



Genetic Variability and Association Among Yield and Yield Related Traits of Bread Wheat (*Triticum aestivum* L.) Genotypes at Adet Research Station, Ethiopia

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Abstract: Wheat is one of the most important cereal crops grown in Ethiopia. Study of genetic variation provides the basis for increasing yield and successful breeding programme. So far, little information is generated about genetic variability of yield and yield component traits in the exotic bread wheat germplasm in Ethiopia. Therefore this study was conducted to evaluate the extent of genetic variability and association among yield and yield related traits of bread wheat genotypes. The study was carried out with the following objectives; to assess the nature and magnitude of genetic diversity for yield and yield related traits and to estimate the genotypic and phenotypic association and path coefficient analysis of yield and yield related traits. To achieve the above objectives; total of sixty-four bread wheat (*Triticum aestivum* L.) genotypes were evaluated at Adet Agricultural Research Centre in 2018/2019 cropping season. The experiment was conducted by using 8x8 simple lattice design. Data were subjected to analysis of variance which revealed that there was highly significant difference ($p \leq 0.01$) among the genotypes for all characters studied. The highest grain yield (6.42 t ha^{-1}) was recorded from G50 followed by G4 (6.4 t ha^{-1}) and G8 (6.4 t ha^{-1}) while low yield of 2.83 t ha^{-1} was obtained from genotype G42. Phenotypic coefficient of variation ranged from 1.75 for starch content to 17.85% for number of effective tillers per plant whereas genotypic coefficient of variation ranged from 1.65 for starch content to 14.48% for number of total tillers per plant. Very high heritability ($\geq 80\%$) was estimated for grain yield, plant height, number of kernels per spike, number of spikelets per spike and starch content. Very high heritability ($\geq 80\%$) coupled with high genetic advance as percent of mean ($\geq 20\%$) values were scored for number of spikelet per spike, number of kernels per spike and grain yield. Grain yield had positive and highly significant ($P \leq 0.01$) correlation with biomass yield, harvest index, plant height, number of spikelets per spike and number of kernels per spike at both genotypic and phenotypic levels. However, grain yield with grain protein content showed negative and significant ($P \leq 0.05$) correlation at both genotypic and phenotypic levels. Path coefficient analysis at genotypic level revealed that biomass yield exerted highest positive direct effect on grain yield followed by harvest index. Whereas path analysis at phenotypic level revealed that biomass yield exerted highest direct effect on grain yield followed by harvest index, and number of spikelet's per spike.

Keywords: Correlation, Genetic Advance, Heritability, Path Coefficient and Variability

1. Introduction

Bread wheat (*Triticum aestivum* L.), a hexaploid species with $2n=6x=42$, and a self-pollinating annual plant in the true grass family Gramineae (Poaceae), is the largest cereal

crop extensively grown as staple food sources in the world [24]. It is one of the most important export and strategic cereal crop in the world and in Ethiopia in terms of production and utilization [27]. It has been described as the 'King of cereals' because of the largest it occupies, high

productivity and the prominent position it holds in the international food grain trade [28]. Currently it is also becoming most important cereals grown on a large scale [4], because of its significance as cash crop, high level of production per unit area, its major role in supplying the dietary requirements of the society.

Wheat is grown at an altitude ranging from 1500 to 3000 m.a.s.l, between 6-16° N latitude and 35-42° E longitude in our country. The most suitable agro-ecological zones, however, fall between 1900 and 2700 m.a.s.l [2]. Ethiopia is the largest wheat producer in sub-Saharan Africa next to South Africa in terms of total wheat area coverage and production. It ranks fourth after teff (*Eragrostis tef*), maize (*Zea mays*) and sorghum (*Sorghum bicolor*) in total area coverage of 1.7 million ha and third in total production of 4.6 million tons after teff and maize with productivity of 2.74 t/ha among cereal in different regions of Ethiopia [15]. The major wheat producing areas in Ethiopia are located in Oromiya (Arsi, Bale, Shewa, Ilubabor, and Western Harerghe), in SNNPR (Hadiya, Sidamo, Silte, Guraghe, Kambata), Tigray, Amhara (Northern Gondar and Gojam zones) [36]. The productivity of wheat in Amhara region is 2.53 t/ha [15].

A wide gap in the yield is attributed to shortage of improved varieties for different agro ecological zone of the country, poor agronomic practices, drought, poor soil fertility, diseases and insect pests, etc. are the major constraints of wheat production in Ethiopia. Hence, the first step in the development of varieties is assessing the genetic variability of available genotypes for the characters of interest [26]. For a successful breeding program, the presence of genetic variability plays a vital role. It is true that the more diverse plants, the greater chance of exploiting high heterotic crosses or to generate productive recombinants and broad variability in segregating generations during genetic improvement [33]. Reduction in the genetic variability makes the crops increasingly vulnerable to diseases and adverse climatic changes [8]. So, precise information on the nature and degree of genetic diversity present in wheat collections from its principal areas of cultivation would help to select parents for evolving superior varieties.

The effectiveness of selection for any successful breeding programme depends upon the existence of genetic variability present in the base population [34]. It is proved that the larger the variability is the greater scope of selection and improvement of character under study.

In plant breeding program, direct selection for yield as such could not be effective [9], because yield is polygenically controlled. For effective utilization of the genetic stock in crop improvement, information of mutual association between yield and yield components is necessary. It is therefore, necessary to know the correlation and path coefficient analysis of various component characters with yield and among themselves. Correlation studies along with path analysis provide a better understanding of the association of different characters with grain yield. Hence, in the present study, exotic as well as improved genotypes were

used and an attempt was made to generate fertile genetic variability information among bread wheat genotypes is very important tool because the information will help the wheat breeders to breed for many characters (earliness, yield increase, drought tolerance, wider adaptation, desirable quality, etc.). Keeping the above fact in view, the current study was carried out to assess the nature and magnitude of genetic diversity for yield and yield related traits, to estimate the genotypic and phenotypic association among characters and to determine the direct and indirect effect of yield related traits on grain yield.

2. Materials and Methods

2.1. Description of the Study Area

The study was conducted at Adet Agricultural Research Centre (West Gojam, Amhara Region) which is a Regional Research Center in 2018/2019 cropping season. The study area is located 40km south west of Bahir Dar town. Adet is located 11°16'N latitude, 37°29'E longitude and at 2240 meters above sea level (m.a.s.l). The area's minimum and maximum temperature recordings are 10.81° and 25.55° respectively with annual rainfall of 1432 mm. The dominant soil types are vertisol and nitosol types with PH 5.43 (Source: National meteorological Agency Bahir- Dar branch, 2018).

2.2. Experimental Materials

The experimental material consists of sixty-four genotypes including four standard checks (Lemu, King brid, Wane and Tay). Lemu, King brid and Wane were obtained from Kulmsa Agricultural Research Center (KARC) and Tay obtained from Adet Agricultural Research Centre (AARC), while the rest of 60 exotic bread wheat genotypes were introduced from CIMMYT were evaluated for genetic variability.

2.3. Experimental Design and Trial Management

The trial was laid out using 8 x 8 simple lattice designs with two replications. Each experimental plot consisted six rows spaced 0.2m x 0.2m long. The plot area was 3m² (2.5m length x 1.2m width). The spacing between plots, blocks and replications were 0.4 m and 1.5 m, and 1.5m, respectively. There were 128 plots with total area 859.95m². A seed rate of 150 kg/ha (45 g/plot) were used for the study. Blended fertilizer (NPSB) and urea fertilizer was applied as recommended by Adet Agricultural Research Center. Sowing was done by hand drilling on July 11, 2018. All other agronomic practices were done uniformly to the entire plots as recommended for wheat production in the area during the growing season to raise healthy crop.

2.4. Methods of Data Collection

Data were collected both on plant basis for some characters (i.e. from ten random plants with in a plot) and plot basis for other traits.

2.4.1. Data Collected on Plot Basis

(i). Days to Heading (DH)

The number of days from date of sowing to the stage where 75% of the spikes have fully emerged.

(ii). Days to Physiological Maturity (DM)

The number of days from sowing to the stage when 90% of the plants in a plot have reached physiological maturity or 90% of the spike on the plots turned golden yellow color.

(iii). Grain Filling Period (GFP)

The number of days from heading to maturity.

(iv). Grain Yield (GY, t ha⁻¹)

The grain yield per plot was measured in grams using sensitive balance from the central four rows of each plot, after moisture of the seed is adjusted to 12.5% and converted to t ha⁻¹ for analysis.

(v). Thousand Kernel Weight (TKW, g/pl)

The weight of 1000 seeds from a random sample of seed harvested per plot.

(vi). Biomass Yields (BMY, t ha⁻¹)

The plants with in the four central rows were harvested and weighed in grams to obtain the biomass yield for each experimental plot and expressed in (t ha⁻¹).

(vii). Harvest Index (HI) (%)

It was estimated by dividing grain yield per plot to biomass yield per plot or it is ratio of grain yield to the above ground biomass yield and multiplied by 100.

2.4.2. Data Collected on Plant Basis

The data for the following characters were recorded from four central rows by randomly ten plants taken each experimental plot and the average was carried out.

(i). Plant Height (PH, cm)

The average height in cm from ground level to the tip of the spike excluding the awns of ten randomly taken plants from the central four rows of each plot.

(ii). Number of Effective Tiller Number (NEPP)

The numbers of tillers per plant bearing productive heads excluding the main plant was counted at the time of harvest and average were record for the ten randomly taken plants from the central four rows.

(iii). Number of Total Tiller Per Plant (NTPP)

The total numbers of tillers were counted on ten randomly sampled plants from central four rows in each plot.

(iv). Number of SPIKELET Per Spike (NSPS)

Total numbers of spikelets on main spike of all ten plants from four central rows were counted at the time of maturity and averages were recorded.

(v). Number of Kernels Per Spike (NKPS)

Total number of grains in the main spike was counted at

the time of harvest from ten randomly taken plants and to be expressed as an average and recorded from central rows of each plot.

(vi). Spike Length (SL, cm)

The main spikes from the ten sampled plants from the central four rows of each plot were measured in cm and averaged to represent the spike length in cm (excluding awns).

2.4.3. Quality Traits

Random homogeneous sample in replicates each harvested genotypes were used for laboratory analysis. Grain samples of each genotype were analyzed separately. The samples were cleaned manually in order to remove soil particles, broken and foreign seeds. The following quality determining traits were determined:

Hectoliter Weight (HLW) (kg/hL)

Grain weights of one hectoliter volume (random sample) of grain were estimated for each experimental plot.

Traits like, starch content, protein content, wet gluten content, and zeleny sedimentation value of the grain were determined using Mininfra Smart Grain Analyzer. For each of the test entries, samples of 500 g were taken of each plot for quality analysis and the NIR spectrophotometer (NIR Infracat 1241 Grain Analyzer, Sweden) was used to analyze bread wheat samples.

2.5. Data Analysis

2.5.1. Analysis of Variance (ANOVA)

The data collected for each trait were subjected to analysis of variance (ANOVA) for simple lattice design. Analysis of variance was done using Proc GLM (General Linear Model) procedures of SAS version 9.4.

2.5.2. Estimates of Variance Components

The phenotypic and genotypic variability of each trait were estimated as phenotypic and genotypic variances and coefficients of variation. The phenotypic and genotypic coefficient of variation was estimated according to the method suggested by Burton and de Vane [14] as follows: -

$$\text{Genotypic variance } (\sigma^2_g) = \left[\frac{MS_g - MS_e}{r} \right]$$

Where, σ^2_g = genotypic variance,

MS_g = mean square of genotype,

MS_e = mean square of error,

r = number of replication.

$$\text{Phenotypic variance } (\sigma^2_p) = \sigma^2_g + \sigma^2_e$$

Where, σ^2_p = phenotypic variance,

σ^2_g = Genotypic variance,

σ^2_e = Environmental variance in which Environmental variance = mean square of error.

$$\text{Phenotypic Coefficient of variation (PCV)} = \frac{\sqrt{\sigma^2_p}}{\bar{x}} \times 100$$

$$\text{Genotypic Coefficient of variation (GCV)} = \frac{\sqrt{\sigma^2_g}}{\bar{x}} \times 100$$

Where: \bar{x} = grand mean of a character.

According to Deshmukh *et al.* [16], PCV and GCV can be categorized as low (<10%), moderate (10-20%) and high (>20%).

2.5.3. Estimation of Heritability in Broad Sense

Broad sense heritability (h^2) expressed as the percentage of the ratio of the genotypic variance (σ^2_g) to the phenotypic variance (σ^2_p) and was estimated on genotype mean basis as described by Allard, R. W [6] as:

$$h^2 = \left[\frac{\sigma^2_g}{\sigma^2_p} \right] \times 100$$

Where, h^2 = heritability in broad sense,

σ^2_p = phenotypic variance,

σ^2_g = Genotypic variance.

Heritability was classified into very high ($\geq 80\%$); values between (60–79%) are moderately high; values between (40–59%) are medium; and low (<40%) as suggested by Singh, B., [31].

2.5.4. Estimation of Genetic Advance

Genetic advance in absolute unit (GA) and percent of the mean (GAM), assuming selection of superior 5% of the genotypes was estimated in accordance with the methods illustrated by [21] as:

$$\text{GA} = K \sigma_p h^2$$

Where, GA = Genetic advance.

K = the standardized selection differential at 5% selection intensity (K = 2.063).

σ_p = Phenotypic standard deviation on mean basis.

h^2 = heritability in broad sense.

2.5.5. Genetic Advance as Percent of Mean (GAM)

Genetic advance as percent of mean were calculated to compare the extent of predicted advance of different traits under selection, using the following formula.

$$\text{GAM} = (\text{GA}/\bar{x}) \times 100$$

Where, GAM = Genetic advance as percent of mean.

GA = Genetic advance.

The GA as percent of mean was categorized as low, moderate and high as suggested by Johnson, H. W *et al.* [21] as follows.

0 - 10% = Low, 10 - 20% = Moderate, and >20% = High.

2.5.6. Association of Characters

(i). Estimation of Correlation Coefficients

Phenotypic and genotypic correlation coefficient was estimated using the standard procedure suggested by Miller, P. A., *et al.* [23] from corresponding variance and covariance

components as:

$$\text{Phenotypic correlation coefficient (rp}_{xy}) = \frac{\sigma_{pxy}}{\sqrt{\sigma^2_{p_x} * \sigma^2_{p_y}}}$$

Where, rp_{xy} = phenotypic correlation coefficient between character x and y.

Genotypic correlation coefficient was tested with the following formula suggested by Robertson [29].

$$\text{Genotypic correlation coefficient (rg}_{xy}) = \frac{\sigma_{gxy}}{\sqrt{\sigma^2_{g_x} * \sigma^2_{g_y}}}$$

rg_{xy} = genotypic correlation coefficients between character x and y.

(ii). Path Coefficient Analysis

Path coefficient analysis was performed using the phenotypic and genotypic correlation coefficients to know the direct and indirect effect of yield components on grain yield using the general formula of [17] by considering grain yield per hectare as dependent variable. The path coefficients were obtained by solving the following simultaneous equations, which express the basic relationship between correlation and path coefficient.

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

Where, r_{ij} = Mutual association between the independent character (i) and dependent character, grain yield (j) as measured by the correlation coefficients.

P_{ij} = Components of direct effects of the independent character (i) as measured by the path coefficients and

$\sum r_{ik} P_{kj}$ = summation of components of indirect of a given independent character.

(i) on a given dependent character (j) via all other independent characters (k).

The contribution of the remaining unknown factor was measured as the residual factor (P_R), which is calculated as: $P_R = \sqrt{(1 - \sum r_{ij} P_{ij})}$ the magnitude of P_R indicates how best the causal factors account for the variability of the dependent factor [32].

3. Results and Discussion

The analysis of variance showed that there was highly significant ($p \leq 0.01$) difference for all traits. The study showed that the presence of considerable variations among genotypes for the traits. This indicates the presence of appreciable level of differences and variability among genotypes for most of the characters and justifies carrying out further genetic analysis. Similar results were reported by several investigators [18]. Highly significant variability was observed among genotypes for grain yield $t ha^{-1}$, which ranged from 2.83 to 6.42 with the mean value of $4.91 t ha^{-1}$.

Table 1. Mean squares values from analysis of variances for 18 characters of 64 bread wheat genotypes grown at AARC 2018 /2019 cropping season.

Trait	Mean	MST	MSE	CV	R ²
DH	59.45	23.88**	4.74	3.66	0.88
DM	110.06	35.68**	7.40	2.47	0.88
GFP	50.73	6.1**	1.77	2.61	0.84
PH	75.77	43.43**	3.74	2.55	0.95
NETP	4.92	1.24**	0.3	11.13	0.87
NTTP	5.39	1.48**	0.26	9.41	0.90
SL	7.74	1.16**	0.24	6.32	0.88
NSPS	15.98	3.49**	0.29	3.35	0.95
NKPS	45.7	32.5**	3.4	4.04	0.93
BMV	13.18	4.91**	1.04	7.73	0.88
GY	4.91	1.19**	0.08	5.91	0.96
HI	37.06	33.65**	12.58	9.57	0.81
TKW	36.51	19.54**	9.27	8.34	0.77
HLW	74.18	8.31**	1.78	1.8	0.88
Trait	Mean	MST	MSE	CV	R ²
GPC	11.04	0.95**	0.17	3.75	0.90
SC	66.33	2.54**	0.14	0.57	0.96
WGL	22.01	11.04**	2.05	6.51	0.90
ZSV	29.08	23.08**	3.86	6.75	0.91

** = highly significant at 1% probability level, CV= Coefficient of variation, MST= Mean squares of treatment, R² = Coefficient of determination, DH= Days to heading (days), DM = Days to maturity (days), GFP = Grain filling period (days), PH = Plant height (cm), NETP = Number of effective tillers per plant, NTTP= Number of total tillers per plant, NSPS = Number of spikelets per spike, NKPS = Number of kernels per spike, SL= Spike length (cm), BMV= Biomass yield (t ha⁻¹), GY= Grain yield (t ha⁻¹), HI = Harvest index (%), TKW = Thousand kernel weight (g), HLW = Hectoliter weight (kg/hl), GPC = Grain protein content (%), SC = Starch content (%), WGL = Wet gluten content (%) and ZSV = Zeleny sedimentation value.

3.1. Estimates of Variance Components

Estimates of phenotypic (σ^2_p), genotypic (σ^2_g) variances; phenotypic and genotypic coefficients of variations; heritability in broad sense, genetic advance and genetic advance as percent of means were estimated for quantitative traits and qualitative traits measured from bread wheat genotypes (Table 3).

3.2. Estimates of Genotypic and Phenotypic Coefficients of Variation

The phenotypic coefficient of variation (PCV) ranged from 1.75 for starch content to 17.85% for number of effective tillers per plant while genotypic coefficient of variation (GCV)

ranged from 1.65 for starch content to 14.48% for number of total tillers per plant. In the present study, none of the traits had high PCV and GCV values. Moderate phenotypic coefficient of variation coupled with moderate genotypic coefficient of variation was observed for number of effective tillers per plant, number of total tillers per plant, biomass yield, grain yield and zeleny sedimentation value indicating the effectiveness of selection based on the phenotypic performance of the genotypes. Similar observations showing moderate values for the phenotypic and genotypic coefficients of variation in wheat were reported by [22, 12] for grain yield, biomass yield and number of effective tillers per meter.

Low values (<10) of both genotypic coefficient of variation and (GCV) and phenotypic coefficient of variation (PCV) were obtained for traits days to heading, days to maturity, grain filling period, plant height, number of spikelets per spike, number of kernels per spike, hectoliter weight, grain protein content and starch content. Similar findings were reported by [13] reported that number of spikelets per spike, days to heading, hectoliter weight, harvest index, grain filling period and days to maturity exhibited least genotypic and phenotypic coefficients of variation. [35] also reported low PCV and GCV were obtained for days to heading, days to maturity and hectoliter weight.

3.3. Estimates of Heritability and Expected Genetic Advance

The broad sense heritability estimates ranged from 35.65% for thousand-kernel weight to 89.55% for starch content (Table 2). In this study, very high heritability noticed for starch content followed by grain yield, number of spikelets per spike, plant height and number of kernels per spike. In agreement with the current result, [19] who reported high heritability was observed for number of spikelets per spike in germplasm. Genetic advance as percent of the means (GAM) in this study ranged from 4.43 to 40.01% for starch content and grain yield respectively. Very high heritability and high genetic advance as percent of mean values were recorded only number of spikelet per spike, number of kernels per spike and grain yield.

Table 2. Range, mean, variance, broad sense heritability, genotypic and phenotypic coefficient of variability, genetic advance as percent of mean for the 18 traits of bread wheat genotypes studied at AARC 2018 / 2019 cropping season.

Traits	Mean \pm SE	Range		σ^2_p	σ^2_g	PCV (%)	GCV (%)	H ² b (%)	GA (k=2.06)	GAM (%)
		Min	Max							
DH	59.45 \pm 3.6	54	71	14.31	9.57	6.36	5.20	66.88	6.73	11.32
DM	110.06 \pm 4.5	101	122.5	21.54	14.14	4.22	3.42	65.65	8.08	7.34
GFP	50.73 \pm 1.8	47	54	3.94	2.17	3.91	2.90	55.02	2.80	5.52
PH	75.77 \pm 5.24	64.2	87	23.59	19.85	6.41	5.88	84.14	11.42	15.08
NETP	4.92 \pm 1.08	2.8	7.1	0.77	0.47	17.85	13.94	61.04	1.40	28.48
NTTP	5.39 \pm 0.95	3.4	7.8	0.87	0.61	17.30	14.48	70.11	1.76	32.59
SL	7.74 \pm 0.78	5.1	10.1	0.70	0.46	10.81	8.76	65.71	1.46	18.84
NSPS	15.98 \pm 1.38	13	18.4	1.89	1.60	8.60	7.92	84.66	3.26	20.39
NKPS	45.7 \pm 4.28	34.5	54	17.95	14.55	9.27	8.35	81.06	9.52	20.83
BMV	13.18 \pm 2.33	10.3	16.7	2.98	1.94	13.09	10.55	65.04	2.97	22.53
GY	4.91 \pm 0.85	2.83	6.42	0.64	0.56	16.23	15.17	87.40	1.96	40.01
HI	37.06 \pm 4.21	24.25	44.24	23.12	10.54	12.97	8.76	45.58	5.45	14.70
TKW	36.51 \pm 3.32	29.60	44.20	14.41	5.14	10.39	6.21	35.65	3.25	8.89

Traits	Mean \pm SE	Range		σ^2_p	σ^2_g	PCV (%)	GCV (%)	H ² b (%)	GA (k=2.06)	GAM (%)
		Min	Max							
HLW	74.18 \pm 2.21	68.6	78.20	5.05	3.27	3.03	2.44	64.72	3.84	5.18
GPC	11.04 \pm 0.74	9.7	13.10	0.56	0.39	6.78	5.66	69.64	1.40	12.67
SC	66.33 \pm 1.21	63.50	69.35	1.34	1.20	1.75	1.65	89.55	2.94	4.43
WGL	22.01 \pm 2.61	17.2	30.45	6.55	4.50	11.62	9.63	68.68	4.70	21.36
ZSV	29.08 \pm 3.86	16.90	38.95	13.47	9.61	12.62	10.66	71.34	7.06	24.28

σ^2_p =Phenotypic variance, σ^2_g =Genotypic variance, PCV (%) = phenotypic coefficient of variance, GCV (%) = Genotypic coefficient of variation, H² b =Broad sense heritability, GA= genetic advance, GAM = Genetic advance as percent of mean, DH= Days to heading (days), DM = Days to maturity (days), GFP = Grain filling period (days), PH = Plant height (cm), NETP = Number of effective tillers per plant, NTTP= Number of total tillers per plant, NSPS = Number of spike lets per spike, NKPS = Number of kernels per spike, SL= Spike length (cm), BMY= Biomass yield (t ha⁻¹), GY= Grain yield (t ha⁻¹), HI = Harvest index (%), TKW = Thousand kernel weight (g), HLW = Hectoliter weight (kg/hl), GPC = Grain protein content (%), SC = Starch content (%), WGL = Wet gluten content (%) and ZSV = Zeleny sedimentation value.

3.4. Estimation of Phenotypic and Genotypic Correlation

Grain yield had positive and highly significant ($P \leq 0.01$) correlation with biomass yield, harvest index, plant height, number of spikelets per spike and number of kernels per spike, at both genotypic and phenotypic levels respectively (Table 3). Similar result was reported by [5] reported strong correlation of grain yield with biomass yield, harvest index, plant height, number of spikelets per spike and number of kernels per spike at genotypic and phenotypic levels. The various characteristics of crop plants are generally

interrelated or correlated [1]. Such correlations can be either negative or positive. Arega *et al* [7] reported at genotypic level, grain yield had a very strong positive correlation with plant height, biomass yield and number of kernels spike⁻¹. Grain yield also showed positive and significant ($P \leq 0.05$) genotypic correlation with days to maturity, hectoliter weight and starch content at both genotypic and phenotypic levels. However, grain yield showed negative and significant ($P \leq 0.05$) correlation with grain protein content at both levels. Similar results were also founded by [10, 12].

Table 3. Estimate of genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients for 18 traits of 64 bread wheat genotypes studied at AARC in 2018/2019 cropping season.

Traits	DH	DM	GFP	PH	NETP	NTTP	SL	NSPS	NKPS
DH	1	0.89**	0.24*	0.18	-0.13	-0.04	0.16	0.08	0.06
DM	0.89**	1	0.61**	0.22	-0.09	-0.027	0.25*	0.12	0.14
GFP	0.20*	0.58**	1	0.16	-0.02	0.03	0.32*	0.02	0.1
PH	0.18*	0.21*	0.15	1	0.08	0.10	0.15	0.35**	0.39**
NETP	-0.10	-0.06	-0.01	0.08	1	0.79**	0.08	0.32*	0.25*
NTTP	-0.01	0.00	0.03	0.10	0.77**	1	0.14	0.14	0.09
SL	0.13	0.21*	0.26**	0.14	0.07	0.16	1	0.04	0.10
NSPS	0.07	0.12	0.03	0.33**	0.26**	0.12	0.04	1	0.89**
NKPS	0.06	0.13	0.09	0.35**	0.21*	0.09	0.10	0.86**	1
BMY	0.21*	0.20*	-0.00	0.68**	0.16	0.15	0.09	0.45**	0.43**
GY	0.15	0.24*	0.21*	0.68**	0.19*	0.16	0.12	0.58**	0.52**
HI	-0.10	0.02	0.21*	0.2*	0.13	0.12	0.08	0.31**	0.28**
TKW	0.24*	0.24*	0.11	0.4**	-0.13	-0.09	0.02	0.02	-0.07
HLW	0.18*	0.16*	0.08	0.3**	0.17	0.06	0.06	0.10	0.11
GPC	-0.03	-0.01	0.04	-0.22*	-0.17*	-0.12	0.01	-0.09	-0.05
SC	0.06	0.10	0.08	0.19*	0.08	0.05	-0.16	0.12	0.09
WGL	0.02	0.04	0.10	-0.11	-0.08	0.00	0.01	-0.04	-0.02
ZSV	-0.01	-0.02	-0.04	0.05	-0.06	-0.06	0.05	0.07	0.14

Table 3. Continued.

Traits	BMY	GY	HI	TKW	HLW	GPC	SC	WGL	ZSV
DH	0.24	0.16	-0.11	0.26*	0.19	-0.06	0.08	-0.01	-0.03
DM	0.24*	0.26*	0.01	0.25*	0.18	-0.04	0.13	0.03	-0.03
GFP	0.06	0.24	0.21	0.10	0.08	0.06	0.09	0.14	-0.01
PH	0.76**	0.73**	0.25*	0.47**	0.34*	-0.24*	0.19	-0.12	0.06
NETP	0.21	0.19	0.11	-0.18	0.19	-0.21	0.08	-0.09	-0.06
NTTP	0.21	0.19	0.13	-0.12	0.09	-0.14	-0.04	0.01	-0.06
SL	0.09	0.17	0.15	0.05	0.09	0.02	-0.18	0.01	0.06
NSPS	0.49**	0.61**	0.39**	0.02	0.13	-0.12	0.14	-0.07	0.06
NKPS	0.48**	0.55**	0.36**	-0.07	0.14	-0.07	0.09	-0.04	0.14
BMY	1	0.76**	-0.01	0.28*	0.22	-0.34*	0.26*	-0.19	-0.03
GY	0.71**	1	0.58**	0.33*	0.25*	-0.27*	0.26*	-0.1	-0.02
HI	-0.1	0.53**	1	0.13	0.14	0.06	-0.03	0.08	0.12
TKW	0.22*	0.26**	0.06	1	0.44**	-0.12	0.22	-0.05	-0.07

Traits	BMY	GY	HI	TKW	HLW	GPC	SC	WGL	ZSV
HLW	0.22*	0.23*	0.07	0.44**	1	0.07	-0.04	0.14	0.36*
GPC	-0.3**	-0.22*	0.1	-0.08	0.05	1	-0.64**	0.89**	0.79**
SC	0.25*	0.24*	-0.05	0.19*	-0.03	-0.64**	1	-0.44**	-0.64**
WGL	-0.17*	-0.07	0.11	-0.01	0.12	0.9**	-0.46**	1	0.72**
ZSV	-0.04	-0.001	0.12	-0.03	0.3**	0.81**	-0.63**	0.75**	1

*and **, significant at $P \leq 0.05$ and $P \leq 0.01$, respectively, and the rest are not significant, DH= Days to heading (days), DM = Days to maturity (days), GFP = Grain filling period (days), PH = Plant height (cm), NETP = Number of effective tillers per plant, NTTTP = Number of total tillers per plant, NSPS = Number of spike lets per spike, NKPS = Number of kernels per spike, SL = Spike length (cm), BMY = Biomass yield ($t ha^{-1}$), GY = Grain yield ($t ha^{-1}$), HI = Harvest index (%), TKW = Thousand kernel weight (g), HLW = Hectoliter weight (kg/hl), GPC = Grain protein content (%), SC = Starch content (%), WGL = Wet gluten content (%) and ZSV = Zeleny sedimentation value.

3.5. Path Coefficient Analysis

path coefficient analysis can identify the direct and indirect causes of association and can measure the relative importance to each other [30]. In the present study, grain yield was selected as dependent variable and the other that had significant correlation of characters were selected as casual variable. The results of path analysis for direct and indirect effects of the characters studied both at genotypic and phenotypic level are illustrated in (Tables 4 and 5).

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

The results of path coefficient analysis at genotypic level (Table 4) revealed that biomass yield exerted the highest positive direct effect followed by harvest index. Similar results were reported by [3, 25] for biomass yield and harvest index. In addition, days to maturity, plant height, number of spikelet's per spike, thousand kernels weight and starch content exerted positive and less magnitude direct effect on grain yield. On the other hand, number of kernels per spike, hectoliter weight, grain protein content had negative genotypic directs effect on grain yield. The

positive indirect effect of days to maturity was scored via biomass yield. The positive indirect effect of plant height was scored via biomass yield and harvest index. Traits like, thousand kernel weight and starch content exerted positive, but negligible genotypic direct effect on grain yield. They exerted positive indirect effect on grain yield via biomass yield. Numbers of spikelets per spike also exerted positive genotypic direct effect on grain yield. It exerted positive indirect effect on grain yield via biomass yield and harvest index. Therefore, the observed positive and high significant genotypic correlations of these traits with grain yield were due to the indirect effects.

Number of kernels per spike had negative direct effect on grain yield and it had positive and high significant genotypic correlation. It exerted positive indirect effect on grain yield via biomass yield, harvest index and number of spikelets per spike. Hectoliter weight and grain protein content exerted negative direct effect via biomass yield 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. This result is in agreement with [12, 20] who reported negative direct effect of grain protein content on grain yield.

Table 4. Estimates of direct (bold and underlined diagonal) and indirect effects (off diagonal) of different traits on grain yield at genotypic level in 64 bread wheat genotypes tested at AARC 2018/2019 cropping season.

Traits	DM	PH	NSPS	NKPS	BMY	HI	TKW	HLW	GPC	SC	Rg
DM	0.0713	0.0047	0.0153	-0.0181	0.1732	0.0027	0.0008	-0.0021	0.0000	0.0096	0.26*
PH	0.0158	0.0213	0.0429	-0.0519	0.5456	0.1458	0.0015	-0.0039	0.0001	0.0149	0.73**
NSPS	0.0088	0.0074	0.1234	-0.1200	0.3515	0.2275	0.0001	-0.0015	0.0000	0.0104	0.61**
NKPS	0.0096	0.0082	0.1102	-0.1344	0.3417	0.2090	-0.0002	-0.0016	0.0000	0.0068	0.55**
BMY	0.0172	0.0162	0.0605	-0.0641	0.7166	-0.0033	0.0009	-0.0026	0.0001	0.0200	0.76**
HI	0.0003	0.0053	0.0483	-0.0483	-0.0041	0.5814	0.0004	-0.0016	0.0000	-0.0030	0.58**
TKW	0.0191	0.0101	0.0030	0.0093	0.1976	0.0777	0.0031	-0.0050	0.0000	0.0166	0.33*
HLW	0.0130	0.0072	0.0166	-0.0183	0.1603	0.0804	0.0014	-0.0114	0.0677	-0.0393	0.25*
GPC	-0.0031	-0.0052	-0.0146	0.0100	-0.2411	0.0348	-0.0004	-0.0008	-0.0002	-0.0488	-0.27*
SC	0.0090	0.0042	0.0169	-0.0121	0.1883	-0.0230	0.0007	0.0004	0.0001	0.0762	0.26*

Residua = 0.253, DM = Days to maturity (days), PH = Plant height (cm), NSPS = Number of spike lets per spike, NKPS = Number of kernels per spike, BMY= Biomass yield ($t ha^{-1}$), HI = Harvest index (%), TKW = Thousand kernel weight (g), HLW = Hectoliter weight (kg/hl), GPC = Grain protein content (%), SC = Starch content (%) and Rg = Genotypic correlation.

3.7. Direct and Indirect Effects of Various Characters on Grain Yield at Phenotypic Level

The results of path coefficient analysis for phenotypic correlations among traits revealed that the biomass yield exerted highest direct effect on grain yield followed by

harvest index and number of spikelets per spike (Table 5). Traits like, days to maturity, grain filling period, plant height, thousand kernel weight, starch content and hectoliter weight exerted positive and less magnitude direct effect on grain yield. However, number of effective tillers per plant, number of kernels per spike and grain protein

content had negative phenotypic direct effect on grain yield. The low direct effect of the above traits and their highly significant and significant phenotypic correlation with grain yield was due to the cumulative indirect effect of these traits through other. This means even if their direct effect on grain yield is small still improvement of these traits may favor on grain yield. Traits like, plant height, starch content, hectoliter weight and thousand kernel weights were showed positive direct effect on grain yield. The positive indirect effects of this trait were via biomass yield. In addition,

number of spikelets per spike exerted positive direct effect on grain yield via biomass yield and harvest index. Number of effective tillers per plant, number of kernels per spike and grain protein content had showed negative phenotypic direct effect on grain yield via in direct effect of biomass yield. Similar result was reported by [11] who obtained negative direct effect of grain protein content and number of kernels per spike on grain yield at dhera. Generally, attention should be given to indirect effect not only direct effect on grain yield for each trait.

Table 5. Estimates of direct (bold and underlined diagonal) and indirect effects (off diagonal) of different traits on grain yield at phenotypic level in 64 bread wheat genotypes tested at AARC 2018/2019 cropping season.

Traits	DM	GFP	PH	NETP	NSPS	NKPS	BMY	HI	TKW	HLW	GPC	SC	Rp
DM	0.0246	0.0407	0.0152	0.0014	0.0184	-0.0128	0.1307	0.0121	0.0008	0.0023	0.0004	0.0060	0.24*
GFP	0.0143	0.0701	0.0104	0.0003	0.0042	-0.0092	-0.0001	0.1166	0.0004	0.0011	-0.0009	0.0046	0.21*
PH	0.0052	0.0102	0.0714	-0.0019	0.0527	-0.0356	0.4468	0.1089	0.0014	0.0043	0.0051	0.0113	0.68**
ETP	-0.0015	-0.0008	0.0057	-0.0234	0.0418	-0.0213	0.1082	0.0703	-0.0005	0.0022	0.0040	0.0046	0.19*
SPS	0.0028	0.0019	0.0236	-0.0061	0.1594	-0.0865	0.2968	0.1731	0.0001	0.0014	0.0021	0.0073	0.58**
KPS	0.0031	0.0064	0.0253	-0.0049	0.1369	-0.1007	0.2867	0.1565	-0.0002	0.0016	0.0013	0.0051	0.52**
BMY	0.0049	0.0000	0.0484	-0.0038	0.0717	-0.0438	0.6596	-0.055	0.0008	0.0031	0.0071	0.0149	0.71**
HI	0.0005	0.0148	0.0141	-0.0030	0.0499	-0.0285	-0.0661	0.5529	0.0002	0.0010	-0.0025	-0.0033	0.53**
TKW	0.0059	0.0077	0.0287	0.0031	0.0027	0.0067	0.1451	0.0331	0.0034	0.0062	0.0020	0.0112	0.26*
HLW	0.0040	0.0053	0.0219	-0.0037	0.0163	-0.0113	0.1471	0.0398	0.0015	0.0139	-0.0011	-0.0020	0.23*
GPC	-0.0004	0.0026	-0.0156	0.0040	-0.0146	0.0055	-0.2008	0.0581	-0.0003	0.0007	-0.0234	-0.0383	-0.22*
SC	0.0025	0.0054	0.0135	-0.0018	0.0195	-0.0086	0.1642	-0.0300	0.0006	-0.0005	0.0150	0.0599	0.24*

Residual effects= 0.335 DM = Days to maturity (days), GFP = Grain filling period, PH = Plant height (cm), NETP = Number of effective tillers per plant, NSPS = Number of spike lets per spike, NKPS = Number of kernels per spike, BMY= Biomass yield (t ha⁻¹, HI = Harvest index (%), TKW = Thousand kernel weight (g), HLW = Hectoliter weight (kg/hl), GPC = Grain protein content (%), SC = Starch content (%) and Rp = Phenotypic correlation.

4. Conclusions

Information on the nature and magnitude of genetic variability present in a crop species is important to develop many essential characters for any breeding strategy and crop improvement program. In order to generate fertile genetic variability information, a total of sixty-four bread wheat genotypes which included four standard checks (Lemu, King brid, Wane and Tay) were tested in simple lattice design (8x8) under rain fed condition at Adet Agricultural Research Centre in 2018/2019 cropping season. The data obtained from the experiment were subjected to the analysis of variance, genotypic and phenotypic coefficient of variations, estimations of heritability in broad sense and expected genetic advance, correlation and path analysis. The analysis of variance revealed highly significant differences among the genotypes for all characters.

5. Recommendations

The present study showed the presence of considerable variability for the tested wheat genotypes and the possibility of improving yield and other desirable characters through selection. However, this study was conducted for one season and at one location, further testing at many wheat growing areas and cropping seasons is required to verify the results and to draw more valid conclusions that could be utilized for

developing high yielding bread wheat varieties with better grain quality characters.

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