Estimate of Correlation Coefficients and Path Analysis for Yield Component Traits in Bread Wheat (*Triticum aestivum. L*) Genotypes under Lowland Temperature Stress

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ABSTRACT

Trait based study of bread wheat genotypes information under lowland temperature stress situation is limited. The association and analysis of path coefficient were studied in 36 diverse bread wheat genotypes in order to understand the relationship and contribution of seventeen traits towards the grain yield in the area of temperature stress. These field experiments were done in the arrangement of Triple Lattice Design replicated three times at Werer agricultural research center, Afar region in 2017. The data generated from the experiment was laid open to analysis of variance, correlation and path analysis. Analysis of variances of bread wheat genotypes assessed for the traits shown strong significant difference among the genotypes for most characters and significant difference between genotypes for total tillers and for fertility of spike and non-significant difference for days to emergence. The study of correlation suggested that spike fertility, thousand kernels weight, biomass yield per hectare and harvest index were the most essential characters which possessed positive and highly significant genotypic and phenotypic correlation with grain yield. The phenotypic analysis of path coefficient indicated that harvest index and biomass yield exerted highest positive direct effect on grain yield. Similarly path coefficient analysis at genotypic level showed harvest index exhibited highest positive direct effect on grain yield per hectare followed by biomass yield. Therefore, from the present outcomes it has been observed important traits which influence positive associated and direct effect on grain yield. These study suggest that harvest index and biomass yield per hectare can be used as selection standards in breeding to improve bread wheat genotypes with high yielding under stress condition.

Keywords: Bread wheat; Correlation; Path coefficient; Yield component

Introduction

Wheat (*Triticum aestivum L.*) is one of the most important cereal crop world-wide and it is the most important crop in Ethiopia and ranked 4th in area (13.38%) and grain production (15.17%) of total grain crops next to Tef, Maize and Sorghum which has resulted increase in a production mainly by smallholder farmers using rain-fed based production system and used mainly for food [1]. Most of Ethiopia's irrigation potential is found in the lowlands. Producing wheat in an irrigated cotton-wheat rotation system in the lower Awash Valley has shown promising wheat productivity levels. Growing wheat in the lowlands during the dry season avoids the challenge of wheat rust disease a major problem in the traditional wheat growing highlands. Thus, breeding in the lowland temperature stress condition and heat tolerant bread wheat genotypes with relevant traits that improving grain yield is the key point to enhance productivity in the stress environments and also identifying a symmetrical association between two traits that helps in considering the nature and magnitude of association between yield and yield related traits as well as partition of the association in to direct and indirect effect is a key concern.

Information concerning interrelationships among quantitative inherited crop characters and their direct and indirect effects on grain yield is of great importance for achievement in selections to be conducted in breeding programs [2]. Studies on genotypic and phenotypic correlations among traits of crop plants are useful in planning, evaluating and setting selection criteria for the desired characters for selection in breeding program [3,4]. Correlation between various physiological and morphological characters results from complex interrelationships among grain yield and yield related traits themselves. But it does not give a particular picture of the relative importance of direct and indirect effects of the various yield attributes

[5]. Thus, in order to get a clear representation of the inter-relationship between grain yield and other traits, direct and indirect effects should be worked out using path coefficient analysis at genotypic level [6]. Using path coefficient analysis, it is easy to determine which yield component is influencing the yield substantially [2]. Thus, to make a good choice for high grain yield a systematic understanding of grain yield component traits and their interaction with yield and themselves is very necessary. Path coefficient analysis has been used by plant breeders to assist in identifying traits that are useful as selection criteria to improve crop yield [2].

Materials and Methods

The experimentation was done at Amibara district Werer Agricultural Research Center under Ethiopian Institute of Agricultural Research during main cropping season in 2017. Geographically, the location of the research site is 9° 16'8"N latitude and 40° 9'41"E longitudes and altitude of 740 m above sea level in Afar region where crop husbandry is mainly grown using irrigation following cotton production. The annual and monthly temperature of the testing site has a mean maximum and minimum of 34°C and 19°C and 38.06°C and 21.06°C during main season, respectively. The precipitation in

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study area is characterized by unpredictable and uneven distribution with annual average rainfall about 571 mm which is not sufficient for crop production. Hence crop production in the region was mostly furrow irrigation method from the source of nearby Awash River. The soil in the testing field of Werer is predominantly Fluvisols, while vertisol are the second dominant soil that occupies about 30% of the total area. The field trial was arranged in Triple Lattice Design comprised of 36 entries which replicated three times. The plot size was 10 rows of 3 m length and 0.3 m between rows (9 m2). 100 kg ha-1 seeds were sown by hand drilling on the prepared ridges. The water was applied at interval of 10 days using furrow application method (Werer Agricultural Water management preliminary data) and other agronomic practices were applied for each treatment uniformly. Data were collected for Phenological and physiological as well as yield and yield related parameters Days to Emergence(DE), Days to Heading/flowering (DH), Days to Maturity (DM), Grain Filling Period (GFP), Plant Height (cm), Spike Length (cm), Canopy Temperature(CT), Chlorophyll content, Number of tillers/plant, 1000 grain wt. (gm) Number of effective tillers/plant, Number of spikelet/spike, Number of seed/spike, Grain yield (g/plot), Spike fertility/tipping, Biomass yield (Kg/ha) and Harvest index (HI) (%).

Statistical analysis

Analysis of variance: The recorded data were exposed to analysis of variance (ANOVA) as suggested by Gomez et al. using SAS Software (Version 9.0) [7]. The ANOVA model of the data was given below in Table 1 and the linear model equation of analysis of variance was as follows:

Source of variation	DF	MS	EMS
Replication	r-1	-	-
Block	r(k-1)	MSb	-
Genotypes	K2-1	MSg	σ2e+rσ2g
Intra block error	K-1 (rk-k-1)	MSe	σ2e
Total	(r)(k2)-1	-	-

Note: Here r=number of replications, k=block size, g= number of genotypes; DF=degree of freedom, MSb=mean square of block, MSg=mean square of genotypes, MSe=mean square of error, σ2g= genotype variance

Table 1: An outline of the analysis of variance of 6*6 triple lattice design.

Yij=Mean+Repi+Block(rep)j+Trtk+Errorijk

Correlation analysis

Estimation of genotypic and phenotypic correlation coefficients was done based on the procedure of Dabholkar [8].

Genotypic correlation coefficient (rg)=covg(xy)/σ²g(x)˙σ²g(y)

Phenotypic correlation coefficient (rp)=covp(xy)/σ²p(x)˙σ²p(y)

Where:

COVg (xy) and COVp (xy) are the genotypic and phenotypic covariance's of two variables (X and Y), respectively.

σg (x) and σg (y) are the genotypic standard deviations for variables

X and Y respectively. σp (x) and σp (y) are the phenotypic standard deviations of variables X and Y, respectively.

The calculated phenotypic correlation values were tested for its significance using t-test:

t=r_p/SE (r_p)

Where, r_p=Phenotypic correlation;

SE (r_p)=Standard error of phenotypic correlation obtained using the following formula.

SE (r_p)=√1-r2p/n-2

Where, n is the number of genotypes tested,

r2p is phenotypic correlation coefficient.

The coefficients of correlations at genotypic levels were also tested for their significance by the formula described by Robertson as indicated below:

t=rgxy/SErgxy

The calculated "t" values were compared with the tabulated "t" value at (n-2) degree of freedom at 5% level of significance. Where, n is number of genotypes.

SErgxy=√1-r²gxy/h²x˙h²y

Where, h²x=Heritability of trait x and h²y=Heritability of trait y

Path coefficient analysis

Path coefficient Analysis was computed for each parameter separately to partition the correlation coefficient to direct and indirect effects of the components on bread wheat yield and as illustrated by Dewey et al. [9].

The formula: rij=pij+Σrikpkj

where, rij=Mutual association between the independent character (i) and dependent character(j) as measured by the correlation coefficient.

pij=Components of direct effects of the independent character (i) on the dependent character (j) as measured by the path coefficient.

Σrikpkj=summation of components of indirect effect of a given independent character (i) on the given independent character (j) via all other independent characters (k).

The residual effect, which determines how best the causal factors account for the Variability of the dependent factor was calculated using the following formula:

1=p²r+Σpiy.riy

Where: p2r=is the residual factor,

piy is the direct effect of yield with i[th] trait.

riy is the correlation of yield with the ith trait.

Results and Discussion

Analysis of variance

The analysis of variances of bread wheat genotypes assessed for seventeen traits revealed that highly significant (P ≤ 0.01) difference between genotypes for most traits and significant difference (P ≤ 0.05)

among genotypes for total tillers and for spike fertility and non-significant difference for days to emergence (Table 2). The significant difference between genotypes for the traits indicated the existence of a considerable amount of variability among genotypes which is an essential to the study of plant breeders for enhancement of these traits through breeding. The mean square due to replication indicated highly significant difference for biomass yield and significant difference for days to emergence, spike length and grain yield which showed the heterogeneity present in the field.

Traits	Mean squares				CV%
	Replication	Block (group)	Genotype	Error	
	d.f=2	d.f=15	d.f=35	d.f=55	
DE	2.23*	0.6	0.62ns	0.64	12.07
DH	2.12	2.85	108.46**	2.94	3.16
DM	8.08	5.82	117.93**	7.23	3.09
GFP	6.23	4.56	17.56**	7.01	8.07
PH	75.58	29.85	124.20**	27.35	8.5
SL	1.638*	0.83*	2.77**	0.41	8.06
TT	0.41	0.12	0.54*	0.31	13.13
ET	0.37	0.32	0.94**	0.3	14.22
NSSP	2.36	0.49	4.10**	0.86	6.21
NKSP	26.96	22.56	59.12**	18.94	12.15
SPF	23.68	20.89	61.23*	24.14	5.69
CT	36.80**	2.43	12.98**	2.62	4.72
CLC	2.14	2.82	17.64**	3.54	3.85
BY	11287194.60**	1493156	4950469.40**	1024605	14.62
TKW	6.38	4.13	26.40**	4.08	7.3
YLD	736350.08*	122589	482329.00**	105636	16.76
HI	5.11	9.22	77.84**	12.43	12.32

Note: *, ** and ns, significant at 5%, 1% probability level and non-significant, respectively. Where: CV=coefficient of variation, d.f=degree of freedom, HI=harvest index, kernels per spike, NSSP=number of spikelet per spike, ET=effective tillers, TT=total tillers, SL=spike length, PH=plant height, GFP=grain filling period, DM=days to maturity, DH=days to heading, DE=days to emergence.YLD=yield kg/ha, TKW=thousands kernel weight, BY=biomass yield kg/ha, CLC=chlorophyll content, CT=canopy temperature, SPF=spike fertility, NKSP=number of

Table 2: The mean squares for different sources of variation and CV% for 17 Traits.

Genotypic and phenotypic correlation coefficients

The correlation coefficients of genotypic and phenotypic were estimated for all possible pair of traits and results are presented in (Tables 3 and 4). In current study the correlation analysis indicated the correlation coefficients of genotypic values were higher than their phenotypic correlation values for most of the traits, indicating inherent association of the traits which showed that the association was largely due to genetic factors. These results agreed with the findings of Jayasudha et al. [10].

Traits	DH	DM	GFP	PH	SL	TT	ET	NSSP	NKSP	SPF	CT	CLC	BMS	TKW	YLD	HI
DH	-	0.89**	-0.07	0.42**	0.40**	-0.23*	-0.35**	0.22*	0.11	-0.43**	-0.61**	-0.07	0.46**	-0.23*	0.01	-0.47**
DM	-	-	0.40**	0.45**	0.35**	-0.17	-0.35**	0.17	0.15	-0.44**	-0.65**	-0.03	0.47**	-0.14	0.05	-0.43**
GFP	-	-	-	0.15	-0.04	0.09	-0.05	-0.07	0.1	-0.09	-0.20*	0.08	0.11	0.17	0.09	-0.01
PH	-	-	-	-	0.49**	0.02	0.01	0.31**	0.37**	-0.04	-0.60**	0.17	0.67**	0.18	0.31**	-0.38**
SL	-	-	-	-	-	-0.15	-0.14	0.54**	0.26**	-0.23**	-0.28**	0.18	0.30**	0.12	0.07	-0.22*
TT	-	-	-	-	-	-	0.81**	-0.11	0.08	0.14	0.02	0.22*	0.1	0.01	0.09	0
ET	-	-	-	-	-	-	-	-0.06	0.11	0.27**	0.09	0.24**	0.02	0.18	0.11	0.11
NSSP	-	-	-	-	-	-	-	-	0.39**	0.04	-0.15	0.28**	0.12	0	-0.12	-0.22*
NKSP	-	-	-	-	-	-	-	-	-	0.22*	-0.28**	0.23**	0.19*	-0.18	0.13	-0.04
SPF	-	-	-	-	-	-	-	-	-	-	0.1	0.1	-0.04	0.11	0.28**	0.35**
CT	-	-	-	-	-	-	-	-	-	-	-	0.09	-0.67**	-0.13	-0.32**	0.37**
CLC	-	-	-	-	-	-	-	-	-	-	-	-	0	0.01	0.01	0.06
BMS	-	-	-	-	-	-	-	-	-	-	-	-	-	0.1	0.61**	-0.41**
TKW	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.24**	0.15
YLD	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.46**
HI	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Note: * and ** indicate significant at 0.05 and 0.01 probability levels, respectively.

Where: HI=harvest index, YLD=yield kg/ha, TKW=thousands kernel weight, BY=biomass yield kg/ha, CLC=chlorophyll content, CT=canopy temperature, SPF=spike fertility, NKSP=number of kernels per spike, NSSP=number of spikelet per spike, ET=effective tillers, TT=total tillers, SL=spike length, PH=plant height, GFP=grain filling period, DM=days to maturity, DH=days to heading.

Table 3: Phenotypic correlation coefficient for 16 traits in bread wheat genotypes under heat stress condition.

Traits	DH	DM	GFP	PH	SL	TT	ET	NSSP	NKSP	SPF	CT	CLC	BMS	TKW	YLD	HI
DH	-	-	-	·	-	-	-	-	-	-	-	-	-	-	-	-
DM	0.93**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
GFP	-0.04	0.34*	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PH	0.55**	0.55**	0.1	-	-	-	-	-	-	-	-	-	-	-	-	-
SL	0.49**	0.41**	-0.12	0.49**	-	-	-	-	-	-	-	-	-	-	-	-
TT	-0.35*	-0.28	0.12	0.01	-0.33*	-	-	-	-	-	-	-	-	-	-	-
ET	-0.47**	-0.44**	0.01	-0.03	-0.29	0.88**	-	-	-	-	-	-	-	-	-	-
NSSP	0.27	0.2	-0.16	0.33*	0.67**	-0.06	0.04	-	-	-	-	-	-	-	-	-
NKSP	0.18	0.2	0.08	0.31	0.17	0.18	0.18	0.41**	-	-	-	-	-	-	-	-
SPF	-0.54**	-0.57**	-0.15	-0.15	-0.38*	0.43**	0.55**	-0.07	0.2	-	-	-	-	-	-	-
CT	-0.77**	-0.79**	-0.19	-0.63**	-0.26	0.11	0.17	-0.12	-0.26	0.18	-	-	-	-	-	-
CLC	-0.08	-0.05	0.08	0.25	0.24	0.32	0.32	0.27	0.40*	0.16	0.12	-	-	-	-	-
BMS	0.59**	0.62**	0.18	0.70**	0.3	0.04	-0.06	0.19	0.2	-0.05	-0.76**	0.11	-	-	-	-
TKW	-0.24	-0.17	0.17	0.06	0.08	0	0.19	-0.03	-0.37*	0.17	-0.03	0.01	-0.02	-	-	-
YLD	0.03	0.04	0.04	0.26	-0.07	0.04	0.06	-0.1	0.17	0.48**	-0.32*	0.11	0.52**	0.19	-	-
HI	-0.54**	-0.56**	-0.12	-0.45**	-0.35*	0.02	0.12	-0.26	-0.02	0.54**	0.44**	0.06	-0.44**	0.2	0.51**	-

Note: * and ** indicate significant at 0.05 and 0.01 probability levels, respectively.

Where: DH=days to heading, DM=days to maturity, GFP=grain filling period, PH=plant height, SL=spike length, TT=total tillers, ET=effective tillers, NSSP=number of spikelet's per spike, NKSP=No of kernel per spike, SPF=spike fertility, CT=canopy temperature, CLC=chlorophyll content, BMS=biomass kg/ha, TKW=thousands kernel weight, YLD=yield kg/ha, HI=harvest index.

Table 4: Genotypic Correlation coefficient for 16 traits in bread wheat genotypes under heat stress condition.

Genotypic and phenotypic correlations among phenological, morphological and physiological traits: Days to heading has positive and highly significant genotypic and phenotypic correlations with days to maturity (r=0.93** and 0.89**), plant height (r=0.55** and 0.42**), spike length (r=0.49** and 0.40**) and biomass (r=0.59** and 0.46**) and it had also positive significant correlation with number of spikelet's per spike(0.22*) only at phenotypic level, showed simultaneous enhancement of these trait is possible and also early heading genotypes had a probability short grain filling period and mature early with significant spike length that contribute for the formation of better spikelet per spike and kernels per spike. Similar findings were observed by Degewione et al. who were reported highly significant association of days to heading with days to maturity and Significant association between days to heading and plant height was also reported by Ali et al. [11,12]. Days to heading also negative and highly significant genotypic and phenotypic correlations with effective tillers per plant (r=-0.47** and -0.35**), spike fertility (r=-0.54** and -0.43**), canopy temperature (r=-0.77** and -0.61**) and harvest index (r=-0.54** and -47**) and also negative significant genotypic and phenotypic association with total tillers per plant (r=-0.35* and -0.23*) and thousand kernel weights(r=-0.23*) at phenotypic level. However this trait showed non-significant correlation with the rest of the traits. Similarly Degewione et al. reported non-significant association of days to heading with different traits [11].

Days to maturity had positive and highly significant genotypic and phenotypic correlation with plant height(r=0.55** and 0.55**), spike length (r=0.41** and 0.35**), biomass(r=0.62** and 0.47**) and grain filling period(r=0.34* and 0.40**), positive significant at genotypic level showed that, genotypes that reached early grain filling period had better chance for early maturing and also late maturing genotypes had taller plant height and higher spike length. This result was agreed with the findings of Gelalcha et al. who reported highly significant association of days to maturity with days to heading, plant height, and spike length, positive and significant with biomass [13]. It had

negative and highly significant genotypic and phenotypic correlation with effective tillers(r=-0.44** and -0.35**), spike fertility(r=-0.57** and -0.44**), canopy temperature(r=-0.79** and -0.65**) and harvest index(r=-0.56** and -0.43**). Both traits, days to heading and days to maturity displayed positive and non-significant genotypic and phenotypic correlation with number of spikelet per spike, number of kernel per spike, and grain yield/ha except number of spikelet per spike which had positive significant at phenotypic level. Therefore, this positive association with grain yield can be used in selection of genotypes for higher yield.

Grain filling period had positive and non-significant genotypic and phenotypic correlation with plant height, total tillers, effective tillers (only at genotypic level), number of kernel per spike, chlorophyll content, biomass yield, thousand kernel weight and yield/ha exhibited genotypes with high grain filling period possessed higher number of tillers per plant and contributing the formation of kernel per spike. Whereas negative and non-significant genotypic and phenotypic association was found with spike length, number of spikelet's per spike, spike fertility, canopy temperature and harvest index. There were positive and highly significant genotypic and phenotypic correlation of plant height was noticed with number of spikelet per spike (r=0.33* and 0.31**), spike length (r=0.49** and 0.49**) biomass yield/ha (r=0.70**and 0.67**) and it had also highly significant and positive phenotypic association with number of kernels per spike (r=0.37**) and grain yield/ha (r=0.31**). While negative and highly significant association with Canopy temperature (r=-0.63** and -0.60**) and harvest index (r=-0.45** and -0.38**). Plant height had also positive genotypic correlation with total tillers per plant, number of kernel per spike, chlorophyll content, thousand kernel weights and grain yield. It showed non-significant and negative with the rest traits.

Positive and highly significant genotypic and phenotypic correlation of canopy temperature at grain filling stage was observed with harvest index (r=0.44** and 0.37**) and positively associated

with chlorophyll content and negatively correlated with thousand kernel weights. It had also negative and highly significant genotypic and phenotypic correlation with biomass (r=-0.76** and -0.67**) and negative significant to highly significant with grain yield/ha (r=-0.32* and -0.32**). Similar results were reported by Bahar et al. significant negative correlation between canopy temperature and grain yield [14]. Similarly Rahman et al. also reported strong and negative correlation of canopy temperature with grain yield. These traits indicating that cell functioning, transpiration and photosynthesis is proper when canopy temperature is low during grain filling period and crop plants relatively better capacity for taking up soil moisture. Rauf et al. observed that high yielding genotypes possess significantly low canopy temperature. It influences grain yield more strongly in the presence of high temperature stress having highly negative correlation with yield. Therefore this trait indicated selection of wheat genotypes that was tolerant to high temperature stress condition. The physiological trait Chlorophyll content showed considerable positive genotypic and phenotypic correlation with most of the traits studied except days to heading and days to maturity, indicating the wheat genotypes with high chlorophyll content can produce high yield under moisture-stressed conditions and there was a positive correlation between chlorophyll content and grain yield. Similar results were reported by Reza et al.

Genotypic and phenotypic correlations of yield components: Spike length was positive and highly significant genotypic association with number of spikelet's per spike (r=0.67**), days to heading(r=0.49**), days to maturity (r=0.41**) and plant height (r=0.49**) and also positive and highly significant phenotypic correlation with number of spikelet's per spike (r=0.54**), number of kernels per spike (r=0.26**) and biomass yield/ha (0.30**) whereas negative and significant genotypic and phenotypic correlation with spike fertility (r=-0.38* and -0.23*) and harvest index (r=-0.35* and -0.22*). It was showed positively associated with number of kernels per spike, chlorophyll content, biomass yield and thousand kernel weights at genotypic level and positive phenotypic association with chlorophyll content, thousand kernel weights and grain yield/ha but negative correlation with the rest traits. Similarly positive association among traits were also reported by Kumer et al. for kernel per spike and spike length; Naghavi et al. for spikelet's per spike and spike length. Total tillers per plant had positive and highly significant genotypic and phenotypic correlation with effective tillers per plant (r=0.88** and, 0.81**), spike fertility (r=0.43**) at genotypic level and chlorophyll content (r=0.22*) at phenotypic level. It had negative and non-significant genotypic and phenotypic association with number of spikelets per spike and positive association with most of the rest traits. Number of spikelet per spike had positive and highly significant genotypic and phenotypic association with number of kernels per spike (r=0.41** and 0.39**) and chlorophyll content (r=0.28**) at phenotypic level. Non-significant and positive genotypic and phenotypic correlations were found with biomass yield/ha and chlorophyll content at genotypic level, while negative non-significant was observed with other traits.

Positive and significant to highly significant genotypic and phenotypic correlation of number of kernel per spike was showed with chlorophyll content (r=0.40* and 0.23**) and also significant positive association with spike fertility and biomass yield/ha while negative significant with thousand kernel weight (r=-0.37*) at genotypic level and negative highly significant with canopy temperature(r=-0.28**) at phenotypic level. Whereas positive non-significant genotypic and phenotypic correlation was observed with most of the traits studied except harvest index which had negative correlated at both level and

canopy temperature at genotypic level and thousand kernel weights at phenotypic level. Similar findings were also reported by Degewione et al. [11]. Spike fertility showed positive and highly significant genotypic and phenotypic correlation with grain yield/ha (r=0.48** and 0.28**) and harvest index (r=0.54** and 0.35**). Whereas positive genotypic and phenotypic association was found with canopy temperature, chlorophyll content and thousand kernel weights and also negatively associated with biomass yield.

Biomass yield/ha showed positive and highly significant genotypic and phenotypic association with grain yield/ha (r=0.52** and, 0.61**), whereas negative and highly significant association with harvest index (r=-0.44** and, -0.41**). This negative association indicated that selection of genotypes for high biomass yield might lower harvest index. These results agreed with the previous findings of kabir et al. who reported relatively biomass yield showed negative and highly significant correlation with harvest index. Positive correlation of thousand kernel weight was observed with grain yield/ha and harvest index both at genotypic and phenotypic levels, but positive and highly significant correlation with yield at phenotypic level indicated that improvement in any one of these traits have positive effects on other traits. These results were in agreement with Akram et al. who reported positive correlation between grain yield and thousand kernel weights [15]. Harvest index had negative and highly significant genotypic and phenotypic correlation with days to heading(r=-0.54** and, -0.47**), days to maturity(r=-0.56** and -0.43**) and negative non-significant with grain filling period indicating that early heading genotypes had higher harvest index than the late heading genotypes.

Genotypic and phenotypic correlations of grain yield with other traits: Grain yield/ha displayed varying trends of correlation with its components at genotypic and phenotypic level (Tables 3 and 4). From the analysis grain yield/ha showed positive and highly significant genotypic and phenotypic correlation with spike fertility (r=0.48** and 0.28**), biomass yield(r=0.52** and, 0.61***) and harvest index (r=0.51** and 0.46**) indicating that genotypes with high spike fertility, biomass yield and harvest index would produce significant grain yield. Therefore, any improvement of this trait would result in a substantial increment on grain yield. These results were agreed with the finding of Bagrei et al. and Ahmadi et al., who were stated positive and highly significant genotypic correlation of grain yield with biomass yield and also in agreement with the finding of Ali et al. but it is in contrast to the findings of Kumar et al., who reported positive and negative non-significant correlation of grain yield with biomass yield and harvest index, respectively [12,16,17].

In other way grain yield/ha was positive and non-significant genotypic and phenotypic association with days to heading, days to maturity, grain filling period, total tillers per plant, effective tillers per plant, number of kernel per spike and chlorophyll content and also plant height and thousand kernel weight at genotypic level indicating difference in this traits can deliver significant variation on yields of genotypes. Similar results were observed by Demelash et al. but not agreed with the finding of Mollasadeghi et al. who reported negative non-significant for the traits days to heading [18]. Other authors reported positive and non-significant correlation of grain yield with plant height, number of kernel per spike and thousand kernel weights [11]. It had also negative and non-significant correlated with spike length at genotypic and number of spikelets per spike at both genotypic and phenotypic level. This result agreed with the finding of Desalegn who reported negative and non-significant correlation of grain yield/ha with spike length [19]. Overall, positive and significant correlation

of grain yield with its component at genotypic and phenotypic level would reflects the presence of interaction among the traits in which a gene conditioning an increase in one traits also influence another traits.

Path coefficient analysis

To differentiate the direct and indirect effect of traits on grain yield, path analysis was conducted. In this study, as dependent variable grain yield was selected while the other traits which had significant to highly significant correlation with grain yield were selected as independent variable. The outcomes of path analysis for direct and indirect effects of the traits studied both at phenotypic and genotypic level are presented in Tables 5 and 6 respectively.

Phenotypic direct and indirect effects of various traits on grain yield: The result of association among yield and yield related significant traits through phenotypic path coefficient analysis of the study shown that nearly all traits exhibited positive direct effects on grain yield except plant height (Table 5). Biomass yield exerted maximum positive and favorable direct effect on grain yield followed by harvest index. In addition, thousand kernel weights, spike fertility and canopy temperature also exerted positive and less magnitude direct effect on grain yield. The promising direct effects of biomass yield and harvest index on grain yield indicated that, other variable reserved constant, enhancement of these traits will raise grain yield.

Traits	PH	SPF	CT	BY	TKW	HI	rp
PH	-0.005	-0.001	-0.012	0.639	0.005	-0.313	0.31**
SPF	0	0.015	0.002	-0.035	0.003	0.295	0.28**
CT	0.003	0.002	0.019	-0.645	-0.003	0.309	-0.32**
BY	-0.003	-0.001	-0.013	0.96	0.003	-0.341	0.61**
TKW	-0.001	0.002	-0.002	0.093	0.026	0.122	0.24**
HI	0.002	0.005	0.007	-0.393	0.004	0.832	0.46**

Note: * and ** indicate significant at 0.05 and 0.01 probability levels, respectively.

Residual effect=0.19 where; PH=plant height, SPF=spike fertility, CT=canopy temperature, BMS=biomass yield/ha, TKW=thousand kernel weight, HI=harvest index, rp=phenotypic correlation.

Table 5: Estimates of direct (bold and diagonal) and indirect effect (off diagonal) of different traits on grain yield at phenotypic level in bread wheat genotypes.

Biomass yield (0.960) exhibited highest and positive direct effect on grain yield and it had also positive and highly significant phenotypic correlation with grain yield (rp=0.61**). Therefore, biomass yield can be used as a key choice in bread wheat development and this finding supported by Bagrei et al. path coefficient results on bread wheat [16]. Similarly, Abderrahmane et al. also indicated that biomass yield had highest direct effect on grain yield [20]. In addition to this, negative direct effects of traits on grain yield were displayed through plant height. This result agreed with the discovery of Mitsiwa who reported negative direct effect of plant height on grain yield. Biomass yield also had negative indirect effect on grain yield via plant height; spike fertility; canopy temperature and harvest index whereas indirect effects via thousand kernel weights were positive. The result showed that the direct selection of biomass yield will increase grain yield effectively. Harvest index had positive direct effects as well as positive highly significant phenotypic correlation with grain yield. The indirect effects of this trait were positive with spike fertility, canopy temperature while it had negative indirect effects with biomass yield. These findings in agreement with the result of Ali and Similarly, Hannachi et al. who reported that biomass and harvest index exerted positive direct effect on grain yield [21].

Thousand kernel weights revealed weak positive direct effects and highly significant positive phenotypic association with yield. It had exerted positive and high indirect effects on yield through biomass yield and harvest index. But, it had negative and insignificant indirect effects via other traits. The consequence of this findings showed that even though it had weak positive direct effects, the association was strong because the positive and high indirect effects with harvest index, biomass yield renders its correlation to be stronger. Awale et al. reported thousand kernels weight exhibited negative direct effect on grain yield which contradicted with this study [22]. Karim et al. also reported the positive indirect effects of thousand kernels weight on grain yield via harvest index. Spike fertility manifested positive weak direct effects and highly significant phenotypic correlation with grain yield. It indicates that the enhancement of this trait via spike fertility will increase grain yield in bread wheat.

Plant height exhibited negative direct effects on grain yield, even though it had positive and highly significant phenotypic correlation, indicating that indirect effects to be cause of correlation. Thus, the negative direct effect of plant height was counter balanced by its positive indirect effects through biomass yield and thousand kernel weights as well as rendered the positive and highly significant phenotypic correlation coefficient. Canopy temperature that correlated highly significant and negatively with grain yield exerted positive weak direct effect on grain yield. In other cases, it had the highest negative and positive indirect effect on grain yield at phenotypic level via biomass yield and harvest index respectively. Thousand kernels weight exerted positive indirect effects on grain yield through spike fertility, biomass yield and harvest index. It had a chief trait which determines the final yield in bread wheat. The indirect selection for these trait would be worthy for improving grain yield in bread wheat genotypes. The residual effect in path analysis determines how best the component (independent) variables account for the variability of the dependent variable, grain yield. Residual effect in the current study was 0.19, Table 5 showing that 81% of the variability in grain yield explained by the component factors. This further clarified that yield attributing

traits chosen for the study of the bread wheat genotypes was quite better, even if other traits are also needed to justify yield per hectare.

Genotypic direct and indirect effects of various traits on grain yield: The result of path coefficient analysis at genotypic level revealed that harvest index exhibited the highest positive direct effect (0.915) on grain yield followed by biomass yield (0.889) (Table 6). The highest positive direct effect of these traits on grain yield indicated their significance in determining traits and therefore it should be kept in mind while selection aimed at the improvement of yield.

Related findings were also reported by Ali et al. [23]. Whereas the lowest positive direct effect was exerted by thousand kernels weight, plant height and spike fertility. In other way, the lowest negative direct effect was displayed by canopy temperature. Harvest index had positive direct effect and highly significant genotypic association with yield which makes the direct selection of this trait is important for improving the yield of bread wheat genotypes.

The indirect effects of this trait were positive with spike fertility and thousand kernels weight. Therefore, giving emphasis to harvest

Traits	PH	SPF	CT	BY	TKW	HI	rg
PH	0.031	-0.005	0.019	0.625	0.001	-0.413	0.26
SPF	-0.005	0.032	-0.005	-0.044	0.003	0.495	0.48**
CT	-0.019	0.006	-0.03	-0.679	-0.001	0.401	-0.32*
BY	0.022	-0.002	0.023	0.889	0	-0.406	0.52**
TKW	0.002	0.006	0.001	-0.02	0.018	0.184	0.19
HI	-0.014	0.018	-0.013	-0.395	0.004	0.915	0.51**

Note: * and ** indicate significant at 0.05 and 0.01 probability levels, respectively.

Residual effect=0.16; where: PH=plant height, SPF=spike fertility, CT=canopy temperature, BY=biomass yield/ha, HI=harvest index, rg=genotypic correlation.

Table 5: Estimates of direct (bold and diagonal) and indirect effect (off diagonal) of different traits on grain yield at phenotypic level in bread wheat genotypes.

index, spike fertility and thousand kernels weight could be important in grain yield enhancement of bread wheat genotypes.

Biomass yield was displayed positive high direct effects and highly significant positive correlation with grain yield. The positive indirect effects of biomass yield through plant height and canopy temperature whereas, negative indirect effects via spike fertility and harvest index. The outcome advised that the direct selection of biomass yield will increase yield of grain yield efficiently. The current result is in nearby agreement with Obsa who reported harvest index and biological yield exerted the highest positive direct effect on grain yield. Both harvest index and biomass yield had negative indirect effect on grain yield via each other. The direct contribution of Spike fertility on grain yield was positive and positively high significant association with a yield, it reflects that this trait is essential to advance grain yield directly. Canopy temperature showed negative direct effects and negative highly significant correlation with grain yield, this indicated that direct selection of this trait is not decisive unless together with indirect effects. On the other hand it exhibited positive indirect effects through spike fertility and harvest index while it had negative indirect effects with the rest of the traits. Residual effect in the present study was 0.16, which indicated the traits in the path analysis expressed the variability in grain yield by 84% (Table 6).

Conclusion

The current study of bread wheat genotypes for their correlation analysis observed genotypic correlation coefficient values were higher than phenotypic correlation for most of the traits, indicating inherent association of the traits was largely due to genetic factors and the phenotypic appearance of correlations had reduced by the environmental effect. The study of correlation between yield and yield component traits under high temperature stress condition need an attention for harvest index, thousand kernels weight, biomass yield/ha and spike fertility those are imperative traits which possessed positive and highly significant genotypic and phenotypic correlation with the yield is an important. In addition to this physiological traits are essential in determining tolerance of genotypes. Hence chlorophyll content positive associated with yield and negative association of canopy temperature with the yield is a supreme trait in bread wheat genotypes identification under high temperature stress situation. Therefore, these traits could be utilized in breeding program to improve bread wheat genotypes for higher yield and simultaneously selection based on these traits would be more effective and also desirable for improving grain yield. Emphasis should also give to path analysis to identify which traits contributing to the yield direct and indirect for handling trait in save manner. The favorable positive direct effects of traits on grain yield is very important because improvement of those traits will increase grain yield and also in determining trait while involved selection aimed at the enhancement of grain yield.

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