Genotypic variation, PCV=Phenotypic coefficient of variation, GCV=Genotypic coefficient of variation, H^2_{BS} . Broad sense heritability, GA=genetic advance, GAM=Genetic advance as percent of mean.

to 136.75 (*shorima*). Grain filling is an important trait that ultimately affects the overall grain yield by increasing grain weight. Therefore, it was ranged from 29.81 (*Danda'a*) to 70.56 (204363) with a mean value of 50.18. Plant height was varies from 82.09 (*Kakaba*) to 155.43 (7459), number of productive tiller was ranged from 1.73 (221735) to 6.98 (222761). Spikelet spike⁻¹ was ranged from 13.33 (222451) to 23.8 (*Kakaba*), spike length varied from 5.89 (243721) to 14.59 (222761). Whereas kernel spike⁻¹, thousand grain weight, biomass yield plot⁻¹, harvest index and grain yield plot⁻¹ were ranged from 18.26 (7946) to 74.35 (*Shorima*), 3.69 (208204) to 32.26 (*Kakaba*), 8004.37 (243720) to 26107.5 (*Huluka*), 4.36 (794) to 52.20 (243720) and 533.37 (7946) to 6335.87 (6844), respectively. Such considerable range of variations provided a good opportunity for yield improvement. Thus, high variability for twelve traits in sixty four bread wheat germplasm and four standard check studies implied that there was reasonably sufficient variability. Generally, the range of variation was wide for all the characters studied. [17] observed high range of variation for yield, 1000-kernel weight, plant height and days to flowering. [18] reported

wide range of variation for plant height, grain filling period, number of spikelet's per spike⁻¹, biological yield per plot⁻¹, grain yield and 1000-kernel weight. Moreover, [19] reported large variation for grain yield, 1000 kernels weight and number of kernels per spike⁻¹.

Correlation among Traits

Correlation of Grain Yield with Other Traits: Phenotypic (p) and genotypic (g) correlation between the various characters are presented in Table 3. Grain yield had positive and significant correlation with grain filling period, number of productive tillers per plant, number of spikelet spike⁻¹, spike length, number of kernels spike⁻¹, thousand kernel weights and biomass yield plot⁻¹ and harvest index at both phenotypic and genotypic levels. Generally, in those characters in which a gene conditioning an increase in one character will also influence another character provided that other conditions are kept constant. The works of [20] showed that wheat grain yield was positively and significantly correlated with spike length, biomass yield per plot⁻¹ and thousand grain weights, which support the present study.

Days to heading and plant height showed significant and negative correlation with grain yield plot⁻¹ at both phenotypic and genotypic levels. 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 finding agrees with the findings of [21] in ten candidate bread wheat lines.

Phenotypic and Genotypic Correlation: Estimates of phenotypic and genotypic correlation coefficient between each pair of characters are presented in Table 3. The results showed that, in general, the genotypic correlation coefficients (rg) were higher than the phenotypic correlation coefficients (rp) except in few cases, which indicated that association among these characters was under genetic control and indicating the presence of inherent association among these characters was under genetic control and indicating the preponderance of genetic variance in expression of characters. Days to heading showed positive and significant association with days to maturity and plant height at both phenotypic and genotypic levels. Selection for these characters can directly be followed for immediate yield improvement of wheat crop. However, it displayed negative and significant association with number of productive tiller plant⁻¹, number of kernels spike⁻¹, thousand kernel weight, biomass yield plot⁻¹, harvest index and grain yield plot⁻¹ at both phenotypic and genotypic levels. Days to maturity showed positive and significant association with grain filling period, plant height, number of productive tiller plant⁻¹, spike length, number of spikelet spike⁻¹, number of kernels spike⁻¹, thousand kernel weight, biomass yield plot⁻¹, at both phenotypic and genotypic level. Grain filling period also revealed that positive and significant association with plant height, spikelet spike⁻¹, spike length, harvest index and grain yield at both levels. Indicating that selection is based on these traits, grain yield could be achieved. The correlation between number of tillers plant⁻¹ and spike length, kernels spike⁻¹, thousand kernel weight, biomass yield plot⁻¹ and grain yield plot⁻¹ was positive and significant association at both phenotypic and genotypic levels. Suggesting that an increase in number of tillers plant⁻¹ could result from increase in all these traits and suggest that selections should be based on tillers plant⁻¹, spike length, number of kernels spike⁻¹, thousand kernels weigh and biomass yield plot⁻¹ for developing new wheat varieties and it may be effective traits to select higher yielding germplasm.

In addition, it showed that number of tillers plant⁻¹ and spike length, kernel spike⁻¹, thousand kernel weigh and biomass yield plot should be given prime importance regarding its contribution to grain yield plot⁻¹. These results are similar with [22]. Number of spikelet spike⁻¹ showed positive and significant association with spike length, kernels spike⁻¹, thousand kernel weight, biomass yield plot⁻¹, harvest index and grain yield plot⁻¹ at both phenotypic and genotypic level. Therefore, indirect selection for these traits may be effective in developing high yielding bread wheat cultivars and the findings of this result emphasized the role of number of spikelet spike⁻¹ upon ultimate increase of grain yield. Similarly, [23] reported that number of spikelet spike⁻¹ showed positive and significant association with thousand grain weights. Number of spikelet spike⁻¹ showed a significant and positive relation with spike length and yield as reported by [24]. Spike length showed positive and significant association with kernels spike⁻¹, thousand grain weights, biomass yield plot⁻¹ and grain yield plot⁻¹ at both phenotypic and genotypic level. The positive and significant association of spike length with spikelet spike⁻¹, thousand grain weight and biomass yield plot⁻¹ indicates that increased spike length would simultaneously increase the spikelet spike⁻¹, thousand grain weight and biomass yield plot⁻¹. Hence directly improve the grain yield. [25] have reported similar positive association between spike length and kernels spike⁻¹. Similar significant positive association among yield and spike length was also observed by [25] and [26]. Kernel spike⁻¹ showed positive and significant association with thousand kernel weight, biomass yield plot⁻¹, harvest index and grain yield plot⁻¹ at both phenotypic and genotypic level. Positive associations suggest that increased grain yield could be achieved if the selection is based on kernels spike⁻¹, harvest index and biological yield Table 4. These results are supported by the findings of [27] and [5] who observed significantly positive association between these traits. Thousand kernels weights showed positive and significant association with biomass yield plot⁻¹, harvest index and grain yield plot⁻¹ at both phenotypic and genotypic level. Suggesting the need of more emphasis on these components for increasing the grain yield in bread wheat. [24] Showed positive phenotypic and genotypic correlation of thousand grain weight with yield plot⁻¹. Biological yield plot⁻¹ showed positive and significant correlation with grain yield plot⁻¹ at both phenotypic and genotypic level. The significant and positive correlations

Table 3: Estimates of phenotypic (above diagonal) and genotypic (below diagonal) correlation coefficients among yield and yield components in 68 bread wheat germplasm

	HD	MD	GFP	PH	PT	SPS	SL	NK	TGW	BIM	HI	GY
HD	1	0.36**	-0.14 ^{ns}	0.87**	-0.32**	0.02 ^{ns}	-0.05 ^{ns}	-0.89**	-0.62**	-0.38**	-0.38**	-0.64**
MD	0.37**	1	0.52**	0.39**	0.24*	0.70**	0.43**	0.26*	0.57**	0.37**	0.05 ^{ns}	0.22 ^{ns}
GFP	-0.14 ^{ns}	0.52**	1	0.42**	0.16 ^{ns}	0.31**	0.25*	0.08 ^{ns}	0.18 ^{ns}	0.06 ^{ns}	0.24*	0.34**
PH	0.88**	0.39**	0.43**	1	-0.38**	-0.05 ^{ns}	-0.06 ^{ns}	-0.84**	-0.59**	-0.40**	-0.09 ^{ns}	-0.31**
PT	-0.34**	0.25*	0.16 ^{ns}	-0.39**	1	0.17 ^{ns}	0.32**	0.45**	0.41**	0.28*	0.05 ^{ns}	0.25*
SPS	0.02 ^{ns}	0.73**	0.32**	-0.05 ^{ns}	0.18 ^{ns}	1	0.77**	0.98**	0.81**	0.44**	0.29*	0.54**
SL	-0.05 ^{ns}	0.43**	0.29*	-0.06 ^{ns}	0.33**	0.81**	1	0.74**	0.53**	0.32**	0.05 ^{ns}	0.25*
NK	-0.91**	0.26*	0.08 ^{ns}	-0.85**	0.47**	0.99**	0.94**	1	0.98**	0.62**	0.77**	0.98**
TGW	-0.63**	0.58**	0.19 ^{ns}	-0.59**	0.43**	0.84**	0.67**	0.98**	1	0.61**	0.71**	0.98**
BIM	-0.38**	0.37**	0.06 ^{ns}	-0.40**	0.23*	0.46**	0.40**	0.63**	0.61**	1	-0.22 ^{ns}	0.44**
HI	-0.39**	0.05 ^{ns}	0.25*	-0.09 ^{ns}	0.06 ^{ns}	0.30*	0.07 ^{ns}	0.78**	0.71**	-0.22 ^{ns}	1	0.98**
GY	-0.65**	0.22 ^{ns}	0.35**	-0.31**	0.26*	0.57**	0.32**	0.98**	0.99**	0.44**	0.99**	1

t =0.23 (P<0.05) and t =0.302 (P<0.01) 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 spikelet spike⁻¹, NKPS= No. of kernels spike⁻¹, TKW=1000 kernel weight (g), BMY= Biomass yield plot⁻¹, HI= harvest index, GY= Grain yield plot⁻¹

Table 4: Estimate of direct effect (bold face and diagonal) and indirect effects (off diagonal) at genotypic level in 68 bread wheat germplasm tested at Kulumissa (2013)

Character	HD	MD	GFP	PH	PT	SPS	SL	NG	TGW	BIM	HI	r _e
HD	-0.088	-0.023	-0.006	0.045	-0.020	0.001	0.001	-0.021	-0.028	-0.108	-0.255	
MD	-0.025	-0.081	0.024	0.021	0.016	0.037	0.014	0.006	0.027	0.111	0.035	
GFP	0.010	-0.038	0.051	0.003	0.011	0.018	0.009	0.006	0.017	0.029	0.195	0.35**
PH	-0.057	-0.024	0.025	0.070	-0.024	-0.002	0.002	-0.020	-0.027	-0.115	-0.062	
PT	0.023	-0.017	0.007	-0.022	0.075	0.009	-0.011	0.012	0.020	0.090	0.043	0.26*
SPS	-0.001	-0.042	0.013	-0.002	0.010	0.071	-0.024	0.023	0.035	0.121	0.185	0.57**
SL	0.003	-0.028	0.011	-0.003	0.020	0.040	-0.042	0.018	0.025	0.095	0.040	0.32**
NK	0.046	-0.013	0.007	-0.035	0.023	0.040	-0.019	0.040	0.048	0.145	0.417	0.98**
TGW	0.030	-0.027	0.011	-0.023	0.019	0.030	-0.013	0.024	0.081	0.130	0.356	0.99**
BIM	0.023	-0.022	0.003	-0.020	0.016	0.021	-0.010	0.014	0.026	0.407	-0.140	0.44**
HI	0.028	-0.003	0.012	-0.005	0.004	0.016	-0.002	0.021	0.036	-0.072	0.792	0.99**

Residual= 0.2583

DH=days to heading, DM= days to maturity, GFP=grain filling period, PH= plant height (cm), NPTPP= No. of productive tillers plant⁻¹, SL= spike length (cm), NSPS =No. of spikelet spike⁻¹, NKPS=No. of kernels spike⁻¹, TKW=1000 kernel weight (g), GY= Grain yield kg ha⁻¹, BMY= Biomass yield kg ha⁻¹, HI =Harvest index

of biological yield and grain yield plant⁻¹ suggest that indirect selection for biological yield will also increase the grain yield. The positive association of biological yield with grain yield was also reported earlier by [28]. Harvest index also showed positive and significant association with grain yield plot⁻¹ at both phenotypic and genotypic level respectively. These findings indicated that increase in harvest index would increase grain yield in bread wheat.

Path Coefficient Analysis: Results presented in Table 4 shows path coefficient analysis of all traits on grain yield plot⁻¹. The harvest index which had positive and significant association with yield exerted maximum direct effect on grain yield. The second direct effect was exerted by biomass yield which had also positive and significant association with grain yield. These indicate the true relationship between these traits and grain yield. As a result these traits could be considered as important traits for selection in a breeding program for higher grain yield of the bread wheat germplasm. However, spike length had negative direct effect on grain yield and showed

significant and positive correlation on grain yield. It had also exerted considerable direct effect on grain yield. These results are consistent with the findings of [29] for biomass yield plot⁻¹ and harvest index. The indirect effect of number of tillers plant⁻¹, number of spikelet spike⁻¹, spike length, number kernel spike⁻¹, thousand kernel weight and biomass yield plot⁻¹ on grain yield mostly through biomass yield plot⁻¹ and harvest index respectively. Similarly, the indirect effect of harvest index on grain yield mostly through biomass yield plot⁻¹ and thousand grain weights. Residual effect in the present study was (0.2583) (Table 4) which means the characters in the path analysis expressed the variability in grain yield by 74.17% and the remaining 25.86% needs additional characterization for the future breeding program. Similar, result reported by [24], [1].

CONCLUSIONS

The present study comprises sixty four bread wheat germplasm with four standard checks were evaluated at Kulumsa Agricultural Research Center with the objective

of estimate the extent of association between pairs of characters at genotypic and phenotypic levels and thereby compare the direct and indirect effects of the characters. Analysis of variance (ANOVA) study revealed that highly significant differences were obtained among the treatments for all the twelve selected quantitative characters, which indicated adequate variability exists among the germplasm considered in this study. The estimates of ranges of mean values revealed that bread wheat germplasm possess good amount of genetic variability. Correlation analysis showed that grain yield per plot had a positive and significant phenotypic and genotypic association with grain filling period, number of productive tillers per plant, number of spikelet spike⁻¹, spike length, number of kernels spike⁻¹, thousand kernel weights, biomass yield plot⁻¹ and harvest index. By selecting for those traits showing positive and significant correlation with grain yield there is possibility to increase grain yield of bread wheat. Path analysis revealed that maximum positive direct effects with significant positive correlation on grain yield was exerted by harvest index followed by biomass yield plot⁻¹. Since harvest index and biomass yield had positive correlation with grain yield in the process of selection much attention should be given to them as these characters are helpful for in direct selection. Thus, there is an opportunity to bring about improvement of the crop yield through direct selection as well as improving of these characters through hybridization using the germplasm collections in Ethiopia. Harvest index and biological yield showing positive and significant correlation and positive direct effect, these for indirect selection to increase grain yield. Productive tillers per plant, spikelet spike⁻¹, spike length, kernel spike⁻¹ thousand grain weight and harvest index showed positive correlation and direct effect on grain yield, these traits may be included as components of indirect selection. This finding, being the result of one year with single location, it is recommended that the experiment should be repeated at multi locations for several years to confirm the obtained results.

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REFERENCES

1. Mollasadeghi, V. and R. Shahryari, 2011. Important morphological markers for improvement of yield in bread wheat. *Advances Environ. Biol.*, 5(3): 538-542.
2. Ranjana and Suresh Kumar, 2013. Study of genetic variability and heritability over extended dates of sowing in bread wheat (*Triticum aestivum* L.). *Research in Plant Biology*, 3(1): 33-36.
3. Shashikala, S.K., 2006. Analysis of genetic diversity in wheat. M.Sc. (Agri.) Thesis, University of Agricultural Sciences, Dharwad, India.
4. Rizwana Maqbool, Muhammad Sajjad and Ihsan Khaliq, 2010. Morphological diversity and traits association in bread wheat (*Triticum aestivum* L.). *American-Eurasian J. Agric. Environ. Sci.*, 8(2): 216-224.
5. Akram, Z., S. Ajmal and M. Munir, 2008. Estimation of correlation coefficient among some yield parameters of wheat under rain fed conditions Pakistan *J. Bot.*, 40(4): 1777-1781.
6. Gomez, K.A. and A.A. Gomez, 1984. *Statistical Procedures for Agricultural Research*. 2nd (ed). John Wiley & sons, Inc. New York.
7. Falconer, D.S. and T.F.C. Mackay, 1996. *Introduction to Quantitative Genetics*. 4th Ed. Longman, Essex, England.
8. Bhatt, G.M., 1973. Significance of path coefficient analysis in determining the nature of character association. *Euphytica*, 22: 338-343. *Biotechnology and Conventional Approaches*. Narosa Publishing House, New Delhi, pp: 604.
9. Sidwell, R.J., E.L. Smith and R.W. McNew, 1967. Inheritance and interrelationships of grain yield and selected yield related traits in a hard red winter wheat cross. *Crop. Sci.*, 16: 650-654
10. Wright, S., 1921. Correlations and causations. *Journal of Agricultural Research*, 20: 557-587.
11. Roy, D., 2000. *Plant Breeding Analysis and Exploitation of Variation*. Narosa Publishing House. New Delhi. India.

12. Federer, W.T., 1956. Augmented (or hoonuiaku) designs. Hawaii. Plant. Rec., 55: 191-208.
13. SAS, 2008. Statistical Analysis System. Version 9.2, SAS Institute Inc., Cary, NC., USA.
14. GENRES statistical software, 1994. Data entry module for Pascal intlsoft ware solution.
15. Dewey, D.R. and K.H. Lu, 1959. A correlation and path-coefficient analysis of components of crested wheat grass seed production. Agronomy Journal, 42: 515-517.
16. Kalimullah, S.J. Khan, M. Irfaq and H.U. Rahman, 2012. Genetic variability, correlation and diversity studies in bread wheat (*Triticum aestivum* L.) germplasm. The Journal of Animal and Plant Sciences, 22(2), Page: 330-333, ISSN: 1018-7081, Page: 330-333 ISSN: 1018-7081, Khan, Pakistan.
17. Radhu, A.S., S.K. Solanki and I. Singh, 1995. Genetic diversity in some Indian and exotic wheat varieties. Crop Improvement, 22(2): 214-217.
18. Maqbool, R., M. Sajjad, I. Khaliq, Aziz-ur-Rehman, A.S. Khan and S.H. Khan, 2010. Morphological diversity and traits association in bread wheat (*Triticum aestivum* L.). Am. Eurasian J. Agric. Environ. Sci., 8: 216-224.
19. Sajjad, M., S.H. Khan and A.S. Khan, 2011. Exploitation of germplasm for grain yield improvement in spring wheat (*Triticum aestivum*). Int. J. Agric. Biol., 13: 695-700.
20. Virk, T.S. and S.C. Anand, 1970. Studies on correlation and their implication in wheat (*Triticum aestivum* L.). Madras Agric. J., 57: 713-717.
21. Mohammad, S. Haider, M. Amin, M.I. Khan and R. Zamir, 2005. Path coefficient and correlation studies of yield and yield associated traits in candidate bread wheat (*T. aestivum* L.) Lines. Suran. J. Sci. Technol., 13: 175-180.
22. Inamullah, H. Ahmad, F. Muhammad, Sirajuddin, G. Hassan and R. Gul, 2006. Diallel analysis of the inheritance pattern of agronomic traits of bread wheat. Pak. J. Bot., 38(4): 1169-1175.
23. Khokhar, M.I., M. Hussain, M. Zulkiffal, N. Ahmad and W. Sabar, 2010. Correlation and path analysis for yield and yield contributing characters in wheat (*Triticum aestivum* L.). Afr. J. Plant Sci., 4(11): 464-466.
24. Ali, Y., B.M. Atta, J. Akhter, P. Monneveux and Z. Lateef, 2008. Genetic variability, association and diversity studies in wheat (*Triticum aestivum* L.) germplasm. Pak. J. Bot., 40: 2087-2097.
25. Khaliq, I., N. Parveen and M.A. Chowdhry, 2004. Correlation and Path Coefficient Analyses in bread wheat. Int. J. Agri. Biol., 6: 633-635.
26. Saleem, U., I. Khaliq, T. Mahmood and M. Rafique, 2006. Phenotypic and genotypic correlation coefficients between yield and yield components in wheat. J. Agric. Res., 44: 1-5.
27. Akhtar, N. and M.A. Chowdhary, 2006. Estimation of genetic and phenotypic correlation coefficients among grain yield and its components in bread wheat. Int'l. J. Agric. Biol., 8(4): 516-522.
28. Singh, K.N., S.P. Singh and G.S. Singh, 1995. Relationship of physiological attributes with yield components in bread wheat (*Triticum aestivum* L.) under rain-fed condition. Agric. Sci. Digest (Karnal) India, 15: 11-4.
29. Ali, I.H. and E.F. Shakor, 2012. Heritability, variability, genetic correlation and path analysis for quantitative traits in durum and bread wheat under dry farming conditions. Mesopotamia J. Agri., 40(4): 27-39.