SciencePG
Science Publishing Group

Associations Studies Among Yield, Yield Components and Quality Traits in Advanced Bread Wheat (*Triticum aestivum* l.) Genotypes at Sinana, South Eastern Ethiopia

Hiwot Sebsibe[1, *], Bulti Tesso[2], Tesfaye Letta[3]

[1]Sinana Agricultural Research Centre, Robe, Ethiopia

[2]College of Agriculture and Environmental Sciences, Haramaya University, Haramaya, Ethiopia

[3]Oromia Agricultural Research Institute, Addis Ababa, Ethiopia

Email address:

hiwotsebsibe@yahoo.com (Hiwot Sebsibe)
[*]Corresponding author

To cite this article:

Abstract: Information on the extent of genetic variation and associations among characters is important to design optimum breeding strategies and to develop varieties for the targeted area of production. Therefore, this research was conducted at Sinana Agriculture Research Centre on testing site, south eastern Ethiopia, with the objectives of to assess associations among yield, yield components and quality traits, and to determine the extent of direct and indirect effects of yield related traits on yield. The experiment was conducted in 2020/21 cropping season using 21 promising lines and 4 released varieties in lattice Design with three replications. Data were recorded for 9 agronomic and 13 grain quality characters. Analysis of variance revealed the presence of highly significant ($P \leq 0.01$) variation among genotypes. Grain yield had high genotypic correlation with day to heading, spike length and spikelet per spike in the process of selection much attention should be given to them as these characters are helpful. Day to heading and spikelets per spike had strong and positive direct effect on grain yield, but, spike length had negative direct effect.

Keywords: Association, Genetic Variation, Quality Traits

1. Introduction

Wheat is cultivated in every continent except Antarctica. It is grown at a wide elevation ranging from 260 m.a.s.l (Jordan Valley) up to 4,000 m.a.s.l (Tibetan plateau) [15]. The crop is adapted to a broad range of moisture conditions from xerophytic to littoral. Although about three-fourths of the land area where wheat is grown receives an average between 375 and 875 mm of annual precipitation, it can also grow in most locations where rainfall ranges from 250 to 1750 mm [8]. The various characteristics of crop plants are generally interrelated or correlated. Such correlations can be either negative or positive. In plant genetics and breeding studies, correlated characters are of prime importance because of genetic causes of correlations through pleiotropic action or developmental interactions of genes and changes brought about by a natural or artificial selection [27, 9, 25]. The association between two characters that can be directly observed is the correlation of phenotypic values or phenotypic correlations (rp). Phenotypic correlations measure the extent to which the two observed characters are linearly related. It is determined from measurements of the two characters in a number of individuals of the populations.

Genetic correlation (rg) is the associations of breeding values (*i.e.* additive genetic variance) of the two characters. Genetic correlation measures the extent to which degree the same genes or closely linked genes cause co-variation (simultaneous variations) in two different characters. The correlation of environmental deviations together with non-additive genetic deviations (*i.e.* dominance and epistatic genetic deviations) is referred to as environmental

correlations (re) [28, 9, 25] Studies on genotypic and phenotypic correlations among characters of crop plants are useful in planning, evaluating and setting selection criteria for the desired characters for selection in breeding program [14, 3]. Correlations between different characters of a crop plant may arise either from genotypic factor or environmental factors. Environmental correlations arise from the effect of overall environmental factors and that vary at different environments [27, 9]. Estimate of correlations and significance test was previously discussed by several workers [28, 25]. Depending on the sign, genetic correlations between two characters can either facilitate or impede selection progress.

Wright, S. [31] developed path coefficient analysis, which is a standardized partial regression analysis that helps in partitioning the correlation coefficients in to direct and indirect effects. The use of this method requires a cause and effect situation among the variables, and the experimenter must assign direction in the causal system based upon priori grounds or experimental evidences [16]. Grain yield in wheat is a complex character affected directly or indirectly by every gene present in the plant. Genotypic and phenotypic correlations are of value to indicate the degree to which various morpho-physiological characters are associated with economic productivity [1]. 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.

2. Materials and Methods

Description of experimental sites and experimental materials the experiment was conducted during the cropping season of 2020/21 at two locations, Sinana Agricultural Research Center (SARC) on station. SARC station is located 070 07' N latitude and 400 10' E longitude and at an altitude of 2400 meters above sea level. The soil texture type of the area is clay loam having black color and the soil pH ranges between 6.3-6.8 (SARC, 2013). The amount of rainfall from August to December 2020/21, during crop growing seasons, was 401.5 mm. The monthly mean maximum and minimum temperatures were 24.5°C and 14.4°C, respectively. The experimental materials comprised of 21 bread wheat genotypes and 4 released varieties obtained from SARC. The genotypes were retained from the 2019 bread wheat regional variety trials at SARC. The details of the genotypes are summarized in Table 1.

2.1. Experimental Design and Trial Management

The experiment was laid out in 5×5 triple lattice design. The plot size was 6 rows of 2.5 m length with 0.2 m spacing between rows (with a gross plot size of 3m^2), and the spacing between plots and blocks was 0.4 m and 1m, respectively. Planting was done by hand drilling. Seed rate was 150 kg/ha

(45 g/plot) and Urea and DAP fertilizers were applied at the rate of 50 kg/ha and 100 kg/ha, respectively. The field was weeded twice by hand (at 25 and 45 days after planting). For data collection, the middle four rows were used (2 m^2 area). All cultural practices were applied uniformly to all experimental units.

Data Collected: Random homogeneous grain samples in replicates each genotype were used for laboratory analysis.

Days to heading: It was recorded as the number of days from planting to 50% heading on plot basis.

Days to physiological maturity: The number of days from date of planting to the stage when 75% of the plants in the plot reached at physiological maturity.

Plant height (cm): Measured from the soil surface to the tip of the spike excluding the awns at physiological maturity.

Number of tillers per plant: Tillers were counted on 10 randomly sampled plants from central rows of each plot and the average of the ten observations was used for analysis.

Spike length (cm): This was measured from the bottom of the spike to the tip of the spike excluding the awns from 10 randomly selected spikes from each plot.

Spikelets per spike: The average number of spikelets per spike of ten plants in each plot.

Kernel per spike: The average number of kernels per spike of ten plants in each plot.

Grain yield (t/ ha): Grain yield was estimated from grain yield (g/plot). Grain yield in grams per plot was measured from plants in the central four rows of each plot and adjusted to 12.5% moisture content. Then, grain yield (g/plot) of each plot was used to estimate grain yield per hectare in tons.

Harvest Index: It was calculated as the ratio of grain yield to total above ground biomass.

Thousand kernel weight (g): The weight of randomly sampled 1000 kernels.

Hectolitre weight (kg/hl): Weight of one-liter volume random sample of grain for each experimental plot.

Average kernel length (AKL): Was determined using a digital caliper by aligning 10 sets of 25 seeds end to end (brush to germ) putting crease down.

Average kernel width (KW): Was measured on the respective sets of 25 seeds by placing the seed crease down, side by side so that each contacted adjacent seed was taken at their widest points using digital caliper.

Average kernel thickness (AKT): Was measured in the same manner on respective sets of 25 seeds by placing them with the edge of the kernels.

Protein content (%) and moisture content (%): Were determined using Mininfra SmarT Grain Analyzer.

Wet and dry gluten content: Wet Gluten was prepared from whole meal by the Glutomatic 2200 gluten wash chamber. Gluten Index Centrifuge 2015 was used to force the wet gluten through a specially designed sieve cassette. The wet gluten is further dried in the Glutork 2020 for dry gluten content.

$$\text{Gluten index (\%)} = \frac{\text{Gluten remaining on the sieve (g)}}{\text{Total gluten (g)}} \times 100$$

Wet Gluten content (WGC) = Total wet gluten (g) × 10

Dry Gluten content (DGC) = Dry gluten weight (g) × 10

Sodium Dodecyl Sulfate (SDS) sedimentation test: The SDS sedimentation volume was measured according to AACC Method No. 56-70 (AACC, 2000).

Vitreoussneous: Kernel vitreosity was estimated by using transmitted light according to ICC standard number 129 (ICC, 2000).

Grain hardness (%): was determined by particle size index (PSI) method as described in the AACC method 55-31 (AACC, 2000).

Data Analysis: The SAS GLM (General Linear Model) procedure SAS Institute Inc (2002) was employed for the analysis of variance. Duncan's Multiple Range Test (DMRT) at 5% probability level was used for mean comparisons, whenever genotypes differences were significant. Comparison of the relative efficiency of lattice design to Randomized Complete Block Design (RCBD) was done after data were analyzed for both designs and it showed that less efficient than RCBD. Therefore, for the flexibility of lattice design the data were analyzed as per RCBD.

2.2. Estimation of Phenotypic and Genotypic Correlations

Phenotypic and genotypic correlations between yield, yield related and quality traits were estimated using the method described by Miller [19].

$$\text{Phenotypic correlation} = \frac{\text{Phenotypic covariance of X and Y}}{\sqrt{(\sigma^2_{ph}\,X \times \sigma^2_{ph}\,Y)}}$$

$$\text{Genotypic Correlation} = \frac{\text{Genotypic covariance of X and Y}}{\sqrt{(\sigma^2_{g}X \times \sigma^2_{g}\,Y)}}$$

Where; $\sigma^2_{ph}x$ = Phenotypic variance of trait x, $\sigma^2_{ph}y$ = Phenotypic variance of trait y, $\sigma^2_{g}x$ = Genotypic variance of trait x, and $\sigma^2_{g}y$ = Genotypic variance of trait y.

2.3. Path Coefficient Analysis

The direct and indirect effect of yield related and quality traits on grain yield per plot has been analyzed through path coefficient analysis. This analysis was computed as suggested by Dewey [7] using the following formula.

$$rij = Pij + \Sigma rikpkj$$

Where: rij= mutual association between the independent (i) and dependent character (j) as measured by the correlation coefficient. Pij= component of direct effects of independent character (i) and dependent character (j) as measured by the path coefficient and, Σrikpkj= summation of components of indirect effect of a given independent character (i) on the given dependent character (j) via all other independent character (k). The residual effect was estimated by the formula:

Table 1. Description of bread wheat genotypes used in the experiment.

S.N	Genotype	Pedigree
1	ETBW 7866	CHUANMAI32//2*INQALAB 91*2/KUKUNA
2	ETBW 7524	PBW343*2/KUKUNA//AKURI
3	ETBW 7402	QUAIU/5/FRET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ
4	ETBW 7559	ROLF07*2/5/FCT/3/GOV/AZ//MUS/4/DOVE/BUC
5	ETBW 7661	TUKURU//BAV92/RAYON/3/FRNCLN
6	ETBW 7409	ROLF07*2/5/REH/HARE//2*BCN/3/CROC_1/AE.SQUARROSA (213)//PGO/4/HUITES
7	ETBW 7528	BABAX/LR42//BABAX*2/3/KUKUNA/4/TINKIO #1
8	ETBW 7527	JUCHI/HUIRIVIS #1
9	ETBW 6114	SOKOLL//SUNCO/2*PASTOR
10	ETBW 7698	FRNCLN/4/WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1
11	ETBW 7638	ATTILA/3*BCN*2//BAV92/3/KIRITATI/WBLL1/4/DANPHE
12	ETBW 7797	SERI.1B*2/3/KAUZ*2/BOW//KAUZ/4/PFAU/MILAN
13	ETBW 6873	WBLL*2/KUKUNA/5/PSN/BOW//SERI/3/MILAN/4/ATTILA/6/WBLLI*KKTS
14	ETBW 7729	MUNAL/3/KIRITATI//PRL/2*PASTOR/4/MU
15	ETBW 8005	SERI.1B//KAUZ/HEVO/3/AMAD/4/FLAG-2
16	ETBW 7998	SERI.1B//KAUZ/HEVO/3/AMAD/4/FLAG-2
17	ETBW 8003	SERI.1B//KAUZ/HEVO/3/AMAD/4/FLAG-2
18	ETBW 7715	MILAN/S87230//BAV92/3/AKURI#1/4/MILAN/S87230//BAV92
19	ETBW 7595	SKAUZ/BAV92//2*WBLL1*2/KKTS
20	ETBW 7435	WAXWING*2/4/BOW/NKT//CBRD/3/CBRD
21	ETBW 7718	MUNAL/3/KIRITATI//PRL/2*PASTOR/4/MUNAL
22	Dambel (2015)	AGUILAL/3/PYN/BAU//MILAN
23	Sanete (2014)	14F/HAR1685
24	Sofumer (2000)	LIRA/TAN
25	Madawalabu (2000)	TL/3/FN/NAR59*2/4/BOL'S'

3. Results and Discussion

Results of analysis of variance for 22 characters of bread wheat genotypes tested is presented in Table 2. ANOVA results based on simple lattice and RCBD designs gave similar coefficient of variation (CV) values for most traits and were comparable in efficiency. Thus, ANOVA based on RCBD was used because of easiness in analysis for estimation of components of variances. Significant

differences among genotypes (with P values from <0.05 to <0.01) were observed for all traits Table 2).

Table 2. Mean squares from analysis of variance for 22 characters of 25 bread wheat genotypes evaluated.

Character	Replication (Df=2)	Genotype (Df=24)	Error (Df=48)	CV (%)
DH	7.20[ns]	12.2**	4.90	3.50
DM	306.41**	6.10*	3.76	1.57
NT	1.43[ns]	1.08*	1.19	14.58
PH	12.60[ns]	53.72**	7.14	3.07
SL	0.057[ns]	1.89**	0.17	4.33
SPS	3.92**	2.34**	0.72	5.22
KPS	14.42[ns]	70.31**	13.82	8.93
YpHa	0.59[ns]	0.60*	0.38	11.2
HI	40.42[ns]	42.57*	26.89	11.52
TKW	13.10**	21.54**	1.56	2.67
HLW	5.26[ns]	3.50*	3.20	2.12
WGC	0.66[ns]	140.88**	1.29	3.43
DGC	1.68[ns]	19.02**	0.67	6.80
GI	81.33[ns]	200.14**	60.14	10.03
GH	23.48[ns]	10.22*	15.09	16.95
KL	0.006[ns]	0.14**	0.009	1.43
KW	0.006[ns]	0.036**	0.003	1.72
KT	0.008[ns]	0.03**	0.004	2.31
VI	42.87**	12.86**	5.03	2.36
MC	0.01[ns]	0.21**	0.04	2.28
PC	33.19**	1.91**	0.72	6.36
SDS	28.49[ns]	412.7**	14.09	5.71

*, ** and ns, significant at P<0.05, P<0.01 and non-significant, respectively Df=degrees of freedom. CV= coefficient of variation, DH=days to heading, DM= days to maturity, NT=number of tillers per plant, PH= plant height, SL= spike length, SPS= spikelets per spike, KPS= kernel per spike, YpHa= grain yield (t ha^{-1}), HI= harvest index, TKW= thousands kernel weight, HLW=hectolitre weight, WGC= wet gluten content, DGC= dry gluten content, GI= gluten index, GH=grain hardness, KL=kernel length, KW= kernel width, KT=kernel thickness, VI= vitreousness, MC=moisture content, PC= protein content, SDS= sodium dodecyl sulfate sedimentation test.

3.1. Genotypic Correlation of Grain Yield with Other Characters

The analysis revealed that grain yield per hectare had positive and highly significant genotypic correlation with days to heading, spike length and number of spikelets per spike, indicating that genotypes with late heading, long spike and large number of spikelets per spike produce higher grain yield than those with early heading, short spike and small number of spikelets per spike. Grain yield per hectare also showed positive and significant correlation with harvest index and thousand kernel weight. Mohammed and Kifle [20, 17] also reported significant positive association between grain yield and day to heading. The highly significant positive association between grain yield and spike length found in the present study agrees well with the reports of Khan, Tazeen and Waleed [16, 29 and 30]. Several previous studies had also reported positive association of grain yield with the number of spikelets per spike Ihsan and Yakubu [13, 32] and thousand kernel weight [22]. [4] also found positive and significant association of harvest index with grain yield in some triticale genotypes. Ermias, Yonas and Yuksel [8, 33, 34] reported weak negative associations of grain yield with

grain quality characters and with grain protein content and similar results were observed in the current study.

3.2. Genotypic Correlations Among Other Characters

Days to heading had highly significant positive genotypic correlation with spike length, number of spikelets per spike and number of kernel per spike, whereas it exhibited positive and significant association with kernel width and moisture content. The results indicate that, late heading genotypes had long spikes and more number of spikelets per spike. Similar results were also reported by Shashikala and Shahnawaz [26, 24] for the association of the same trait with spike length and number of spikelet per spike. Related results were also reported by [6] who reported highly significant association of days to heading with spikelets per spike. Days to maturity showed significant positive association with grain moisture and protein contents, negatively associated with harvest index recorded. Alemu [2] also found similar result for harvest index. Plant height had significant positive correlations with spike length, thousand kernels weight and kernel length. The result agrees with previous reports for correlation between plant height and spike length [35], and for correlation between plant height and thousand kernel wheat Ihsan and Berhanu [13, 5]. The number of tillers showed highly significant negative association with the number of spikelets per spike. It showed significant negative association with kernel per spike. Khan [16] reported a similar result for the association of the number of tillers with the number of spikelet per spike. Spike length had positive and highly significant correlation with number of spikelets per spike, number of kernel per spike and thousand kernel weight, which was in close agreement with the finding of Shahnawaz [24]. Significant positive association was observed between spike length and kernel length and between kernel width and moisture content.

Thousand kernels weight showed positive and highly significant association with spike length and kernel width and significant positive association with kernel length, plant height, and gluten index. Moslem [21] also reported similar result. However, highly significant negative association of thousand kernel weight with grain protein content was observed. Berhanu [5] also reported similar result. Wet gluten content exhibited highly significant positive correlation with dry gluten content, and significantly correlated with grain protein content. The result indicated that genotypes with high wet gluten content would generate significant dry gluten content. These results are consistent with the findings of Berhanu and Mohammed [5, 20]. However, wet gluten content showed significant negative association with gluten index and kernel length. Gluten index had significant positive association with SDS sedimentation, and similar result also reported by Mohammed [20] for SDS sedimentation. The degree of vitreousness of bread wheat is related to protein and its composition in the grain, which signifies the observed positive correlation. Yonas [33] also found similar association between these traits. Similarly, grain vitreousness had significant positive correlation with SDS sedimentation.

Table 3. *Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients of 22 yield, yield related and quality traits in bread wheat genotypes at Sinana (2016).*

Traits	DH	DM	NT	PH	SL	SPS	KPS	YpHa	HI	TKW	HLW	WGC
DH		0.35	-0.08	0.14	0.59**	0.54**	0.60**	0.63**	-0.09	0.31	-0.01	0.12
DM	0.16		0.12	0.26	0.05	0.06	-0.13	0.18	-0.42*	0.04	-0.33	0.34
NT	-0.01	0.01		-0.16	-0.15	-0.52**	-0.46*	0.06	0.05	-0.01	0.03	-0.06
PH	0.04	0.11	0.03		0.41*	0.30	-0.09	0.35	0.09	0.44*	-0.06	-0.06
SL	0.36**	0.02	-0.04	0.34**		0.53**	0.50**	0.51**	0.23	0.58**	-0.04	-0.07
SPS	0.27*	0.27*	-0.18	0.21	0.53**		0.49*	0.46**	0.08	0.32	-0.01	-0.17
KPS	0.42**	-0.02	-0.21	-0.09	0.43**	0.44**		0.26	-0.04	0.29	-0.10	0.19
YpHa	0.34**	-0.14	0.15	0.35**	0.37**	0.29**	0.16		0.42*	0.41*	0.12	-0.17
HI	0.07	0.14	0.05	0.10	0.13	-0.07	-0.12	0.47**		0.40*	0.16	-0.30
TKW	0.24*	0.04	-0.06	0.38**	0.48**	0.28*	0.25*	0.25*	0.21		0.15	0.02
HLW	0.11	0.15	0.06	0.02	0.00	0.01	-0.01	-0.02	0.11	0.15		-0.03
WG	0.07	-0.03	-0.04	-0.05	-0.07	-0.12	-0.02	-0.12	-0.19	0.01	-0.02	
DG	-0.17	0.07	-0.10	-0.12	-0.14	-0.14	0.16	-0.18	-0.11	-0.02	-0.06	0.69**
GI	0.17	-0.22	-0.11	-0.13	0.20	0.29*	0.06	0.09	0.09	0.00	-0.01	-0.32*
GH	-0.04	-0.02*	0.03	0.16	-0.08	-0.19	0.27*	0.22*	0.14	0.03	0.03	0.11
KL	0.18	0.05	0.04	0.36**	0.41**	0.24*	-0.12	0.20	0.00	0.39**	-0.05	-0.39*
KW	0.23*	0.00	-0.18	0.24*	0.38**	0.24*	0.14	0.23*	0.21	0.54**	0.04	0.17
KT	-0.21	-0.02	0.06	0.04	0.10	-0.23*	0.23*	-0.01	0.25	0.21	-0.01	0.01
VI	0.07	-0.33**	0.02	-0.03	0.08	0.00	-0.05	0.18	0.20	-0.20	0.24*	-0.08
MC	0.30**	0.04	-0.09	0.39**	0.36**	0.25*	0.17	0.20	-0.21	0.34**	0.03	-0.08
PC	-0.09	-0.42**	0.20	-0.09	-0.12	-0.21	-0.05	-0.03	0.03	-0.52*	-0.23*	0.22
SDS	-0.12	-0.17	-0.14	-0.17	0.14	-0.07	0.16	-0.08	0.22*	-0.16	-0.12	-0.05

Table 3. *Continued.*

Traits	DGC	GI	GH	KL	KW	KT	VS	MC	PC	SDS
DH	-0.21	0.12	-0.23	0.26	0.40*	-0.30	-0.14	0.49*	-0.05	-0.17
DM	0.13	-0.37	0.07	-0.09	0.22	-0.01	-0.16	0.39*	0.41*	-0.29
NT	-0.18	-0.34	0.05	-0.01	-0.25	0.04	-0.28	-0.22	-0.02	-0.20
PH	-0.12	-0.09	0.26	0.42*	0.25	-0.02	-0.04	0.53**	-0.23	-0.19
SL	-0.14	0.32	-0.15	0.46*	0.44*	0.15	0.11	0.40*	-0.28	0.18
SS	-0.12	0.33	-0.18	0.28	0.35	-0.31	0.23	0.28	-0.14	-0.05
KPS	0.08	0.28	-0.13	0.21	0.37	-0.14	-0.05	0.18	-0.02	0.21
YpHa	-0.31	0.18	-0.04	0.31	0.24	-0.16	0.16	0.32	-0.27	-0.15
HI	-0.18	0.29	0.13	0.06	0.30	0.33	0.29	-0.23	-0.36	0.34
TKW	0.00	-0.04	0.00	0.41*	0.55**	0.23	-0.16	0.35	-0.62**	-0.14
HLW	0.02	-0.08	-0.21	-0.17	0.08	-0.14	0.38	0.04	-0.32	-0.21
WG	0.72**	0.42*	0.21	0.42*	0.20	0.00	-0.07	-0.08	0.39*	-0.05
DG		-0.23	0.25	-0.36	0.06	0.20	0.13	-0.23	0.29	0.13
GI	-0.25*		-0.21	0.20	0.21	0.22	0.28	-0.14	0.03	0.49*
GH	0.13	-0.07		0.12	-0.11	0.10	0.17	-0.16	0.25	0.31
KL	-0.37*	0.19	0.07		-0.12	-0.10	-0.25	0.43*	0.43*	0.01
KW	0.05	0.15	0.01	-0.07		0.31	0.15	0.12	0.06	0.16
KT	0.17	0.16	0.09	-0.06	0.24*		0.12	-0.08	0.04	0.25
VS	0.11	0.08	0.17	-0.19	0.06	0.01		-0.30	0.26	0.41*
MS	-0.19	-0.07	0.00	0.37**	0.11	-0.05	-0.15		-0.24	0.45*
PR	0.21	-0.14	0.12	-0.23*	-0.01	0.00	0.38**	-0.17		0.36
SDS	0.12	0.37**	0.17	0.02	0.14	0.18	0.29**	0.40**	0.26*	

*and ** significant at P<0.05 and P<0.01, respectively, DH=days to heading, DM= days to maturity, NT=number of tiller, PH= plant height, SL= spike length, SPS= spikelet per spike, KPS= kernels per spike, YpHa= grain yield t ha-1, HI= harvest index, TKW= thousands kernel weight, HLW=hectolitre weight, WGC= wet gluten content, DGC= dry gluten content, GI= gluten index, GH=grain hardness, KL=kernel length, KW= kernel with, KT=kernel thickness, VI= vitreousness, MC=moisture content, PC= protein content, SDS= sodium dodecyl sulfate sedimentation test.

3.3. Phenotypic Correlation of Grain Yield with Other Characters

Grain yield was positively and highly significantly correlated with day to heading, number of spikelets per spike and harvest index. It also showed significant positive correlation with thousand kernels weight, grain hardness and kernel width. This is in good agreement with the findings of Gupta and Khan [10, 16]. Hasan and Obsa [11, 22] had also reported significant positive association of grain yield with number of spikelets per spike and thousand kernels weight at phenotypic level. Similar associations were also reported by Majumder [18], indicating that improvement of these characters can increase the grain yield of bread wheat. However, Degewione [6] reported negative correlation between grain yield and day to heading, which is contrary to

the present result.

Grain yield was positively and highly significantly correlated with spike length and plant height at phenotypic level, indicating that, genotypes with tall plant height and long spikes produce high grain yield than those with short plant height and short spikes. Hectolitre weight, wet gluten content and dry gluten content, kernel thickness, and SDS sedimentation volume had non-significant negative correlation with grain yield. Majumder and Degewione [18, 6] reported non-significant positive correlations of grain yield with plant height, spike length and thousand kernels weight, while also reported non-significant positive association between grain yield and SDS sedimentation volume. However, non- significant negative correlation of grain yield with other characters was reported by Ermias [8].

The association between grain yield and protein content was negative, which is consistent with known theoretical facts related to the inverse relationship between starch and protein accumulation during grain development. The inverse relationship between protein content and grain yield was found in numerous works in wheat [22, 8, 33]. Protein content, which is one of the most important traits in quality evaluation and breeding of bread wheat, is known to be influenced mainly by climatic parameters, genotype and nitrogen fertilizer rate, time of nitrogen application, residual soil nitrogen and available moisture during grain filling. The percentage protein in the grain increases with the increase of temperature and nitrogen supply, whereas the quality of proteins per grain is affected negatively by high temperatures. Selection for protein content in environmental conditions on protein content is a further constraint in bread wheat breeding. Correlation between different characteristics generally results from the environment and genetic factors such as the presence of linked genes and the epistatic effect of different genes [21].

3.4. Path Coefficient Analysis

Phenotypic and genotypic correlations were analyzed to identify the important yield attributes by estimating their direct and indirect effects on grain yield. The analysis was conducted using grain yield as dependent variable and all other traits studied as independent variables.

3.5. Direct and Indirect Effects of Various Characters on Grain Yield at Genotypic Level

Study of relationship between yield, yield contributing characters and quality traits through genotypic path coefficients analysis revealed that days to heading, number of tillers, plant height, number of spikelets per spike, harvest index, days to maturity, wet gluten content, gluten index, kernel length, kernel thickness, number of kernel per spike, vitreousness, grain moisture content and SDS sedimentation had exerted positive direct effects on grain yield with the range of values 0.06 for kernel thickness and 0.84 for number of kernel per spike. Traits with large direct effects have high contribution to grain yield and could be considered as main

components of selection in a breeding program for obtaining higher grain yield. Similar results were also reported by Obsa [22] for the number of spikelets per spike by Yonas and Degewione [33, 6] also reported consistent with present finding. Negative and small direct effects on grain yield were exerted through spike length, thousand kernels weight, hectolitre weight, dry gluten content, grain hardness, kernel width and grain protein content in the range of values -0.07 for hectolitre weight and -0.99 for grain protein content. The negative direct effects of these traits on grain yield indicate that selection for these traits will hinder improvement for yield. Days to heading showed negative indirect effects on grain yield via number of tillers, spike length, harvest index, thousand kernel weight, kernel width, kernel thickness, vitreousness and SDS sedimentation volume.

The indirect effects of days to heading via plant height, number of spikelets per spike, day to maturity, wet gluten and dry gluten content, gluten index, grain hardness, kernel length, number of kernel per spike, grain moisture content and protein content were positive.

This result is in line with the finding of Kifle [17] who reported positive indirect effect of days to heading through the number of spikelets per spike and plant height. Spike length had exerted a positive indirect effect on grain yield via day to heading, day to maturity, plant height, number of spikelets per spike, harvest index, dry gluten content, gluten index, grain hardness, kernel length and kernel thickness, number of kernel per spike, vitreousness, moisture content, grain protein content and SDS sedimentation, and indirect negative effects via tiller number, thousand kernel weight, wet gluten content and kernel width. This result was in agreement with the reports of different authors [19, 24].

The observed positive direct effect (0.27) of the number of spikelets per spike on grain yield agrees with the report of Degewione [6], but is contradictory with the finding of Johnson [14] who reported a negative direct effect of this character on grain yield. The indirect effects of spikelets per spike via the number of tillers, spike length, thousands kernel length, wet gluten, kernel width and kernel thickness were to be negative. Conversely, it exerted positive indirect effects on grain yield via the rest of the other traits. Mohammed [20] reported a similar result regarding the indirect effect of the number of spikelets per spike on grain yield via the number of tillers and spike length. Thousand grain weight exerted negative direct effect (-0.66) on grain yield, which indicates that direct selection for this character alone for grain yield improvement is not effective unless it is looked for its positive indirect effect via other characters. It had positive indirect effects via days to heading, days to maturity, plant height, number of spikelets per spike, harvest index, wet gluten content, kernel length, kernel thickness, grain moisture content, and protein content. On the contrary, it was observed that thousand kernel weight had negative indirect effect on grain yield via the number of tillers, spike length, hectolitre weight, gluten index, kernel width, vitreousness and SDS sedimentation. Amsal [3] also reported positive indirect effect of thousand grain weight on grain yield via days to

heading and harvest index, but negative indirect effect via vitreousness, which is similar to the present result.

Positive and significant indirect effects of harvest index on grain yield were exhibited through the number of tillers, plant height, number of spikelets per spike, dry gluten content, gluten index, kernel length and kernel thickness, vitreousness, grain protein content and SDS sedimentation. The positive indirect effect of harvest index on grain yield through these traits signifies the importance of harvest index for indirect selection for grain yield improvement. Conversely, it was observed that harvest index had negative indirect effect on grain yield *via* day to heading, day to maturity, spike length, thousand kernel weights, hectolitre weight, wet gluten content, grain hardness, kernel width, number of kernels per spike and grain moisture content (Table 3). Shahnawaz [24] also reported a similar result for indirect effect of harvest index on grain yield *via* plant height and number of spikelets per spike. The present result is in partial agreement with

Berhanu [5], who obtained negative direct effect of days to heading on grain yield and positive indirect effect of this character *via* days to maturity. Mohammed [20] reported similar result for vitreousness and harvest index and for number of spikelet per spike.

The direct effect of number of kernel per spike on grain yield was low but positive (0.11). It also exerted positive indirect effects on grain yield *via* days to heading, day to maturity, spike length, grain hardness, harvest index, wet gluten content, kernel length, kernel width and hectolitre weight. However, it exerted negative indirect effects on grain yield *via* number of tillers, plant height, number of spikelets per spike, moisture content, thousand kernel weight, protein content, vitreousness, dry gluten content, gluten index, SDS sedimentation and kernel thickness (Table 4). Previous reports also documented positive indirect effect of kernel per spike through harvest index [18], and plant height and spikelets per spike [13].

Table 4. *Genotypic path coefficients of direct (main diagonal) and indirect effects of 22 bread wheat traits at Sinana.*

Traits	DH	DM	NT	PH	SL	SPS	KPS	HI	TKW	HLW	WGC	DGC
DH	0.14	0.27	-0.06	0.06	-0.39	0.14	0.51	-0.06	-0.20	0.00	0.06	0.02
DM	0.05	0.77	0.10	0.12	-0.03	0.02	-0.11	-0.27	-0.03	0.02	0.16	-0.01
NT	-0.01	0.10	0.82	-0.07	0.10	-0.14	-0.39	0.03	0.01	0.00	-0.03	0.02
PH	0.02	0.20	-0.13	0.46	-0.27	0.08	-0.07	0.05	-0.29	0.00	-0.03	0.01
SL	0.08	0.04	-0.12	0.19	-0.65	0.14	0.42	0.14	-0.38	0.00	-0.04	0.01
SPS	0.07	0.05	-0.42	0.14	-0.35	0.27	0.42	0.05	-0.21	0.00	-0.08	0.01
KPS	0.08	-0.10	-0.38	-0.04	-0.33	0.13	0.84	-0.03	-0.19	0.01	0.09	-0.01
HI	-0.01	-0.33	0.04	0.04	-0.15	0.02	-0.04	0.62	-0.27	-0.01	-0.14	0.02
TKW	0.04	0.03	-0.01	0.20	-0.38	0.09	0.24	0.25	-0.66	-0.01	0.01	0.00
HLW	0.00	-0.25	0.02	-0.03	0.03	0.00	-0.09	0.10	-0.10	-0.07	-0.01	0.00
WGC	0.02	0.26	-0.05	-0.03	0.05	-0.04	0.16	-0.19	-0.01	0.00	0.47	-0.07
DGC	-0.03	0.10	-0.15	-0.06	0.09	-0.03	0.07	-0.11	0.00	0.00	0.34	-0.10
GI	0.02	-0.28	-0.28	-0.04	-0.21	0.09	0.24	0.18	0.03	0.01	-0.20	0.02
GH	-0.03	0.06	0.04	0.12	0.10	-0.05	-0.11	0.08	0.00	0.01	0.10	-0.03
KL	0.04	-0.07	-0.01	0.19	-0.30	0.07	0.17	0.04	-0.27	0.01	-0.20	0.04
KW	0.05	0.17	-0.21	0.12	-0.29	0.09	0.31	0.19	-0.36	-0.01	0.09	-0.01
KT	-0.04	-0.01	0.03	-0.01	-0.10	-0.08	-0.12	0.20	-0.15	0.01	0.00	-0.02
VI	-0.02	-0.12	-0.23	-0.02	-0.07	0.06	-0.04	0.18	0.10	-0.03	-0.03	-0.01
MC	0.07	0.30	-0.18	0.24	-0.27	0.07	0.15	-0.14	-0.23	0.00	-0.04	0.02
PC	-0.01	0.31	-0.02	-0.11	0.18	-0.04	-0.01	-0.23	0.40	0.02	0.18	-0.03
SDS	-0.02	-0.22	-0.17	-0.09	-0.12	-0.01	0.18	0.21	0.09	0.01	-0.02	-0.01

DH=days to heading, DM= days to maturity, NT=number of tiller, PH= plant height, SL= spike length, SPS= spikelet per spike, KPS= kernels per spike, YpHa= grain yield t ha-1, HI= harvest index, TKW= thousands kernel weight, HLW=hectolitre weight, WGC= wet gluten content, DGC= dry gluten content, GI= gluten index, GH=grain hardness, KL=kernel length, KW= kernel with, KT=kernel thickness, VI= vitreousness, MC=moisture content, PC= protein content, SDS= sodium dodecyl sulfate sedimentation.

Table 4. *Continued.*

Traits	GI	GH	KL	KW	KT	VI	MC	PC	SDS	rg
DH	0.05	0.03	0.03	-0.04	-0.02	-0.09	0.15	0.05	-0.01	0.63**
DM	-0.16	-0.01	-0.01	-0.02	0.00	-0.10	0.12	-0.41	-0.02	0.18
NT	-0.15	-0.01	0.00	0.02	0.00	-0.18	-0.07	0.02	-0.01	0.06
PH	-0.04	-0.03	0.05	-0.02	0.00	-0.02	0.16	0.23	-0.01	0.35
SL	0.14	0.02	0.06	-0.04	0.01	0.07	0.13	0.28	0.01	0.51**
SPS	0.14	0.02	0.03	-0.03	-0.02	0.15	0.09	0.14	0.00	0.46**
KPS	0.12	0.02	0.03	-0.04	-0.01	-0.03	0.06	0.02	0.01	0.26
HI	0.13	-0.01	0.01	-0.03	0.02	0.19	-0.07	0.36	0.02	0.42*
TKW	-0.02	0.00	0.05	-0.05	0.01	-0.10	0.11	0.61	-0.01	0.41*
HLW	-0.03	0.02	-0.02	-0.01	-0.01	0.24	0.01	0.32	-0.01	0.12
WGC	-0.18	-0.02	-0.05	-0.02	0.00	-0.05	-0.03	-0.39	0.00	-0.17
DGC	-0.10	-0.03	-0.05	-0.01	0.01	0.08	-0.07	-0.29	0.01	-0.31
GI	0.43	0.02	0.02	-0.02	0.01	0.18	-0.04	-0.03	0.03	0.18
GH	-0.09	-0.11	0.01	0.01	0.01	0.11	-0.05	-0.25	0.02	-0.04

Traits	GI	GH	KL	KW	KT	VI	MC	PC	SDS	rg
KL	0.09	-0.01	0.12	0.01	-0.01	-0.16	0.13	0.43	0.00	0.31
KW	0.09	0.01	-0.01	-0.10	0.02	0.10	0.04	-0.06	0.01	0.24
KT	0.09	-0.01	-0.01	-0.03	0.06	0.08	-0.02	-0.04	0.02	-0.16
VI	0.12	-0.02	-0.03	-0.01	0.01	0.65	-0.09	-0.26	0.03	0.16
MC	-0.06	0.02	0.05	-0.01	0.00	-0.19	0.31	0.24	-0.03	0.32
PC	0.01	-0.03	-0.05	-0.01	0.00	0.17	-0.07	-0.99	0.02	-0.27
SDS	0.21	-0.04	0.00	-0.02	0.01	0.27	-0.14	-0.35	0.07	-0.15

Residual = 0.266, DH=days to heading, DM= days to maturity, NT=number of tiller, PH= plant height, SL= spike length, SPS= spikelet per spike, KPS= kernels per spike, YpHa= grain yield t ha-1, HI= harvest index, TKW= thousands kernel weight, HLW=hectolitre weight, WGC= wet gluten content, DGC= dry gluten content, GI= gluten index, GH=grain hardness, KL=kernel length, KW= kernel with, KT=kernel thickness, VI= vitreousness, MC=moisture content, PC= protein content, SDS= sodium dodecyl sulfate sedimentation.

4. Conclusion

Information on the extent and pattern of interrelationship among different agronomic and quality characters and their direct and indirect effects on grain yield are essential to design efficient breeding strategies in crop improvement. The present study was designed to generate such information on advanced bread wheat genotypes at Sinana, South eastern part of the Ethiopia in 2020 cropping season. Twenty five bread wheat genotypes including four released varieties (Dambel, Sanete, Sofumer and Mada walabu) were tested in lattice design with three replications. Data were collected on phenological and developmental traits, agronomic characters, and quality traits. The data were subjected to analysis of variance and then variance components were estimated for each trait. Correlation and path coefficients were also estimated both at phenotypic and genotypic levels.

Grain yield (ha⁻¹) had significant and positive genotypic and phenotypic correlation with day to heading, spike length, number of spikelets per spike and harvest index. On other hand, grain yield was negatively correlated with grain protein content at both phenotypic and genotypic levels, which is consistent with known theoretical principles. The significant positive correlations observed between grain yield and other traits at both genotypic and phenotypic levels indicate that these characters should be considered when selecting for high grain yield.

The path analysis results showed high positive direct genotypic effects on grain yield for days to maturity, number of tiller, number of kernel per spike, harvest index and vitreousness at genotypic level. This justifies the presence of true relationship between these characters and grain yield, thereby direct selection through these characters would result in reasonable improvement of grain yield. However, spike length, thousand kernels weight and grain protein content had highest negative direct genotypic effects on grain yield. Regarding phenotypic path coefficients, harvest index and spike length had high and positive direct phenotypic effects on grain yield. However, the highest negative direct phenotypic effect on grain yield was exhibited by dry gluten content and wet gluten content. Generally, the present study revealed the presence of ample genetic variation for most of the studied traits among the tested genotypes and this could be exploited in future bread wheat breeding in the studied area. The study also exposed the importance of considering quality characters in the process of selection of genotypes for grain yield and quality character.

References

[1] Alam. K., G. Shabbir, M. A. Chowdhry and I. Khaliq. 1992. Correlation of post-emergence characters with yield in bread wheat. Pakistanian Journal of Agricultural Science. 29: 449-452.

[2] Alemu Dabi, Firew Mekbib and Tadesse Desalegn. 2016. Estimation of Genetic and Phenotypic Correlation Coefficients and Path Analysis of Yield and Yield Contributing Traits of Bread Wheat (Triticum aestivum L.) Genotypes. International Journal of Natural Resource Ecology and Management, 1 (4): 145-154.

[3] Amsal T. 2001. Studies on Genotypic Variability and Inheritance of Water logging Tolerance in Wheat. Ph.D. Dissertation, University of the Free State, Bloemfontein, South Africa.

[4] Basazen Fantahun. 2006. Genetic variability and character associations in some triticale genotypes at Kulumsa and Assasa, Arsi. M.Sc Thesis, Harmaya University, Harmaya, Ethiopia.

[5] Berhanu Mamo, 2004. Genetic variability and character associations in bread wheat (Triticum aestivum l.) genotypes developed for semiarid areas. M.Sc Thesis, Harmaya University, Harmaya, Ethiopia.

[6] Degewione, A. and Alamerew, S. 2013. Genetic diversity in bread wheat (Triticum aestivum L.) genotypes. Pakistan journal of biological sciences, 16 (21): 1330-1335.

[7] Dewey, R. R. and K. H. Lu. 1959. A correlation coefficient analysis of components of crested seed production. Agronomy Journal, 51: 515-518.

[8] Ermias Estifanos. 2005. Assessment for quality traits, yield and yield related characters in advanced Ethiopian bread Wheat (Triticum aestivum l.) breeding lines. M.Sc Thesis, Haramaya University, Haramaya, Ethiopia.

[9] Falconer, D. S., Trudy F. C. and Mackay. 1996. Introduction to Quantitative Genetics. 4th ed., Longman Group Limited, Malaysia, p464.

[10] Gupta AK, Mittal RK and Ziauddin A. 1999. Association and factor analysis in spring wheat. Ann. Agri. Res, 20: 481-485.

[11] Hasan Kilic and Tacettin Yagbasanlar. 2010. The Effect of Drought Stress on Grain Yield, Yield Components and some Quality Traits of Durum Wheat (Triticum turgidum ssp. durum) Cultivars. Journal of Notulae Botanicae Horti Agrobotanici, 38 (1): 164-170.

[12] Hussain T., Tariq M. A., Akram Z., Iqbal J., Rehman A. U., and Rabbani G. 2014. Estimation of Some Genetic Parameters and Inter-Relationship of Grain Yield and Yield Related Attributes in Certain Exotic Lines of Wheat (Triticum aestivum L.). Journal of Biology, Agriculture and Healthcare, 4 (2): 48-53.

[13] Ihsan Khaliq, I. H. S. A. N., Parveen, N. A. J. M. A. and Chowdhry, M. A. 2004. Correlation and path coefficient analyses in bread wheat. Int. J. Agric. Biol, 6 (4): 633-635.

[14] Johnson, H. W., H. F. Robinson and R. F. Comstock. 1955a. Estimates of Genetics and environmental variability in soya bean. Agronomy Journal, 47: 314-318.

[15] KEW, 2017. Royal Botanical Gardens. Accessed on August 10, 2017. Website: htttp://www.kew.org.

[16] Khan, M. H., and Dar, A. N. 2009. Correlation and Path coefficient Analysis of some quantitative traits in wheat. African Crop Science Journal, 18 (1): 9 -14 452.

[17] Kifle Zerga, Firew Mekbib and Tadesse Dessalegn. 2017. The Mean Performance of Different Bread Wheat (Triticum Aestivum. L) Genotypes in Gurage Zone, Ethiopia. International Journal of Plant Breeding and Crop Science, 3 (2): 123-126.

[18] Majumder, D. A. N., Shamsuddin, A. K. M. Kabir, M. A. and Hassan, L. 2008. Genetic variability, correlated response and path analysis of yield and yield contributing traits of spring wheat. Journal of Bangladesh Agricultural University, 6 (2): 227- 234.

[19] Miller, B., Afework S., Pomeranz Y., Bruinsma B. L. and Booth, G. D. 1982. Measuring the hardness of wheat. Cereal Food World, 27: 61–64.

[20] Mohammed Abinasa, Amsalu Ayana and Geremew, Bultosa. 2011. Genetic variability, heritability and trait associations in durum wheat (Triticum turgidum L. var. durum) genotypes. African Journal of Agricultural Research, 6 (17): 3972-3979.

[21] Moslem Abdipour, Mohsen Ebrahimi, Ali Izadi-Darbandi, Anna Maria Mastrangelo, Goodarz Najafian, Yousef Arshad, Gita Mirniyam. 2016. Association between Grain Size and Shape and Quality Traits, and Path Analysis of Thousand Grain Weight in Iranian Bread Wheat Landraces from Different Geographic Regions. Not Bot Horti Agrobo, 44 (1): 228-236.

[22] Obsa Chimdesa. 2014. Genetic variability among bread wheat (Triticum aestivum L.) genotypes for growth characters, yield and yield Components in bore district, Oromia regional state. M.Sc Thesis, Haramaya University, Haramaya, Ethiopia.

[23] Schuler, S. F., R. K. Bacon and E. E. Gbur. 1994. Kernel and spike character influence on test weight of winter wheat. Crop Science Journal. 34: 1309-1313.

[24] Shahnawaz Khan and Shailesh Marker. 2016. Correlation and path coefficient analysis of some quantitative traits in wheat (Triticum aestivum L.). International Journal of Multidisciplinary Research and Development, 3 (7): 15-20.

[25] Sharma, J. R. 1998. Statistical and biometrical techniques in plant breeding. New Age International (P) limited, publishers. New Delhi. P432.

[26] Shashikala, S. K. 2006. Analisis of genetic diversity in wheat (Triticum aestivum L.). M.Sc Thesis, Dharawad university of Agricultural science, Dharawad, India.

[27] Singh, B. D. Plant breeding: principles and methods. Kalyani publishers, 2015.

[28] Singh, R. K. and Chaudhary. 1977. Biometrical methods in quantitative genetic analysis. Kalyani publishers, New Delhi-Ludhiana, India.

[29] Tazeen Mohsin, Nadia Khan and Farzana Nasir Naqvi. 2009. Heritability, phenotypic correlation and path coefficient studies for some agronomic characters in synthetic elite lines of wheat. Journal of Food, Agriculture and Environment, 7 (3 and 4): 278-282.

[30] Waleed Khaled, Shailesh Marker and G. Roopa Lavanya, 2014 Investigation of genetic variability and correlation analysis of wheat (Triticum aestivum L.) genotypes for grain yield and its Component traits European Academic research, 2 (5): 2286-4822.

[31] Wright, S. 1923. The Theory of Path Coefficients a reply to niles criticism. Genetics, 8 (3): 239-255.

[32] Yakubu Yahaya. 2014. Estimate of genetic variability and correlation coefficients for some quantitative characters in bread wheat (Triticum aestivum L.). World Journal of Agricultural Sciences, 2 (7): 163-167.

[33] Yonas Shimelis. 2015. Genetic variability and association of grain yield, Yield components and quality traits in durum wheat (triticum turgidum l. Var. Durum) genotypes at hera liphitu, Southern Ethiopia. M.Sc Thesis, Haramaya University, Haramaya, Ethiopia.

[34] Yuksel Kaya and Mevlut Akcura. 2014. Effects of genotype and environment on grain yield and quality traits in bread wheat (T. aestivum L.). Food Sci. Technol (Campinas) vol. 34 no. 2.

[35] Zeeshan, M., Arshad, W., and Ali, S. 2013. Genetic Diversity and Trait Association among Some Yield Parameters of Wheat Elite Lines Genotypes under Rainfed Conditions. *Journal of Renewable Agriculture.*