

Full Length Research Paper

Genetic variability, correlation and path analysis of yield and grain quality traits in bread wheat (*Triticum aestivum* L.) genotypes at Axum, Northern Ethiopia

Berhanu Meles^{1*}, Wassu Mohammed² and Yemane Tsehaye³

¹Plant Breeding Department, Axum Agricultural Research Center, Axum, Ethiopia.

²Department of Plant Breeding and Genetics, Haramaya University, Dire Dawa, Ethiopia.

³Department of Plant Breeding and Genetics, Mekelle University, Mek'ele, Ethiopia.

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Forty-nine bread wheat genotypes were tested at Axum, Northern Ethiopia in 2016/17, with the objective of assessing the extent of genetic variation, correlation and path analysis of wheat genotypes in yield and grain quality traits using 7 x 7 triple lattice design. Data were collected for 17 agronomic and grain quality characters. For each of the test entries, samples of 500 g grains were taken from each plot for quality analysis. The NIR spectrophotometer (NIR Infratec 1241 Grain analyzer, Sweden) was used to analyze wheat samples for their protein, wet gluten, zeleny sedimentation volume and starch content based on dry weight basis. Data were subjected to analysis of variance which revealed significant differences among the genotypes for all the characters. The genotypic coefficient of variation (GCV) ranged from 1.63 (for starch content) to 13.30% (for grain yield). The broad sense heritability (H^2) ranged from 15.89 (for number of tillers) to 97.16% (for days to heading), while genetic advance as percent of mean (GAM) from 2.01 (for starch content) to 19.63% (for days to heading). The GCV and phenotypic coefficient of variation (PCV) differences were low in magnitude for days to heading and days to maturity, and H^2 values were coupled with moderate to high GAM. This suggests selection based on phenotype of genotypes could be effective to improve these characters. Grain yield was positively and significantly correlated with biological yield (0.72), harvest index (0.65), plant height (0.51), thousand kernel weight (0.31), hectoliter weight (0.37) and starch content (0.32), of which biomass yield (0.85) and harvest index (0.70) had the highest positive direct effect on grain yield. Thus, selection for higher mean values of biomass yield and harvest index could be considered simultaneously for selection of higher grain yield.

Key words: Bread wheat, correlation, genetic coefficient of variation, genetic advance, grain quality, heritability.

INTRODUCTION

Wheat is one of the most important export and strategic cereal crops in the world and in Ethiopia in terms of production and utilization (Suresh, 2013). It is the second

most important staple food crop of the world; it provides more calories in human diet than any other crop worldwide. It accounts for nearly 30% of global cereal

*Corresponding author. E-mail: bhortic@gmail.com.

production, covering an area of 222.42 million hectares with total production of 725.12 million tons (FAO, 2015). Given its predominance in human diets, cultivated wheat has to meet the specific quality criteria for the manufacture of a wide range of food products derived from it.

Wheat is one of the most important small cereal crops in Ethiopia, which ranks fourth both in area coverage (1,663,845.63 hectares) and in total annual production (4,231,588.716 tons). The productivity of the crop remains low (2.54 t ha⁻¹) (CSA, 2015) in the country as compared to the world average yield (3.19 t ha⁻¹) (FAO, 2013). The low yield per hectare is attributed to many factors, such as unavailability of quality seed for varieties that are high yielding as well as adapted to wide range of agro-ecologies of the country. Hence, the first step in the development of varieties is assessing the genetic variability of available genotypes for the characters of interest (Rahman et al., 2016). High genetic advancement coupled with high heritability estimates offers the most suitable condition for selection (Johnson et al., 1955). The presence of variability, heritability and genetic advance in different yield related characters of bread wheat has been reported by Desalegn and Chauhan (2016), Kifle et al. (2016) and Rahman et al. (2016). However, no variability studies have been conducted in the study area. Moreover, the variability studies in the region were not on moisture stress tolerant bread wheat genotypes. In addition, genetic information is limited to grain quality traits in bread wheat genotypes evaluated in the country. Considering the importance of such information, this research was initiated with the objective of assessing genetic variability for yield and grain quality traits, and determining the association among the yield components of bread wheat genotypes.

MATERIALS AND METHODS

Field experiment was conducted at Axum Agricultural Research Center (AxARC), Northern Ethiopia during 2016-2017. The experimental site is located at latitude 13°15'40.2" N, and 38°34'45.8" E longitudes with an altitude of 2148 m above sea level. It is characterized by uni-modal rainfall pattern concentrated in one season from July to August with total annual rain fall of 500 to 782.8 mm per annum. The mean minimum and maximum temperatures ranged from 12.6 to 25.51°C, respectively. The soil type of the site is clay type with pH ranging from 7.5 to 8.3. A total of 49 bread wheat genotypes introduced from ICARDA-CIMMYT (Table 1) were included in the study. The experiment was laid down in 7x7 triple lattice design. Each genotype was planted in a plot consisting of six rows of 2.5 m long and 1.2 m width; a total of 3 m² with spacing of 20 cm between rows. The distances between plots, blocks and replications were 0.5, 0.5 and 1.5 m, respectively. A seed rate of 150 kg ha⁻¹ and fertilizer rate of 100-100 kg ha⁻¹ N-P₂O₅ in the forms of Urea and DAP (di-ammonium phosphate) were used.

For each of the test entries, samples of 500 g grains were taken from each plot for quality analysis. The NIR spectrophotometer (NIR Infracore 1241 Grain analyzer, Sweden) was used to analyze wheat samples for their protein, wet gluten, zeleny sedimentation, starch

content and moisture content based on dry weight basis. While, hectoliter weight was estimated using grain analyzer computer 2100.

Data collected

Data were collected both from plot and plant basis. The four central rows were used for data collection based on plots, such as days to 50% heading, days to physiological maturity, grain yield, biomass yield and harvest index. Ten randomly selected plants from the four central rows of each plot were used for data collection on plant basis and the averages of the ten plants in each experimental plot were used for statistical analysis for traits such as plant height, productive tillers per plant, number of kernels per spike, number of spike lets per spike and spike length.

Data for grain quality traits

For each of the test entries, samples of 500 g were taken from each plot for quality analysis and the NIR spectrophotometer (NIR Infracore 1241 Grain analyzer, Sweden) was used to analyze wheat samples.

Statistical analysis

The mean values of the genotypes were subjected to analysis of variance based on triple lattice design. Analysis of variance was done using Proc lattice and Proc GLM procedures of SAS version 9.1.3 (SAS Institute Inc, 2004) after testing the ANOVA assumptions. Mean separations were estimated using Duncan's multiple range (DMRT) test at 5% probability levels.

Estimation of variance components and association among characters

The phenotypic and genotypic coefficients of variation were estimated according to the methods suggested by Burton and De Vane (1953).

$$PCV = \frac{\sqrt{\sigma^2_p}}{\bar{X}} \times 100$$

Where, σ^2_p = phenotypic variance and \bar{X} = mean of the characters evaluated.

$$GCV = \frac{\sqrt{\sigma^2_g}}{\bar{X}} \times 100$$

Where, σ^2_g = genotypic variance, \bar{X} = mean of the characters evaluated. Broad sense heritability was computed for each character based on the formula developed by Allard (1960) as: $H^2 = \frac{\sigma^2_g}{\sigma^2_p} \times 100$

The genetic advance (GA) for selection intensity (K) at 5% was calculated by the formula suggested by Allard (1960) as:

$$GA = K \times \sigma_p \times H^2$$

Where, GA = Expected genetic advance, σ_p = the phenotypic standard deviation, H^2 = broad sense heritability, K= selection differential (K=2.06 at 5% selection intensity).

$$GA \text{ (as \% of the mean)} (GAM) = \frac{GA}{\bar{X}} \times 100$$

Where \bar{X} = population mean.

Table 1. Genotypes used in the study.

Name	Pedigree
ETBW8484	MUTUS//WBLL1*2/BRAMBLING/3/WBLL1*2/BRAMBLING
ETBW8486	SNLG/3/EMB16/CBRD//CBRD/4/KA/NAC//TRCH
ETBW9019	MUTUS//KIRITATI/2*TRCH/3/WHEAR/KRONSTAD F2004
ETBW9026	AGUILAL/FLAG-3
ETBW9027	REYNA-29
ETBW9028	MUTUS//ND643/2*WBLL1
ETBW9029	ND643/2*WBLL1/4/CHIBIA//PRLII/CM65531/3/SKAUZ/BAV92/5/BECARD
ETBW9033	DANPHE #1*2/CHYAK
ETBW9034	MUTUS*2/HARIL #1
ETBW9040	T.DICOCCON CI9309/AE.SQUARROSA (409)// MUTUS/3/2*MUTUS
ETBW9042	HUW234+LR34/PRINIA//PFAU/WEAVER/3/CMH83.30
ETBW8489	VORB/6/CPI8/GEDIZ/3/GOO//ALB/CRA/4/AE.SQUARROSA (208)/5/2*WESTONIA/7/ CPI8/ GEDIZ/3/GOO//ALB/CRA/4/AE.SQUARROSA (208)/5/2*WESTONIA
ETBW8492	KRICHAUFF/2*PASTOR//CHONTE
ETBW9015	SUP152//ND643/2*WBLL1/3/ND643/2*WBLL1
ETBW9016	SWSR22T.B./2*BLOUK #1//WBLL1*2/KURUKU
ETBW9017	SWSR22T.B./2*BLOUK #1//WBLL1*2/KURUKU
ETBW9018	SWSR22T.B.//TACUPETO F2001*2/ BRAMBLING/3/2*TACUPETO F2001*2/ BRAMBLING
ETBW9041	T.DICOCCON CI9309/AE.SQUARROSA (409)//MUTUS/3/2*MUTUS
ETBW9051	CROC-1/AE.SQUARROSA (224) //OPATA/3/QAFZAH-21/4/SOMAMA-3
ETBW 8471	WEEBILL-1/BOCRO-3
ETBW 8472	SANOBAR-4
ETBW 8473	SUNCO.6/FRAME//PASTOR/3/PAURAQ
ETBW 8474	1447/PASTOR//KRICHAUFF/3/PAURAQ
ETBW 8475	WORRAKATTA/2*PASTOR//DANPHE #1
ETBW 8476	1447/PASTOR//KRICHAUFF/5/2*SERI*3//RL6010/4*YR/3/PASTOR/4/BAV92
ETBW 8477	C80.1/3*BATAVIA//2*WBLL1/3/EMB16/CBRD//CBRD/4/CHEWINK #1
ETBW 8478	SLVS/3/CROC_1/AE.SQUARROSA(224)// OPATA/5/VEE/LIRA//BOW/3/BCN/4/KAUZ/6/2*KA/NAC//TRCH
ETBW 8479	METSO/ER2000//MUU
ETBW 8480	KA/NAC//TRCH/3/DANPHE #1
ETBW 8481	EMB16/CBRD//CBRD/4/BETTY/3/CHEN/AE.SQ//2*OPATA
ETBW 6861	WAXWING*2/HEILO
ETBW 8506	AGUILAL/FLAG-3
ETBW 8507	DURRA-4
ETBW 7120	QAFZAH-23/SOMAMA-3
ETBW 8508	REYNA-8
ETBW 7213	CHAM-4/SHUHA'S/6/2*SAKER/5/RBS/ANZA/3/KVZ/HYS//YMH/TOB
ETBW 8509	REYNA-29
ETBW 7038	ATTILA/3*BCN//BAV92/3/TILHI/5/BAV92/3/PRL/SARA// TSI/VEE#5/4/CROC_1/AE.SQUARROSA (224)//2*OPATA
ETBW 8510	HIJLEEJ-1
ETBW 8511	BOW #1/FENGGANG 15/3/HYS//DRC*2/7C
ETBW 7147	CROC-1/AE.SQUARROSA(224)// OPATA/3/QAFZAH-21/4/SOMAMA-3
ETBW 8512	BABAX/LR42//BABAX*2/3/KURUKU/4/KINGBIRD #1
ETBW 7871	PAURAQ/4/PFAU/SERI.1B//AMAD/3/WAXWING
ETBW 8513	MUTUS//WBLL1*2/BRAMBLING/3/WBLL1*2/BRAMBLING
ETBW 6940	UTIQUE 96/FLAG-1
Kakaba (PICAFLOR#1)	Kitititi//Seri/Rayon
Shorima (ETBW5483)	UTQE96/3/PYN/BAU//Milan
Ogolcho(ETBW5520)	WORRAKATTA/2*PASTOR
King bird	THELIN # 2/TUKURU

Table 2. Mean squares from analysis of variance for the 17 characters of 49 bread wheat genotypes.

Characters	Mean square						RE to RCBD(%)	CV (%)
	Replication (2)	Treatments (48)		Blocks with in rep(Adj) (18)	Error			
		Un-adj	Adj		Intra(78)	RCBD(96)		
DH	51.76	98.19	83.48**	1.39	0.98	1.06	102.12	1.71
DM	40.62	187.40	169.58**	6.48	8.34	7.99	95.82	2.83
GFP	56.63	43.01	43.42**	7.99	5.28	5.79	103.08	5.22
PH(cm)	60.41	97.33	86.58**	14.92	15.66	15.52	99.11	4.92
NT	0.07	0.23	0.21*	0.23	0.13	0.14	105.98	18.75
KPS	9.69	89.63	82.98**	14.95	22.44	21.03	93.74	10.13
SKPS	0.17	4.49	3.80**	1.12	0.83	0.88	101.69	5.63
SL(cm)	0.26	0.91	0.76**	0.19	0.25	0.23	95.55	5.98
BY(t ha ⁻¹)	20.89	4.39	3.71**	1.02	1.26	1.22	96.40	12.00
GY(t ha ⁻¹)	5.28	1.14	0.97**	0.21	0.25	0.24	97.20	12.53
HI(%)	33.55	71.25	62.61*	32.78	35.45	34.95	98.59	13.91
TKW(g)	58.07	32.80	30.59**	8.68	5.67	6.24	103.24	7.00
HLW	4.85	10.72	10.34**	3.09	2.27	2.42	101.70	1.92
GPC(%)	5.12	1.89	1.70**	0.61	0.47	0.49	101.23	4.95
WG(%)	23.78	14.99	14.13**	3.55	3.41	3.44	100.03	5.85
ZSV(%)	78.77	54.40	46.49**	8.33	11.91	11.24	94.37	7.15
SC(%)	1.89	2.39	2.20**	0.38	0.42	0.41	98.50	1.02

ns= Non-significant,* and ** = significant at 5 and 1% probability level, respectively. Number in parenthesis represented degree of freedom. DH= days to heading, DM = days to maturity, GFP = grain filling period, PH = plant height, NT = number of productive tillers per plant, KPS = number of kernels per spike, SPKS = number of spike lets per spike, SL= spike length, BY= biomass yield, GY= grain yield, HI = harvest index, TKW = thousand kernel weight, HLW = hectoliter weight, GPC = grain protein content, WG = wet gluten, ZSV = zeleney sedimentation value and SC = starch content, ETBW= Ethiopian bread wheat, adj= adjusted, SE= standard error.

Correlation coefficient

Estimation of genotypic and phenotypic correlation coefficients was done based on the procedure of Dabholkar (1992).

Path coefficient analysis

Path coefficient analysis which refers to the estimation of direct and indirect effects of the yield attributing characters on grain yield was calculated based on the method used by Dewey and Lu (1959) as follows:

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

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

$$1 = p^2R + \sum p_{ij} r_{ij}$$

Where, p^2R is the residual effect; $p_{ij} r_{ij}$ = the product of direct effect of any variable and its correlation coefficient with yield.

RESULTS AND DISCUSSION

The mean values for 17 characters of 49 bread wheat

genotypes are presented in Appendix Table 1.

Genotypes had in between 49 to 73.33 days to heading and 87 to 118 days to maturity with a mean of 57.99 and 101.83 days, respectively. The result showed a wide range of variations for days to heading and maturity. Grain yield ranged from 2.37 to 5.44 t ha⁻¹ with a mean of 3.95 t ha⁻¹. Maximum grain yield was obtained from the genotypes ETBW9016 (5.44 t ha⁻¹), ETBW8480 (5.37 t ha⁻¹), ETBW8475 (4.64 t ha⁻¹) and ETBW8486 (4.56 t ha⁻¹). Grain protein content ranged from 11.93% for the check variety King bird to 15.43% for ETBW8489 with a mean value of 13.79%.

Mean squares of 17 characters from analysis of variance (ANOVA) are presented in Table 2. The analysis of variance showed highly significant ($P < 0.01$) differences among genotypes for all the characters except number of effective tillers per plant and harvest index in which genotypes had significant differences ($P < 0.05$). Significant genetic variation among genotypes for various characters suggested that the genotypes were genetically diverse and could be a good opportunity for breeders to select genotypes for trait of interest. Several researchers reported significant differences among bread wheat genotypes studied (Kifle et al., 2016; Kumar et al., 2016; Tesfaye et al., 2016; Birhanu et al., 2016).

Table 3. Phenotypic and genotypic variances and coefficients of variations, heritability in broad sense and genetic advance for 17 characters of 49 bread wheat genotypes

Characters	Ranges	Mean \pm SE	σ^2_g	PCV	GCV	H ²	GA	GAM
DH	47-74	58.17 \pm 0.47	31.52	9.79	9.65	97.16	11.42	19.63
DM	86-120	102.14 \pm 0.65	58.42	7.99	7.48	87.81	14.78	14.47
GFP	36-60	43.97 \pm 0.31	11.88	9.56	7.84	67.18	5.83	13.25
PH	64.4-98.8	80.40 \pm 0.47	26.85	8.08	6.45	63.99	8.55	10.64
NT	1.0-3.60	1.93 \pm 0.02	0.03	21.88	8.72	15.89	0.14	7.17
KPS	31.0-67.1	46.77 \pm 0.45	20.99	14.08	9.79	48.56	6.59	14.08
SKPS	11.8-20.5	16.15 \pm 0.10	1.09	8.68	6.48	55.76	1.61	9.99
SL	6.40-9.90	8.29 \pm 0.05	0.21	8.03	5.49	46.73	0.64	7.74
BY	5.50-13.0	9.29 \pm 0.10	0.99	15.81	10.64	45.29	1.38	14.77
GY	2.37-5.44	3.95 \pm 0.05	0.28	18.21	13.30	52.83	0.79	19.94
HI	26.4-51.5	42.49 \pm 0.40	11.70	16.03	7.99	24.83	3.52	8.21
TSW	26.3-43.6	34.01 \pm 0.27	8.09	11.04	8.45	57.41	4.45	13.08
HLW	73.0-82.7	78.67 \pm 0.16	2.49	2.84	2.00	49.77	2.29	2.92
GPC	11.9-15.4	13.79 \pm 0.07	0.42	6.88	4.71	46.86	0.92	6.65
WG	27.2-36.5	31.49 \pm 0.18	3.74	8.50	6.13	51.97	2.88	9.11
ZSV	34.4-53.1	47.9 \pm 0.35	13.02	10.19	7.48	53.83	5.46	11.32
SC	61.1-65	62.9 \pm 0.07	0.63	1.63	1.26	60	1.27	2.01

DH= Days to heading, DM = days to maturity, GFP = grain filling period, PH = plant height, NT = number of productive tillers per plant, KPS = number of kernels per spike, SPKS = number of spike lets per spike, SL= spike length, BY= biomass yield, GY= grain yield, HI = harvest index, TKW = thousand kernel weight, HLW = hectoliter weight, GPC = grain protein content, WG = wet gluten, ZSV = zeleney sedimentation value and SC = starch content, σ^2_g = genetic variance, PCV= phenotypic variance, GCV= genotypic variance, GA= genetic advance, GAM= genetic advance as percent of mean.

Estimation of variability components

The estimated phenotypic coefficient of variation (PCV) and genotypic (GCV) coefficients of variations are presented in Table 3. The GCV ranged from 1.26% for starch content to 13.30% for grain yield and PCV from 1.63% for starch content to 21.88% for number of productive tillers per plant. The GCV and PCV values were categorized as low (<10%), moderate (10 to 20%) and high (>20%) as indicated by Deshmukh et al. (1986). Accordingly, moderate GCV and PCV was observed for grain yield (13.30 and 18.21%) and biomass yield (10.64 and 15.81%), respectively. This indicated that the genotype could be reflected by the phenotype and the effectiveness of selection based on the phenotypic performance for these characters. Report of Birhanu et al. (2016) is in line with the occurrence of GCV and PCV media in this study.

The PCV value was high for number of productive tillers, while medium PCV values were observed for harvest index, kernels per spike, thousand seed weight and Zeleny sedimentation value. The lowest GCV and PCV were recorded for days to heading, days to maturity, grain filling period, plant height, number of spikelets per spike, hectoliter weight, grain protein content, wet gluten content and starch content. The result indicates the environmental factors had more influence on the expression of these characters than the genetic factors, suggesting the limited scope for improvement of these

characters by direct selection of high performing genotypes. This is in agreement with reports of Naik et al. (2015) and Rahman et al. (2016).

Estimation of heritability and expected genetic advance

The heritability estimates ranged from 15.89% for number of productive tillers per plant to 97.16% for days to heading. According to Singh (1990), for a character with high heritability ($\geq 80\%$), selection is fairly easy, because there would be a close correspondence between genotype and phenotype due to a relatively smaller contribution of environment to phenotype. High heritability was estimated for days to heading (97.16%) and days to maturity (87.81%). This implies the variation observed was mainly under genetic control and was less influenced by the environment and the possibility of progress from selection. The obtained results are in agreement with results reported by Tesfaye et al. (2016). Moderate heritability values (40-80%) were computed for grain filling period, plant height, kernels per spike, spike lets per spike, spike length, biomass yield, grain yield, thousand kernel weight, hectoliter weight, grain protein content, wet gluten content and Zeleny sedimentation value. Low heritability (<40) estimated for number of effective tillers per plant and harvest index indicated that

Table 4. Estimation of genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficient for 17 morphological and quality traits in 49 bread wheat advanced lines.

Traits	DH	DM	GFP	PH	NT	KPS	SKPS	SL	BY	GY	HI	TSW	HLW	GPC	WGC	ZSV	SC
DH	1	0.90**	0.38*	0.26	-0.5*	0.14	0.39*	0.37*	0.14	-0.19	-0.44*	-0.44*	-0.6**	-0.20	0.03	-0.17	0.19
DM	0.87**	1	0.74**	0.36*	-0.4*	0.19	0.46*	0.43*	0.22	-0.05	-0.34*	-0.35*	-0.49*	-0.30*	0.02	-0.25	0.32*
GFP	0.31*	0.74**	1	0.35*	-0.19	0.19	0.37	0.35*	0.24	0.19	-0.04	-0.08	-0.09	-0.31*	-0.01	-0.25	0.38*
PH	0.19*	0.32*	0.34**	1	-0.21	0.29*	0.20	0.12	0.58**	0.51*	0.00	0.08	-0.11	-0.48*	-0.32*	-0.31*	0.31*
NT	-0.27*	-0.17*	0.02	-0.12	1	-0.20	-0.36*	-0.24	-0.04	0.22	0.38*	0.40*	0.38*	0.07	0.05	0.08	-0.06
KPS	0.12	0.16	0.15	0.30*	-0.02	1	0.72**	0.33*	0.21	0.19	0.01	-0.16	-0.11	-0.30*	-0.32*	-0.17	0.04
SKPS	0.33**	0.39**	0.31*	0.25*	-0.15	0.65**	1	0.63**	0.08	0.02	-0.09	-0.33*	-0.27	-0.09	-0.07	-0.07	0.01
SL	0.28*	0.36**	0.30*	0.23*	-0.05	0.42**	0.61**	1	0.06	-0.09	-0.21	-0.03	-0.22	0.03	0.19	0.14	0.09
BY	0.05	0.15	0.22*	0.51**	-0.0	0.15	0.09	0.06	1	0.72**	-0.20	0.06	0.16	-0.43*	-0.24	-0.27	0.34*
GY	-0.18*	-0.01	0.22*	0.47**	0.15	0.13	0.06	-0.03	0.65**	1	0.53**	0.31*	0.37*	-0.38*	-0.27	-0.23	0.32*
HI	-0.28*	-0.19*	0.04	0.02	0.30*	-0.01	-0.02	-0.11	-0.28*	0.53**	1	0.39*	0.35*	-0.01	-0.09	0.00	0.05
TSW	-0.5**	-0.23*	0.02	0.04	0.21*	-0.13	-0.25*	-0.05	0.10	0.26*	0.23*	1	0.71**	-0.04	0.05	0.11	0.34*
HLW	-0.4**	-0.27*	-0.01	-0.07	0.25*	-0.01	-0.19*	-0.11	0.15	0.29*	0.23*	0.65**	1	-0.15	-0.14	-0.06	0.31*
GPC	-0.21*	-0.27*	-0.23*	-0.25*	-0.07	-0.20*	-0.01	0.03	-0.14	-0.14	0.00	-0.14	-0.21*	1	0.81**	0.80**	-0.7**
WG	0.00	0.00	0.01	-0.14	-0.04	-0.21*	0.02	0.14	-0.05	-0.08	-0.03	-0.02	-0.13	0.81**	1	0.71**	-0.22
ZSV	-0.18*	-0.22*	-0.18*	-0.17*	0.01	-0.16*	-0.05	0.08	-0.06	-0.06	-0.00	-0.01	-0.13	0.77**	0.67**	1	-0.43*
SC	0.19*	0.32**	0.34**	0.20*	0.03	0.03	-0.00	0.07	0.19*	0.19*	0.02	0.41**	0.39**	-0.7**	-0.3**	-0.5**	1

*And **=significant at 5% and 1% probability levels, respectively. DH=days to heading, DM = days to maturity, GFP = grain filling period, NT = number of productive tillers per plant, PH = plant height, SL= spike length, SKPS = number of spike lets per spike, KPS = number of kernels per spike, BY = biomass yield, GY = grain yield, HI = harvest index, TKW = thousand kernel weight, HLW = hectoliter weight, GPC = grain protein content, WG = wet gluten content, ZSV = Zeleny sedimentation value and SC = starch content.

selection for these characters would not be effective due to the predominant effects of non-additive genes. In consonance with the current result, Desalegn and Chauhan (2016) reported low heritability for tillers per plant (26.3%) and harvest index (11.1%). It has been suggested that heritability estimates together with genetic advance are more helpful in predicting the gain under selection than heritability estimates alone in selecting best individuals because heritability does not provide indication of amount of genetic progress that would result from selecting the best individuals (Johnson et al., 1955). High heritability is coupled with moderate genetic advance as percent of mean observed for days to heading

and days to maturity. This indicates that most likely the heritability of these characters is due to additive gene effects, and selection might be effective for these characters (Salman et al., 2014; Rahman et al., 2016).

Correlation of grain yield with other characters

Grain yield had positive and highly significant ($P<0.01$) genotypic correlation with biomass yield (0.65) and harvest index (0.53) (Table 4). Grain yield also exhibited positive and significant ($P<0.05$) genotypic correlation with plant height (0.51), thousand kernel weight (0.31), hectoliter

weight (0.37) and starch content (0.32). The positive association of these characters with grain yield might be due to the higher assimilation of photosynthesis as biomass because of the increased plant height and the more photosynthesis partitioned to kernels that increased their weight and thereby harvest index. This suggested that improvement of biomass yield would result in a substantial increment on grain yield that could be used in selection of genotypes for high grain yield at optimum condition. According to Kearsy and Pooni (1996), the positive correlation of these characters with grain yield resulted from the presence of strong coupling linkage of genes or the characters may

be the result of pleiotropic genes that control these characters in the same direction. They further suggested that the presence of such genes effects leads to the improvement of yield as seen in these characters. The positive and significant association of grain yield with biological yield and harvest index had been reported by Kifle et al. (2016), Kumar et al. (2016) and Ebrahimnejad and Rameeh (2016). The work of Surma et al. (2012) showed positive and significant correlation of grain yield with thousand kernel weight, hectoliter weight and starch content. In contrast to the current study result, Singh (2014) reported the presence of negative correlation between grain yield and plant height.

Grain yield was negatively and significantly correlated with grain protein content (-0.38). It also had negative and non-significant association with wet gluten content and Zeleny sedimentation value. The low yielding ability of the high protein genotypes is usually explained by the high energy needed for protein production as compared to starch production (Monaghan et al., 2001). But under ideal environment, assimilates are used more for grain yield than protein content. This indicated the importance of considering harvest index as it contributed more to the grain yield. However, different hypotheses dealing with the cause of this negative correlation have been also proposed, mainly related to genetic incompatibility (linkage, pleiotropy) (Iqbal et al., 2007). Therefore, care should be given while selecting genotypes for grain yield and grain protein content. The results obtained in this study are in agreement with the findings of Surma (2012), in which grain yield was negatively correlated with protein content, wet gluten and Zeleny sedimentation value. Days to maturity had significant and negative association with number of productive tillers (-0.42 and -0.17), harvest index (-0.34 and -0.19), thousand kernel weight (-0.35 and -0.23), hectoliter weight (-0.49 and -0.27) and grain protein content (-0.30 and -0.27) both at genotypic and phenotypic levels (Table 4). The negative association of grain protein content with maturity suggested that early maturity and high protein content can be readily achieved simultaneously.

Genotypic path analysis

Biomass yield (0.85) followed by harvest index (0.70) exerted the highest positive direct effect on grain yield, while plant height had negligible positive direct effect, though it exhibited significant and positive association with grain yield (Table 5). The result indicated that the positive and significant correlation of biomass yield and harvest index with grain yield at genotypic level was due to the direct effect of these characters on grain yield. However, the positive association of plant height with grain yield was due to the indirect effect of this character on yield through other characters such as biomass yield, grain filling period and days to heading. The maximum

positive genotypic direct effect of biomass yield and harvest index on grain yield was reported by many authors (Obsa, 2014; Dargicho et al., 2015; Alemu et al., 2016).

The genotypic correlation coefficients of thousand kernel weight, hectoliter weight and starch content were significant and positive with grain yield; however, these characters had low and negligible negative direct effect on grain yield. This implies that the indirect effects of these characters on grain yield through other characters could be the cause for significant and positive correlation. For instance, the indirect positive effect of thousand kernel weight via harvest index (0.27), hectoliter weight via harvest index (0.25) and starch content via biomass yield (0.29) on grain yield were high. This shows the importance of considering harvest index and biomass yield when selection of wheat genotypes for higher grain yield is desired. In agreement with the current study results, similar results were reported by Ermias (2005), Senayt (2007) and Adhiena (2015). Grain protein content exerted negative direct effect on grain yield, consequently, selection of genotypes for high performance of grain protein content might not be effective when the breeding objective is selection of genotypes for high grain yield. Singh (2014) reported negative direct effect of grain protein content on grain yield.

Conclusion

The study indicated the presence of wide genetic variation among the wheat genotypes which can be exploited to develop high yielding varieties with desirable grain quality and early maturity in the study area and similar agro-ecologies, where terminal moisture stress is the major constraint of wheat production. Moderate GCV coupled with moderate PCV (10 to 20%) was observed for grain yield and biomass yield, indicating the effectiveness of selection based on the phenotypic performance of the genotypes. High heritability (>80%) coupled with moderate genetic advance as percent of mean (10 to 20%) was observed for days to heading and days to maturity. This implies that the variation observed was mainly under genetic control and the possibility of progress from selection. In general, in the context of plant breeding, traits that exhibited good GCV, H^2 and GAM would be useful as a base for selection; hence days to heading, days to maturity, grain yield and biomass yield were identified as the major contributors. Grain yield had positive and highly significant correlation with biomass yield and harvest index, and also significantly correlated with plant height, thousand kernel weight, hectoliter weight and starch content both at genotypic and phenotypic level. This suggested that, grain yield potential can be effectively improved by obtaining maximum expression of these characters. However, grain yield had negative and significant correlation with grain protein content, and protein content exerted negative direct

Table 5. Estimates of direct (bold and diagonal) and indirect effect (off diagonal) of different traits on grain yield at genotypic level in 49 bread wheat genotypes at Laelay-Maichew in 2016.

Traits	DH	DM	GFP	PH	NT	KPS	SKPS	SL	BY	HI	TSW	HLW	GPC	WG	ZSV	SC	r _g
DH	0.088	-0.171	0.027	0.002	0.013	-0.003	0.009	0.002	0.122	-0.309	0.003	0.006	0.033	0.003	-0.005	-0.011	-0.19
DM	0.079	-0.189	0.052	0.002	0.013	-0.004	0.010	0.002	0.190	-0.241	0.003	0.005	0.049	0.002	-0.007	-0.019	-0.05
GFP	0.033	-0.140	0.071	0.002	0.006	-0.004	0.008	0.002	0.214	-0.025	0.001	0.001	0.051	0.000	-0.007	-0.023	0.19
PH	0.023	-0.067	0.025	0.006	0.006	-0.006	0.004	0.001	0.497	0.001	0.000	0.001	0.079	-0.030	-0.009	-0.019	0.51*
NT	-0.040	0.080	-0.015	-0.001	-0.030	0.002	-0.008	-0.001	-0.031	0.266	-0.003	-0.003	-0.012	0.005	0.002	0.004	0.22
KPS	0.013	-0.037	0.014	0.002	0.003	-0.022	0.016	0.002	0.178	0.004	0.001	0.001	0.049	-0.030	-0.005	-0.002	0.19
SKPS	0.035	-0.086	0.026	0.001	0.011	-0.016	0.022	0.004	0.072	-0.055	0.003	0.003	0.015	-0.006	-0.002	-0.001	0.02
SL	0.032	-0.081	0.025	0.001	0.007	-0.007	0.014	0.006	0.048	-0.150	0.000	0.002	-0.004	0.018	0.004	-0.006	-0.09
BY	0.013	-0.042	0.018	0.003	0.001	-0.005	0.002	0.000	0.857	-0.144	0.000	-0.001	0.070	-0.022	-0.008	-0.021	0.72**
HI	-0.038	0.065	-0.002	0.000	-0.011	0.000	-0.002	-0.001	-0.175	0.707	-0.003	-0.003	0.002	-0.009	0.000	-0.003	0.53**
TSW	-0.039	0.066	-0.005	0.000	-0.012	0.003	-0.007	0.000	0.055	0.274	-0.008	-0.007	0.007	0.004	0.003	-0.022	0.31*
HLW	-0.054	0.093	-0.007	-0.001	-0.011	0.002	-0.006	-0.001	0.134	0.248	-0.006	-0.009	0.024	-0.013	-0.002	-0.019	0.37*
GPC	-0.018	0.057	-0.022	-0.003	-0.002	0.007	-0.002	0.000	-0.369	-0.010	0.000	0.001	-0.163	0.075	0.023	0.040	-0.38*
WG	0.003	-0.003	0.000	-0.002	-0.002	0.007	-0.002	0.001	-0.202	-0.067	0.000	0.001	-0.132	0.093	0.021	0.014	-0.27
ZSV	-0.015	0.046	-0.018	-0.002	-0.002	0.004	-0.001	0.001	-0.236	0.003	-0.001	0.001	-0.130	0.067	0.029	0.027	-0.23
SC	0.016	-0.060	0.027	0.002	0.002	-0.001	0.000	0.001	0.293	0.035	-0.003	-0.003	0.108	-0.021	-0.013	-0.061	0.32*

Residual effect= 0.077. DH = Days to heading, DM = days to maturity, GFP = grain filling period, NT = number of productive tillers per plant, PH = plant height, SL = spike length, SKPS = number of spike lets per spike, KPS = number of kernels per spike, BY = biomass yield, HI = harvest index, TKW = thousand kernel weight, HLW = hectoliter weight, GPC = grain protein content, WG = wet gluten, ZSV = zeleny sedimentation value, SC = starch content and r_g= genotypic coefficient of correlation.

effect. This implies simultaneous improvement of these two characters is difficult, thus care should be given during selection of these two traits. The highest positive direct effect on grain yield was exerted by biomass yield followed by harvest index both. Therefore, selection for high mean values of biomass yield and harvest index could be considered as the simultaneous selection of genotypes for high gain yield.

Generally, it is recommended to further evaluate high yielding genotypes with high grain protein content and early maturing once more at similar agro-ecologies to develop varieties. Beside this, genetic information is limited for grain quality characteristics in bread wheat genotypes in the

country (Ethiopia). Hence, due attention should be given to grain quality and yield performance of bread wheat genotypes to exploit genetic potential of the crop via selection or hybridization.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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Abbreviations

DH, Days to heading; **DM**, days to maturity; **GFP**, grain filling period; **PH**, plant height; **NT**, number of productive tillers per plant; **KPS**, number of kernels per spike; **SKPS**, number of spikelets per spike; **SL**, spike length; **BY**, biomass yield; **GY**, grain yield; **HI**, harvest index; **TKW**, thousand kernel weight; **HLW**, hectoliter weight; **GPC**, grain protein content; **WG**, wet gluten; **ZSV**, zeleny sedimentation value; **SC**, starch content;

ETBW, Ethiopian bread wheat; σ^2g , genetic variance; **GCV**, genetic coefficient of variation; **GAM**, genetic advance as percent of mean; **GA**, genetic advance; H^2 , broad sense heritability; **PCV**, phenotypic coefficient of variation.

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Appendix Table 1. Mean values of 17 traits of 49 bread wheat genotypes tested at Axum area in 2016.

Name	DH	DM	GFP	PH	NT	KPS	SKPS	SL	BY	GY	HI	TSW	HLW	GPC	WG	ZSV	SC
ETBW8484	57.33	101.7	44.33	82.40	1.86	39.20	15.5	7.80	9.67	4.16	44.22	33.73	79.33	12.93	28.30	34.95	63.30
ETBW8486	55.33	100.0	44.67	77.30	1.84	47.27	16.0	8.20	11.00	4.56	41.64	35.80	79.27	14.30	31.93	51.93	62.73
ETBW9019	57.33	98.3	41.00	73.77	2.60	48.37	15.2	8.00	8.33	3.84	48.15	35.23	79.13	13.57	30.57	49.33	63.20
ETBW9026	51.67	93.7	42.00	84.53	2.01	43.10	14.9	8.47	9.50	4.49	47.36	38.67	81.60	13.17	29.83	48.87	63.43
ETBW9027	52.67	94.7	42.00	74.93	1.89	41.33	15.3	8.10	10.00	4.35	43.54	37.07	81.40	14.00	32.63	50.63	63.67
ETBW9028	65.67	112.3	46.67	83.37	1.79	57.23	18.5	8.70	9.33	3.71	39.18	29.70	76.27	13.30	30.70	48.80	63.10
ETBW9029	51.67	92.3	40.67	75.40	2.02	48.83	16.5	8.47	9.50	4.24	44.93	36.30	80.67	14.03	31.67	51.50	63.23
ETBW9033	53.00	96.7	43.67	81.67	2.19	54.10	16.9	9.10	11.00	4.09	37.33	38.23	80.10	13.87	31.33	49.60	63.37
ETBW9034	52.33	90.7	38.33	79.53	1.76	49.93	15.6	8.00	8.83	4.15	48.00	34.00	79.30	14.33	31.80	50.63	62.13
ETBW9040	54.33	94.3	40.00	74.17	1.53	51.37	16.6	8.27	8.50	3.26	38.19	29.57	77.93	14.37	30.50	50.60	61.73
ETBW9042	52.67	94.7	42.00	80.37	2.07	50.77	16.3	8.40	9.00	3.68	42.55	33.93	77.83	15.30	33.90	50.03	61.13
ETBW8489	53.67	98.3	44.67	69.47	1.86	36.47	15.0	6.93	5.50	2.59	47.59	35.60	79.20	15.43	33.53	51.33	62.33
ETBW8492	54.67	100.3	46.33	82.87	2.38	47.07	15.4	8.47	9.33	4.19	44.96	39.50	79.70	13.57	30.87	46.60	62.13
ETBW9015	58.33	98.7	40.33	86.53	1.74	51.43	15.8	7.10	10.33	4.46	43.19	30.90	78.20	13.00	27.87	44.40	62.77
ETBW9016	59.33	105.0	45.67	88.13	2.13	50.70	16.7	8.27	13.00	5.44	41.82	33.10	76.90	13.30	30.40	44.37	63.67
ETBW9017	62.33	104.7	42.33	85.10	1.58	43.23	16.1	8.57	9.33	3.64	38.90	30.33	76.17	14.57	33.90	51.70	62.57
ETBW9018	59.67	102.3	42.67	77.43	1.86	51.30	16.6	8.10	8.67	3.64	42.11	30.93	77.20	14.70	31.40	51.07	61.37
ETBW9041	59.33	99.3	40.00	78.03	1.60	54.53	17.7	8.57	8.00	3.82	48.08	29.63	77.13	14.53	31.63	50.50	61.57
ETBW9051	61.67	110.3	48.67	91.83	2.17	51.20	16.8	7.63	10.33	4.36	42.25	31.70	77.03	12.97	31.47	47.45	64.27
ETBW8471	59.33	100.7	41.33	75.63	1.56	49.07	16.7	8.30	8.75	2.43	27.78	28.50	76.50	13.93	30.47	45.30	61.30
ETBW8472	64.33	114.0	49.67	89.63	1.76	41.93	15.5	9.23	9.00	3.46	38.40	31.53	75.30	13.53	30.97	48.87	62.93
ETBW8423	57.00	101.3	44.33	73.43	1.95	45.47	16.5	8.27	9.33	3.85	41.30	30.97	77.40	14.53	33.90	51.93	62.17
ETBW8474	54.00	99.3	45.33	81.80	1.71	42.93	16.4	8.37	9.83	4.21	43.11	37.90	81.10	14.70	33.03	51.43	62.53
ETBW8475	53.67	112.3	58.67	81.53	1.68	49.60	16.5	8.53	11.00	4.64	42.19	33.80	81.30	13.10	31.53	47.30	63.80
ETBW8476	63.00	110.3	47.33	78.27	1.85	42.50	14.7	7.63	10.67	4.42	41.70	33.00	79.60	12.70	29.43	44.57	63.73
ETBW8477	60.67	106.7	46.00	86.07	1.95	50.57	15.9	7.80	10.00	4.43	44.55	33.67	79.33	12.23	27.50	35.90	63.63
ETBW8478	61.67	107.3	45.67	90.43	1.81	50.97	16.4	8.20	9.67	4.04	41.65	35.83	78.27	13.70	30.30	49.43	62.77
ETBW8479	52.00	92.7	40.67	82.07	2.07	36.20	12.8	7.53	8.67	3.75	42.94	37.63	77.87	14.77	35.40	52.40	62.90
ETBW8480	56.67	97.3	40.67	89.43	1.96	41.13	15.7	7.87	11.00	5.37	49.68	36.47	80.13	13.53	28.20	49.97	62.47
ETBW8481	55.67	105.3	49.67	86.37	2.02	59.50	17.6	9.00	8.67	4.47	51.55	41.90	80.80	12.80	30.30	44.50	65.03
ETBW6861	59.33	99.3	40.00	79.60	2.38	52.13	16.6	8.00	9.00	3.84	43.18	32.60	77.90	13.63	29.40	49.87	62.07
ETBW8506	63.00	108.7	45.67	90.93	1.71	45.63	16.6	8.00	10.67	4.12	38.53	32.33	78.37	13.20	31.83	46.83	63.63
ETBW8507	49.33	87.0	37.67	77.97	2.52	36.93	14.0	8.07	9.50	4.21	44.37	35.40	81.00	14.67	34.83	52.03	63.03
ETBW7120	60.67	104.3	43.67	72.90	1.94	46.03	15.5	8.60	8.33	3.12	37.43	28.97	75.90	14.33	33.70	51.00	62.67
ETBW8508	54.00	93.7	39.67	69.03	2.04	37.47	14.1	7.43	7.33	3.54	48.15	33.50	77.73	14.00	31.80	50.27	63.13
ETBW7213	53.00	94.7	41.67	82.33	2.18	43.33	15.2	8.47	10.33	4.38	42.37	40.10	81.50	14.20	33.73	53.13	63.20

Appendix Table 1. Contd.

ETBW8509	59.33	106.7	47.33	80.83	1.62	46.57	18.6	9.60	7.00	3.28	46.92	34.57	76.60	13.90	32.20	50.27	63.77
ETBW7038	55.00	98.0	43.00	66.87	2.51	39.07	16.0	8.33	8.00	3.23	40.68	35.13	81.27	15.40	36.47	52.47	62.50
ETBW8510	72.67	118.0	44.67	82.07	1.66	51.80	18.7	9.33	10.00	3.83	38.49	36.97	79.40	13.93	34.67	50.37	64.03
ETBW8511	64.67	113.0	51.00	82.20	1.69	53.83	18.7	8.83	9.67	4.51	46.75	29.67	78.37	14.07	33.87	49.47	63.20
ETBW7147	49.00	88.0	39.00	74.43	2.29	49.03	16.0	8.13	7.67	3.70	47.61	37.07	79.83	14.00	31.07	51.03	62.17
ETBW8512	56.33	100.0	43.67	76.73	1.93	48.07	17.1	8.80	9.67	4.24	44.15	32.87	80.67	13.10	28.20	43.63	63.53
ETBW7871	66.33	114.7	48.33	82.40	1.87	44.33	17.7	8.97	9.50	4.31	45.46	27.20	73.95	15.17	36.10	51.20	61.53
ETBW8513	73.33	118.0	44.67	77.63	1.55	43.90	16.3	9.07	9.67	3.79	38.93	34.90	74.77	13.77	32.93	47.87	63.67
ETBW6940	52.67	94.0	41.33	82.20	1.69	46.53	14.8	7.47	10.00	4.52	45.21	37.70	80.70	13.53	32.20	47.13	64.50
Kakaba	57.67	101.3	43.67	81.60	1.62	47.10	17.2	8.67	9.00	3.57	39.52	31.23	78.53	12.60	27.23	43.23	63.33
Shorima	61.00	108.0	47.00	78.13	2.33	42.03	14.8	8.13	8.67	4.38	51.27	36.57	79.60	13.57	31.57	46.60	62.93
Ogolcho	72.67	117.0	44.33	78.80	1.60	40.60	14.9	8.50	9.33	2.37	26.35	32.40	77.60	13.57	32.30	47.90	64.07
king bird	59.33	104.7	45.33	81.53	2.04	49.80	16.6	8.17	10.00	4.38	43.85	32.20	79.23	11.93	27.77	34.35	64.70
Mean	58.17	102.1	44.02	80.40	1.93	46.8	16.15	8.29	9.37	3.98	42.82	34.0	78.7	13.8	31.6	48.3	62.99
CV(%)	1.65	2.79	5.48	4.83	20.1	10.1	5.78	5.86	11.69	12.6	13.90	7.21	2.01	4.99	5.89	6.93	1.03
LSD at 1%	2.13	6.19	4.93	8.49	0.81	10.2	1.95	1.06	2.41	1.07	12.78	5.11	3.23	1.45	3.96	7.40	1.38

DH=Days to heading, DM = days to maturity, GFP = grain filling period, NT = number of productive tillers per plant, PH = plant height, SL= spike length, SKPS = number of spike lets per spike, KPS = number of kernels per spike, BY = biomass yield, GY = grain yield, HI = harvest index, TKW = thousand kernel weight, HLW = hectoliter weight, GPC = grain protein content, WG = wet gluten content, ZSV = zeleny sedimentation value and SC = starch content.