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Correlation and Path Analysis for Yield and Yield Component Traits on Bread Wheat (*Triticum aestivum* L.) Genotypes

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ABSTRACT

The research was conducted at Kulumsa Agricultural Research Center Main Station, during July–November, 2021 (Main cropping season) to study the association among traits and estimate the direct and indirect effects of various traits on grain yield of bread wheat genotypes. A total of 64 bread wheat genotypes were evaluated for 16 traits in 8×8 simple lattice design. Grain yields showed positive and highly significant at (p<0.01) genotypic and phenotypic correlation with plant height, number of seeds spike^{-1}, head weight, yield head^{-1}, biomass yield, hectoliter weight, test weight and harvest index. Genotypic correlation coefficients were greater for all significantly correlated with grain yield studied traits than the corresponding phenotypic correlation coefficients, indicating inherent association of the characters, therefore, selection for these characters could improve grain yield. Genotypic path analysis of the direct effects revealed that days to maturity, number of spikelets spike^{-1}, head weight, yield head^{-1}, biomass yield, hectoliter weight, test weight and harvest index exerted direct positive effect on grain yield. Phenotypic path analysis of the direct effects showed that days to maturity, plant height, number of tillers plant^{-1}, number of seeds spike^{-1}, head height, yield head^{-1}, biomass yield, test weight and harvest index had direct positive effect on grain yield. Therefore, these traits should be considered for bread wheat breeding program for yield improvement.

KEYWORDS: Correlation, path analysis, *Triticum aestivum*, yield component traits

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1. INTRODUCTION

Wheat is an important cereal crop that is cultivated worldwide and was one of the first crops to be domesticated about 10000 years ago (Feldmann, 2001; Haas et al., 2018). World wheat production is based almost entirely on two modern species: common or hexaploid bread wheat (*Triticum aestivum* L, 2n=6x=42, AABBDD) and durum or tetraploid wheat (*T. turgidum* subsp. *durum*, 2n=4x=28, AABB) (Feldmann, 2001). Bread wheat (*Triticum aestivum* L.) belongs to the family Gramineae and a monoecious plant with perfect flowers, it is reproducing sexually as an autogamous crop although limited (3%) cross pollination is possible (Mergoum et al., 2009).

Wheat is one of the most important cereal crops in Ethiopia and is produced across a large area of the country (Endale and Getaneh, 2015; Gadisa, 2019). Wheat production in Ethiopia for 2022/23 is projected to 5.7 mt that is greater than that of 2021/2022 (5.18 mt). This is due to more Government of Ethiopia engagement in irrigation, better input supply, and mechanized farming in the lowland and central parts of the country (Anonymous, 2022). However, wheat production and productivity is relatively small by global standards. The main reason is that mostly subsistence farming of wheat is produced by small-scale farmers through rain feed production system with less irrigated production (Adugnaw and Dagninet, 2020) and constrained by several infectious diseases including rust and Septoria leaf blotch diseases which are the major problem of wheat production in the world as well as in Ethiopia (Kasa et al., 2015; Endale and Getaneh, 2015).

Yield is a polygenically controlled complex character and is dependent on a number of component traits that are also may not be quantitatively inherited. This is why Selection by yield is often less effective, making it imperative to go for indirect selection through component traits (Singh, 1983; Sharma, 1998). Thus it is essential to examine various components and give more attention to those having the maximum correlation coefficient with yield. Character association studies provide reliable information on the nature, extent and directions of selection. Correlation measures the degree of association (Genetic or non-genetic) between two traits. It is indicated by a correlation coefficient, and is a measure of a linear association between traits (Falconer and Mackay, 1996). The knowledge of the correlations that exist between important characters may facilitate the interpretations of the results already obtained, and provide the basis for planning a more efficient breeding program in the future (Dewey and Lu, 1995).

The influence of each variable upon another variable and permits the separation of the correlation coefficient into components of direct and indirect effects can be estimated by path coefficient analysis (Bhatt, 1973). The breeders can rank the genetic attributes of each trait according to their contribution and thus can be useful for the indirect selection of elite genotypes from the given diverse genetic populations. Path coefficient analysis is a reliable statistical technique that provides means not only to quantify the interrelationships of different yield components but also indicates whether the influence is directly reflected on the yield or takes some other pathway for ultimate effects for actual yield observed (Ahmed et al., 2003, Kashif and Khaliq, 2004). Hence, the research was conducted with the objective to examine the association among traits and estimate the direct and indirect effects of various traits on grain yield of bread wheat genotypes.

2. MATERIALS AND METHODS

2.1. Experimental site and time

The research was conducted at Kulumsa agricultural research center main station, Ethiopian Institute of Agricultural Research, Asella, Ethiopia during July–November, 2021 (main cropping season). The experimental site is located at 08°01’10”Nlongitude and 39°09’11”E latitude at an altitude of 2200 meters above sea level. The mean annual rain fall of the site is 820 mm with an average annual temperature of 16.5°C.

2.2. Experimental materials

The 64 introduced bread wheat genotypes from International Maize and Wheat Improvement Center (CIMMYT) and International Center for Agricultural Research in Dry Areas (ICARDA) were randomly selected for study (Table 1)

2.3. Experimental design and field management

The experiment was laid out in an 8×8 simple lattice design with two replication; the replication containing with eight incomplete blocks each containing eight genotypes were sown on a plot of (3 m^2) consisting of 6 rows, each 2.5 m long; the spacing between rows was 20 cm. Spacing between plots and replications was 1 m and 1.5 m respectively. The seed rate was adjusted to 150 kg ha^{-1}. Planting was done at the onset of rain in the main cropping season. The trial was conducted with the application of 121 kg ha^{-1} of NPS and 100 kg ha^{-1} of urea. All NPS was applied at planting while urea was applied in split: half at the time of planting and the remaining half at tillering stage. In addition, weeding was carried out uniformly

2.4. Data collected

Data was collected from the mean of ten sample plants for the characters like plant height, effective tillers $plant^{-1}$, tillers $plant^{-1}$ and spikelets $spike^{-1}$, spike length, seeds $spike^{-1}$, head weight, yield $head^{-1}$, peduncle length and spike length. However, plot base data were collected for the characters

Table 1: Materials used in the study

Entry	source	Pedigree
1	CIMMYT	rolf07*2/3/prinia/pastor//huites/4/2*sup152/akuri//sup1
2	ICARDA	06w31476//milan/pastor/4/heilo/3/sw89.5277/borl95//skauz
3	ICARDA	usher-18/wafir-6
4	CIMMYT	nd643/2*trch//mutus/3/sup152/4/kachu #1/kiritati//kachu
5	ICARDA	munia//chen/altar 84/3/chen/aegilops squarrosa (taus)//bcn/4/marchouch-8/5/afif
6	CIMMYT	francolin#1/7/reh/hare//2*bcn/3/croc_1/ae.squarrosa(213)//pgo/4/huites/5/t.speltapi348599/6/reh/hare//2*bcn/3
7	ICARDA	NAVJ07/SHORTENED SR26 TRANSLOCATION/3/ATTILA/BAV92//PASTOR
8	CIMMYT	bavis/3/attila/bav92//pastor/5/croc_1/ae.squarrosa(205)//borl95/3/prl/sara//tsi/vee#5/4/fret2/6/mutus//wbll1*2/brambling/3
9	ICARDA	attila/4/weaver/tsc//weaver/3/weaver/5/brbt1*2//tui/clms/6/teg/mian yang 20//chum18/5*bcn
10	CIMMYT	chipak/3/swsr22t.b./2*blouk #1//wbll1*2/kuruku
11	CIMMYT	sokoll/3/pastor//hxl7573/2*bau*2/6/oasis/5*borl95/5/cndo/r143//ente/mexi75/3/ae.sq/4/2*oc
12	CIMMYT	kachu*2/3/nd643//2*prl/2*pastor/4/kachu/danphe
13	ICARDA	sw89-5124*2/fasan/3/cazo/kauz//kauz/4/wbll1/5/ac8528/sova/6/milan/s87230//babax
14	ICARDA	usher-16//kamb2/pandion/3/huites/pandion
15	CIMMYT	altar 84/ae.squarrosa (221)//3*borl95/3/ures/jun//kauz/4/wbll1/5/mutus*2/6/danphe #1/kenya sunbird//danphe
16	ICARDA	kronstad/3/fret2/kukuna//fret2/6/altar84/ae.squarrosa(jbangor)//esda/3/heilo/5/cno79//pf70
17	ICARDA	nabuq-1//kamb2/pandion/5/02w50807/4/pfau/seri.1b//amad/3/waxwing
18	CIMMYT	wbll1*2/brambling*2//bavis/3/kachu #1/kiritati//kachu
19	ICARDA	nesser/seri//milan/pastor/3/florkwa-2/asfoor-5
20	ICARDA	kronstad/3/fret2/kukuna//fret2/6/altar 84/ae.squarrosa (jbangor)//esda/3/heilo/5/ cno79//pf70354/mus/3/pastor/4/babax
21	CIMMYT	mutus//nd643/2*wbll1/3/swsr22t.b./2*blouk #1//wbll1*2/kuruku
22	CIMMYT	tacupetof2001/brambling//pvn/3/iwa8600211//2*pbw343*2/kukuna/4/pbw343*2/kukuna*2//frtl/pifed/5/mutus/akuri-5
23	ICARDA	attila-7/sunco//05w90045
24	CIMMYT	kachu#1//wbll1*2/kukuna/3/brbt1*2/kiritati/6/rolf07*2/5/reh/hare//2*bcn/3/croc_1/ae.squarrosa(213)//pgo/4/huites/7/borl14
25	CIMMYT	kachu/becard//wbll1*2/brambling*2/3/frncln*2/tecue #1
26	ICARDA	katila-9/3/ning mai 96035/finsi//heilo
27	CIMMYT	grack/tecue #1//frncln*2/5/site/mo//pastor/3/tilhi/4/waxwing/kiritati
28	ICARDA	cham-10/3/tnmu//milan/tui/4/sandall-5
29	ICARDA	02w50807/rsmf8 704//mace
30	CIMMYT	kutz*2//kfa/2*kachu
31	CIMMYT	wbll1*2/kuruku//heilo/3/kanchan*2/juchi/4/parus/francolin #1
32	ICARDA	nejmah-14/4/bl2064//sw89-5124*2/fasan/3/tilhi/5/05w90045
33	CIMMYT	premio/4/croc_1/ae.squarrosa (205)//kauz/3/pifed/5/borl14
34	CIMMYT	trap#1/bow/3/vee/pjn//2*tui/4/bav92/rayon/5/kachu#1/6/toba97/pastor/3/t.dicocconpi94624/ae.squarrosa(409)//bcn/4/bl

Table 1: Continue...

Entry	source	Pedigree
35	ICARDA	girwill-13/2*pastor-2//sids-1/3/gladius
36	CIMMYT	fret2*2/shama//kachu/3/mutus*2/muu
37	ICARDA	bow #1/fengkang 15//nesma*2/261-9/3/ducula/4/sids-1/5/gladius
38	CIMMYT	mayil//mutus*2/haril #1/3/mayil
39	CIMMYT	kiritati/4/2*seri.1b*2/3/kauz*2/bow//kauz/5/cmh81.530/6/manku
40	ICARDA	prl/2*pastor//seri/4/milan/kauz//prinia/3/babax/5/hubara-3*2/shuha-4/6/kamb2/pandion
41	CIMMYT	francolin#1/7/huites/5/t.speltapi348599/6/reh/hare//2*bcn/3/croc1/ae.squarrosa/8/trap#1/bow/3/vee/pjn//2*tui/4/bav92/rayon/5
42	CIMMYT	sntl/3/kachu//wbll1*2/brambling
43	ICARDA	worrakatta/2*pastor//aguilal/flag-3
44	ICARDA	pastor/3/gen*2//buc/flk/4/pastor/5/kamb2/pandion/ 6/02w50807/rsmf8 704
45	CIMMYT	mayil/8/seri.1b*2/3/kauz*2/bow//kauz/4/pbw343*2/tukuru/5/c80.1/3*batavia//2*wbll1/6/cmh75a.66/seri/7/munal #1/9/manku
46	CIMMYT	chrz//bow/crow/3/wbll1/4/croc_1/ae.squarrosa (213)//pgo/5/borl14
47	CIMMYT	becard/frncln//borl14
48	CIMMYT	ATTILA/3*BCN*2//BAV92/3/KIRITATI/WBLL1/4/DANPHE
49	ICARDA	kabowsh-7/5/shuha-6//ns732/her/4/croc-1/ae.squarrosa (205)//fct/3/pastor
50	CIMMYT	borl14*2/7/muu/5/wbll1*2/4/yaco/pbw65/3/kauz*2/trap//kauz/6/wbll1*2/shama
51	CIMMYT	saual/3/achtar*3//kanz/ks85-8-4/4/saual*2/5/attila*2/pbw65//muu #1/3/francolin #1
52	ICARDA	hubara-15/zemamra-8//massira/4/frame//milan/kauz/3/pastor
53	ICARDA	hubara-1/3/munia/chto//milan/4/goumria-8/5/afif
54	CIMMYT	slvs/attila//wbll1*2/3/gondo/cbrd/4/borl14
55	ICARDA	altar84/ae.squarrosa(jbangor)//esda/3/heilo/5/cno79//pf70354/mus/3/pastor/4/babax/6/02w50807_1/rsmf8 704
56	ICARDA	gonglase-4/4/croc_1/ae.squarrosa (205)//kauz/3/2*kauz*2/yaco//kauz/5/teg/mianyang 20//chum18/5*bcn
57	ICARDA	soonot-10/hubara-15//jawahir-14
58	CIMMYT	saar//inqalab 91*2/kukuna/3/villa juarez f2009*2/4/fret2*2/shama//kiritati/2*trch/3/baj #1
59	ICARDA	nada-1/5/milan/munia/3/pastor//munia/altar84/4/milan/ducula/6/huites/pandion
60	ICARDA	kronstad/3/fret2/kukuna//fret2/6/altar84/ae.squarrosa(jbangor)//esda/3/heilo/5/cno79//pf70354/mus/3/pastor/4/babax
61	ICARDA	miskeet-18/3/cbrd/wbll1//pandion/5/ald/coc//ures/3/ducula /4/metso
62	ICARDA	qafzah-33/florkwa-2//excalibur/3/doukkala-33
63	ICARDA	weebill-1/2*qafzah-21//kamb2/pandion/3/teg/mian yang 20//chum18/5*bcn
64	CIMMYT	muu/kbird//2*kachu/kiritati

such as days to heading and maturity, grain yield, harvest index, hectoliter weight, test weight and above-ground biomass yield

2.5. Data analysis

2.5.1. Phenotypic and genotypic correlation analysis

Correlation coefficient analysis was done using R software (R core team, 2021), it helps to determine the nature and degree of relationship between any two measurable characters (Fellahi et al., 2013). The various characteristics of crop plants are generally interrelated or correlated (Abderrahmane et al., 2013). Phenotypic and genotypic correlation coefficients was estimated (Miller et al., 1958) as:

$$\text{Phenotypic correlation coefficient} = \frac{\text{COV}_{pxy}}{\sqrt{(\sigma^2_{px})(\sigma^2_{py})}}$$

Genotypic correlation coefficient $(r_{gxy}) = \frac{COV_{gxy}}{\sqrt{(\sigma^2_{gx})(\sigma^2_{gy})}}$

Phenotypic covariance $(pcovxy)$=gcov$_{xy}$+ecov$_{xy}$

Genotypic covariance $(gcov_{xy})$=gcovxy+ecovxy

Environmental correlation coefficient $(r_{exy}) = \frac{COV_{exy}}{\sqrt{(\sigma^2_{ex})(\sigma^2_{ey})}}$

Where:- rp$_{xy}$=Phenotypic correlation coefficient between traits x and y

rg$_{xy}$=Genotypic correlation coefficient between traits x and y

pcov$_{xy}$=Phenotypic covariance between traits x and y

gcov$_{xy}$=Genotypic covariance between traits x and y

ecov$_{xy}$=Environmental covariance between character x and y

MSPg=Mean square product for genotypes

MSPe=Means square products of error

r=Number of replication

The level of significance of phenotypic and genotypic correlation coefficients was tested using the formula suggested by Robertson (1959) using a t-table at (g-2) degree of freedom at 5% level of significance: where, g is number of genotypes. Accordingly, the phenotypic correlation coefficient value was tested for its significance by employing the following formula: $t = r_p/(SE(r_p)$, $SE(rp) = \sqrt{(1-r^2_p/n-2)}$ Where:- r_p=Phenotypic correlation

SE (r_p)=Standard error of phenotypic correlation

n=Number of genotypes to be tested

The genotypic correlations coefficients were tested for their significance by the formula indicated below:

$$t_{cal} = \frac{r_g}{SE(r_g)}, SE_{rg} = \sqrt{\frac{r^2_g}{2H^2_x \times H^2_y}}$$

Where, SE(r_g)=Standard error of genotypic correlation coefficient

r_g=Genotypic correlation coefficient; n is the number of genotypes test

H^2=Heritability

2.5.2. Path coefficient analysis

Path coefficient analysis was carried out using R software (R core team, 2021) to study the direct and indirect contributions of the traits to the associations. The direct and indirect effects of the independent characters (yield components) on the dependent variable (yield) was estimated as described by Dewey and Lu (1959) using the following formula:

r_{ij}=Pij+Σrikpkj

Where:-r_{ij}=mutual association between the ith independent character and the jth dependent characters as measured by the genotypic and phenotypic correlation coefficient.

P_{ij}=Components of direct effects of the ith independent character on the jth dependent character as measured by the genotypic and phenotypic path coefficients and

Σrikpkj=Summation of components of indirect effects of a given ith independent characters on given jth dependent via all other k independent characters.

3. RESULTS AND DISCUSSION

3.1. Genotypic and phenotypic correlations of grain yield with other traits

Grain yield showed positive and highly significant at ($p<0.01$) genotypic and phenotypic association with plant height, number of seeds per spike, head weight, yield per head, biomass yield, hectoliter weight, test weight and harvest index. Whereas, days to maturity and peduncle length were positive highly significant at ($p<0.01$) at genotypic correlation coefficient and positive significant at ($p<0.05$) at phenotypic correlation coefficient respectively (Table 2).

Similar result reported that plant height, test weight, biomass yield and harvest index had positively and significantly correlated with grain yield at both genotypic and phenotypic correlation coefficient (Ashebr et al., 2020; Getachew et al., 2021) and grain yield had significant positive correlation with days to maturity and hectoliter weight at both genotypic and phenotypic levels (Ashebr et al., 2020). Grain yield showed significant and positive association with yield plant^{-1} and harvest index (Kumar et al., 2023). Contrast to the present finding Chimdesa et al. (2017) reported that grain yield had positive and negative non-significant correlation with number of seeds spike^{-1} and peduncle length respectively at both genotypic and phenotypic levels.

Analyses of genotypic and phenotypic correlation revealed that, genotypic correlation coefficients were greater for all associated with grain yield studied characters than the corresponding phenotypic correlation coefficients, indicating inherent association of the characters therefore, selection for these correlated characters could improve grain yield. The same result reported that the estimates of genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients for most of the character combinations (Ashebr et al., 2020; Mohant et al., 2016). However, days to heading, number of tillers per plant, number of effective tillers plant^{-1}, spike length and number of spikelets spike^{-1} were not significantly correlated with grain yield at both genotypic and phenotypic correlations among studied traits. Therefore, improving these non-correlated traits will not be important to give better grain yield.

Table 2: Genotypic (above diagonal) and Phenotypic (below diagonal) correlation coefficient for 16 traits of 64 bread wheat genotypes tested

Traits	DTH	DTM	PHT	NTPP	NETPP	NSPS	NKPS	PDL
DTH		0.70**	0.26*	0.05^{ns}	-0.03^{ns}	0.49**	0.35**	-0.31*
DTM	0.69**		0.24^{ns}	-0.03^{ns}	-0.10^{ns}	0.34**	0.17^{ns}	-0.14^{ns}
PHT	0.26*	0.23^{ns}		0.26*	0.33**	0.28*	0.36**	0.63**
NTPP	0.03^{ns}	-0.04^{ns}	0.17^{ns}		0.90**	-0.12^{ns}	-0.15^{ns}	0.11^{ns}
NETPP	-0.03^{ns}	-0.09^{ns}	0.27*	0.81**		-0.11^{ns}	-0.08^{ns}	0.10^{ns}
NSPS	0.46**	0.30*	0.26*	-0.12^{ns}	-0.11^{ns}		0.59**	0.02^{ns}
NKPS	0.33**	0.15^{ns}	0.32*	-0.04^{ns}	-0.01^{ns}	0.52**		0.05^{ns}
PDL	-0.30*	-0.13^{ns}	0.60**	0.08^{ns}	0.08 ^{ns}	0.01^{ns}	0.07^{ns}	
SL	0.08^{ns}	0.02^{ns}	0.29*	-0.14^{ns}	-0.10^{ns}	0.61**	0.26*	0.14 ^{ns}
HW	0.21^{ns}	0.28*	0.60**	-0.07^{ns}	-0.02^{ns}	0.39**	0.58**	0.28*
YH	0.18^{ns}	0.24^{ns}	0.64**	-0.01^{ns}	0.08^{ns}	0.30*	0.67**	0.40**
BY	0.20^{ns}	0.39**	0.60**	-0.01^{ns}	0.11^{ns}	0.11^{ns}	0.38**	0.30*
HLW	0.32**	0.17^{ns}	0.59**	0.11^{ns}	0.21^{ns}	0.28*	0.52**	0.33**
TKW	0.04^{ns}	0.13^{ns}	0.66**	0.09^{ns}	0.21^{ns}	0.05^{ns}	0.29*	0.51**
HI	0.10^{ns}	0.02^{ns}	0.38**	0.04^{ns}	0.13^{ns}	0.30*	0.45**	0.29*
GY	0.20^{ns}	0.30*	0.57**	0.01^{ns}	0.12^{ns}	0.22^{ns}	0.49**	0.32*

Table 2: Continue...

Traits	SL	HW	YH	BY	HLW	TKW	HI	GY
DTH	0.08^{ns}	0.23^{ns}	0.19^{ns}	0.20^{ns}	0.33**	0.04^{ns}	0.13^{ns}	0.21^{ns}
DTM	0.04^{ns}	0.32*	0.26*	0.38**	0.18^{ns}	0.15^{ns}	0.04^{ns}	0.32**
PHT	0.33**	0.64**	0.68**	0.64**	0.63**	0.72**	0.42**	0.61**
NTPP	-0.20^{ns}	-0.05^{ns}	0.03^{ns}	0.02^{ns}	0.12^{ns}	0.11^{ns}	0.11^{ns}	0.04^{ns}
NETPP	-0.11^{ns}	-0.02^{ns}	0.11^{ns}	0.14^{ns}	0.23^{ns}	0.23^{ns}	0.17^{ns}	0.15^{ns}
NSPS	0.64**	0.39**	0.29*	0.10^{ns}	0.31*	0.07^{ns}	0.35**	0.23^{ns}
NKPS	0.29*	0.62**	0.70**	0.42**	0.55**	0.28*	0.50**	0.53**
PDL	0.15^{ns}	0.30*	0.42**	0.32**	0.34**	0.54**	0.33**	0.34**
SL		0.44**	0.27*	0.11^{ns}	0.22^{ns}	0.19^{ns}	0.22^{ns}	0.17^{ns}
HW	0.43**		0.90**	0.77**	0.70**	0.75**	0.54**	0.80**
YH	0.27*	0.87**		0.77**	0.81**	0.86**	0.72**	0.88**
BY	0.10 ^{ns}	0.70**	0.72**		0.71**	0.76**	0.49**	0.91**
HLW	0.18 ^{ns}	0.65**	0.76**	0.68**		0.83**	0.80**	0.85**
TKW	0.15 ^{ns}	0.70**	0.81**	0.71**	0.81**		0.77**	0.87**
HI	0.18 ^{ns}	0.50**	0.67**	0.42**	0.73**	0.71**		0.799**
GY	0.14 ^{ns}	0.74**	0.83**	0.87**	0.81**	0.83**	0.796**	

* and ** indicates significant at (p=0.05) and highly significant at (p=0.01) probability levels respectively; ns: non-significant; DTH: Days to heading; DTM: Days to Maturity; PHT: Plant height; NTPP: No. of tillers plant^{-1}; NETPP: No. of effective tillers plant^{-1}; NSPS: No. of spikelet spike^{-1}; NKPS: No. of seeds spike^{-1}; PDL: Peduncle length; SL: Spike length; HW: Head weight; YH: Yield head^{-1}; BY: Biomass yield; GY: Grain yield; HLW: Hectoliter weight; TKW: Test weight; HI: Harvest index

The result agreement with previous finding that reported by Chimdesa et al. (2017) days to heading, number of tillers per plant and effective tillers per plant were not significantly correlated with grain yield at both genotypic and phenotypic level and spike length and number of spikelets spike^{-1} were not significantly correlated with grain yield at genotypic level but opposite to the present result spike length and number of spikelets per spike were significantly correlated with grain yield at phenotypic correlation (Chimdesa et al., 2017). The earlier article report contrasted to the present result that number of spikelets spike^{-1} (Zeeshan et al., 2013). And Productive tillers plant^{-1} (Kumar et al., 2023). had positive correlation with grain yield at both genotypic and phenotypic levels

3.2. Genotypic and phenotypic correlations among yield component traits

Biomass yield revealed positive and highly significant at ($p<0.01$) genotypic and phenotypic correlation with days to maturity ($r_g=0.38^{**}$ and $r_p=0.39^{**}$), plant height ($r_g=0.64^{**}$ and $r_p=0.60^{**}$), number of seeds spike^{-1} ($r_g=0.42^{**}$ and $r_p=0.38^{**}$), head weight ($r_g=0.77^{**}$ and $r_p=0.70^{**}$), yield head^{-1} ($r_g=0.77^{**}$ and $r_p=0.72^{**}$), hectoliter Weight ($r_g=0.71^{**}$ and $r_p=0.68^{**}$), test weight ($r_g=0.76^{**}$ and $r_p=0.71^{**}$) and Harvest index ($r_g=0.49^{**}$ and $r_p=0.42^{**}$). Whereas, peduncle length ($r_g=0.32^{**}$ and $r_p=0.30^{*}$) was observed positive highly significant at ($p<0.01$) at genotypic correlation coefficient and positive significant at ($p<0.05$) at phenotypic correlation coefficient respectively. Similar result reported by Kumar et al. (2020) who reported that biomass yield had positively correlated with plant height, number of spikelets spike^{-1}, Number of seeds spike^{-1}, test weight and number of spikelets spike^{-1}. However, days to heading, number of tillers plant^{-1}, number of effective tillers plant^{-1}, spike length and number of spikelets spike^{-1} were not correlated with biomass yield at both genotypic and phenotypic correlation coefficients among studied bread wheat genotypes. This finding aligned with Chimdesa et al. (2017) for tillers plant^{-1} and spikelet spike^{-1}. Therefore, improving these non-correlated (non-significant) traits may not improve biomass yield.

Harvest index had positive and highly significant at ($p<0.01$) genotypic and phenotypic correlation with plant height ($r_g=0.42^{**}$ and $r_p=0.38^{**}$), head weight ($r_g=0.54^{**}$ and $r_p=0.50^{**}$), yield head^{-1} ($r_g=0.72^{**}$ and $r_p=0.67^{**}$), hectoliter Weight ($r_g=0.80^{**}$ and $r_p=0.73^{**}$), number of seeds spike^{-1} ($r_g=0.50^{**}$ and $r_p=0.45^{**}$), test weight ($r_g=0.77^{**}$ and $r_p=0.71^{**}$). whereas, peduncle length ($r_g=0.33^{**}$ and $r_p=0.29^{*}$) number of spikelets spike^{-1} ($r_g=0.35^{**}$ and $r_p=0.30^{*}$) were positive highly significant at ($p<0.01$) at genotypic correlation coefficient and positive significant at ($p<0.05$) at phenotypic correlation coefficient respectively. Different authors had supported the present result that harvest index had significantly correlated with test weight, biomass yield, hectoliter weight at both genotypic and phenotypic level and plant height at phenotypic level (Alemu et al., 2016).

Yield head^{-1} revealed positive and highly significant at ($p<0.01$) genotypic and phenotypic correlation with plant height ($r_g=0.68^{**}$ and $r_p=0.64^{**}$), number of seeds spike^{-1} ($r_g=0.70^{**}$ and $r_p=0.67^{**}$), peduncle length ($r_g=0.42^{**}$and $r_p=0.40^{**}$), head weight ($r_g=0.90^{**}$and $r_p=0.87^{**}$), hectoliter Weight ($r_g=0.81^{**}$ and $r_p=0.76^{**}$), test weight ($r_g=0.86^{**}$ and $r_p=0.81^{**}$) and spike length ($r_g=0.29^{*}$ and $r_p=0.29^{*}$) and number of spikelets spike^{-1} ($r_g=0.29^{*}$ and $r_p=0.30^{*}$) were observed positive significant at ($p<0.05$) at genotypic and phenotypic correlation coefficient respectively. Whereas, days to maturity was positive significant at genotypic level ($r_g=0.26^{*}$) and non-significant at phenotypic correlation. However, days to heading, number of total tillers plant^{-1} and number of effective tillers plant^{-1} were not significantly correlated with yield head^{-1} at both genotypic and phenotypic correlation coefficients among studied bread wheat genotypes. This indicates, improving these non-significantly associated traits may not contribute to improvement of yield head^{-1}.

Mohant et al. (2016) reported that yield head^{-1} significantly correlated with plant height, spikelets spike^{-1}, number of seeds spike^{-1} and spike length and and Kumar et al. (2023) reported yield per plant significantly correlated with harvest index. Contrast to the present result, days to heading was significantly correlated with yield per head and similar to the present result tillers plant^{-1} not significantly correlated with yield head^{-1} at both phenotypic and genotypic correlation coefficients (Mohant et al., 2016). And incontrasting of the present result Sharma et al. (2023) reported that grain yield was not significantly correlated with harvest index.

Test weight had positively and highly significant at ($p<0.01$) at both genotypic and phenotypic correlation with peduncle length ($r_g=0.54^{**}$ and $r_p=0.51^{**}$) and hectoliter weight ($r_g=0.83^{**}$ and $r_p=0.81^{**}$). Whereas, number of seeds spike^{-1} ($r_g=0.28^{*}$ and $r_p=0.29^{*}$) had positively significantly correlated with test weight at ($p<0.05$) at both genotypic and phenotypic correlations. Days to heading, days to maturity, number of tillers plant^{-1}, number of effective tillers plant^{-1}, number of spikelets spike^{-1} and spike length were not significantly correlated with test weight at both genotypic and phenotypic correlation coefficients among studied bread wheat genotypes. Thus, improving these non-significantly associated traits may not contribute to improvement of test weight.

Similar finding reported by Kabir et al. (2017) that test weight had significant correlation with plant height, number of grains spike^{-1} and harvest index and opposite to the present study days to maturity significantly correlated with test weight. and Kumar et al. (2020) found that test weight showed significant correlation with plant height, biomass yield and harvest index and contrast to the present result days to heading significantly correlated with test weight. Number of seeds spike^{-1} showed positive and highly significant at (p<0.01) at both genotypic and phenotypic correlation with days to heading (r_g=0.35** and r_p=0.33**), number of spikelets spike^{-1} (r_g=0.59** and r_p=0.52**) and hectoliter weight (r_g=0.55** and r_p=0.52**). Whereas, number of tillers plant^{-1}, number of effective tillers per plant and peduncle length were not significantly associated with number of seeds per spike at both genotypic and phenotypic correlation coefficient.

Irfan et al. (2021) and Berhanu et al. (2017) reported number of seeds spike^{-1} showed significant correlation with spikletes spike^{-1} and spike length and contrast to present study Peduncle length had significantly correlated with number of seeds spike^{-1} and similarly, effective tillers plant^{-1} not significantly correlated with number of seeds per spike (Irfan et al., 2021). And seeds spike^{-1} had significantly correlated with days to heading , days to maturity, biological yield, spikelets spike^{-1} and spike length (Alemu et al., 2016).

Generally, most of studied traits revealed positive highly significant and significantly correlated each other at both genotypic and phenotypic correlation coefficient. Therefore, improving these significantly associated characters had contribution to improvement of each other and finally increase grain yield. Analyses of genotypic and phenotypic correlation showed that, genotypic correlation coefficients were greater for all significantly associated studied characters than their corresponding phenotypic correlation coefficients and most of traits which had correlation with grain yield were showed association each other which indicated inherent association of the characters therefore, selection for the correlated characters could give better result to enhance grain yield.

3.3. Genotypic path coefficient analysis

Genotypic path analysis of the direct effects revealed that days to maturity (0.063), number of spikelet spike^{-1} (0.024), head weight (0.020**)**, yield head^{-1} (0.099), biomass yield (0.568**)**, hectoliter weight (0.048), test weight (0.064) and harvest index (0.360) exerted direct positive effect on grain yield (Table 3). Similarly, number of spikelets spike^{-1}, biomass yield and harvest index had positive genotypic direct effect on grain yield (Dutamo et al., 2015) and (Berhanu et al., 2017), and days to maturity, biomass yield, test weight, harvest index and number of spikelet spike^{-1} depict positive genotypic direct effect on grain yield (Mecha et al., 2017). Chimdesa et al. (2017) reported that days to maturity, biomass yield and harvest index and Alemu et al. (2016) hectoliter weight exerted genotypic direct positive effect on grain yield. The maximum positive direct effect and highly significant positive correlation coefficient was recorded between biomass yield and grain yield followed by harvest index and grain yield. This result in agreement with Dutamo et al. (2015b), Alemu et al. (2016), Chimdesa et al. (2017) and Getachew et al. (2021). The positive direct effect of these characters on grain yield indicates that improvement on these traits will be increase grain yield and selection for these traits will be effective for breeding program. Contrast to the present result Mecha et al. (2017) reported that hectoliter weight had negative genotypic direct effect on grain yield.

Whereas, the direct effect of days to heading (-0.049), plant height (-0.032), number of tillers plant^{-1} (-0.005), number of effective tillers plant^{-1} (-0.003), number of seeds spike^{-1} (-0.001), peduncle length (-0.044) and spike length (-0.028) were observed negative. Thus, indicated that the contribution of these traits for grain yield is minimum. Direct effect was negative and correlation coefficient was significantly positive for plant height, number of seeds spike^{-1} and peduncle length with grain yield. This was mainly due to the indirect positive effect through biomass yield and harvest index. Therefore, indirect selection for this trait will be effective to improve grain yield. Similarly, Mohant et al. (2016) reported that days to heading, plant height, number of seeds spike^{-1} and spike length had negative genotypic direct effect on grain yield. The present result aligned with Mecha et al. (2017) who reported that plant height had negative direct genotypic effect on grain yield. Number of seeds spike^{-1} and number of tillers plant^{-1} showed negative genotypic direct effect on grain yield (Berhanu et al., 2017), and days to heading and spike length observed genotypic negative direct effect on grain yield (Dutamo et al., 2015). Number of tillers plant^{-1}, peduncle length, days to heading and number of seeds spike^{-1} showed negative phenotypic direct effect on grain yield (Chimdesa et al., 2017). All traits had positive genotypic indirect effect on grain yield through Head weight, yield head^{-1}, biomass yield, hectoliter weight, test weight and harvest index except number of tillers plant^{-1} via head weight. Head weight (0.438) and yield head^{-1} (0.437) carried highest positive indirect effect on grain yield through biomass yield. However, indirect effect was visible to be highest negative via days to maturity through days to heading followed by plant height via peduncle length. Genotypic path coefficient analyses result in the present study revealed that days to maturity, number of spikelet spike^{-1}, head weight, yield head^{-1}, biomass yield, hectoliter weight, test weight and harvest index are important selection criteria for the development of high yielding bread wheat varieties (Table 4)

3.4. Phenotypic path coefficient analysis

Phenotypic path analysis of the direct effects showed that

Table 3: Genotypic Direct (Italic diagonal) and indirect effects (off diagonal) of 15 traits on grain yield of 64 bread wheat genotypes tested

Traits	DTH	DTM	PHT	NTPP	NETPP	NSPS	NKPS	PDL
DTH	*-0.049*	0.044	-0.009	0.000	0.000	0.012	0.000	0.014
DTM	-0.034	*0.063*	-0.008	0.000	0.000	0.008	0.000	0.006
PHT	-0.013	0.015	*-0.032*	-0.001	-0.001	0.007	0.000	-0.028
NTPP	-0.003	-0.002	-0.008	*-0.005*	-0.003	-0.003	0.000	-0.005
NETPP	0.002	-0.007	-0.011	-0.004	*-0.003*	-0.003	0.000	-0.004
NSPS	-0.024	0.021	-0.009	0.001	0.000	*0.024*	-0.001	-0.001
NKPS	-0.017	0.011	-0.012	0.001	0.000	0.014	*-0.001*	-0.002
PDL	0.015	-0.009	-0.020	-0.001	0.000	0.001	0.000	*-0.044*
SL	-0.004	0.002	-0.011	0.001	0.000	0.016	0.000	-0.007
HW	-0.011	0.020	-0.021	0.000	0.000	0.009	-0.001	-0.013
YH	-0.009	0.017	-0.022	0.000	0.000	0.007	-0.001	-0.019
BY	-0.010	0.024	-0.020	0.000	0.000	0.003	-0.001	-0.014
HLW	-0.016	0.012	-0.020	-0.001	-0.001	0.008	-0.001	-0.015
TKW	-0.002	0.010	-0.023	-0.001	-0.001	0.002	0.000	-0.024
HI	-0.006	0.003	-0.014	-0.001	-0.001	0.008	-0.001	-0.015

Table 3: Continue...

Traits	SL	HW	YH	BY	HLW	TKW	HI	r_g
DTH	-0.002	0.005	0.019	0.112	0.016	0.003	0.045	0.208^{ns}
DTM	-0.001	0.006	0.026	0.217	0.009	0.010	0.015	0.318**
PHT	-0.009	0.013	0.068	0.361	0.030	0.046	0.152	0.605**
NTPP	0.006	-0.001	0.003	0.011	0.006	0.007	0.038	0.041^{ns}
NETPP	0.003	0.000	0.011	0.082	0.011	0.015	0.062	0.153^{ns}
NSPS	-0.018	0.008	0.029	0.058	0.015	0.004	0.125	0.234^{ns}
NKPS	-0.008	0.013	0.069	0.238	0.027	0.018	0.180	0.530**
PDL	-0.004	0.006	0.042	0.184	0.016	0.034	0.118	0.336**
SL	*-0.028*	0.009	0.027	0.063	0.010	0.012	0.081	0.172^{ns}
HW	-0.012	*0.020*	0.089	0.438	0.033	0.048	0.196	0.796**
YH	-0.008	0.018	*0.099*	0.437	0.039	0.054	0.260	0.875**
BY	-0.003	0.016	0.076	*0.568*	0.034	0.048	0.178	0.914**
HLW	-0.006	0.014	0.080	0.402	*0.048*	0.053	0.289	0.847**
TKW	-0.005	0.015	0.085	0.429	0.040	*0.064*	0.275	0.865**
HI	-0.006	0.011	0.072	0.281	0.038	0.049	*0.360*	0.790**

Residual effect =0.1508; * and ** indicates significant at (p=0.05) and highly significant at (p=0.01) probability levels respectively; ns: non-significant; DTH: Days to heading; DTM: Days to Maturity; PHT: Plant height; NTPP: Number of tillers plant^{-1}; NETPP: Number of effective tillers plant^{-1}; NSPS: Number of spikelet spike^{-1}; NKPS: number of seeds spike^{-1}; PDL: Peduncle length; SL: Spike length; HW: Head weight; YH: yield head^{-1}; BY: Biomass yield; GY: Grain yield; HLW: Hectoliter weight; TKW: Test weight; HI: Harvest index

days to maturity (0.072), plant height (0.006) number of tillers plant^{-1} (0.004), number of seeds spike^{-1} (0.011), head height (0.042), yield head^{-1} (0.047), and biomass yield (0.572), test weight (0.026) and harvest index (0.491) had positive phenotypic direct effect on grain yield (Table 4). The present result in agreement with Chimdesa et al.

Table 4: Phenotypic direct (Italic diagonal) and indirect effects (off diagonal) of 15 traits on grain yield of 64 bread wheat genotypes tested

Traits	DTH	DTM	PHT	NTPP	NETPP	NSPS	NKPS	PDL
DTH	*-0.041*	0.050	0.002	0.000	0.000	-0.006	0.004	0.013
DTM	-0.028	*0.072*	0.002	0.000	0.001	-0.004	0.002	0.006
PHT	-0.011	0.017	*0.006*	0.001	-0.003	-0.003	0.003	-0.026
NTPP	-0.001	-0.003	0.001	*0.004*	-0.010	0.001	0.000	-0.004
NETPP	0.001	-0.006	0.002	0.004	*-0.012*	0.001	0.000	-0.004
NSPS	-0.019	0.022	0.002	-0.001	0.001	*-0.012*	0.006	-0.001
NKPS	-0.013	0.011	0.002	0.000	0.000	-0.006	*0.011*	-0.003
PDL	0.012	-0.009	0.004	0.000	-0.001	0.000	0.001	*-0.043*
SL	-0.003	0.002	0.002	-0.001	0.001	-0.007	0.003	-0.006
HW	-0.009	0.020	0.004	0.000	0.000	-0.005	0.006	-0.012
YH	-0.007	0.017	0.004	0.000	-0.001	-0.004	0.007	-0.017
BY	-0.008	0.028	0.004	0.000	-0.001	-0.001	0.004	-0.013
HLW	-0.013	0.012	0.004	0.001	-0.003	-0.003	0.006	-0.014
TKW	-0.002	0.009	0.004	0.000	-0.002	-0.001	0.003	-0.022
HI	-0.004	0.001	0.002	0.000	-0.002	-0.004	0.005	-0.013

Table 3: Continue...

Traits	SL	HW	YH	BY	HLW	TKW	HI	r_g
DTH	-0.002	0.009	0.008	0.112	-0.003	0.001	0.050	0.196^{ns}
DTM	-0.001	0.012	0.011	0.220	-0.002	0.003	0.008	0.304^{*}
PHT	-0.007	0.025	0.030	0.343	-0.006	0.017	0.186	0.572^{**}
NTPP	0.004	-0.003	-0.001	-0.006	-0.001	0.003	0.021	0.006^{ns}
NETPP	0.002	-0.001	0.004	0.060	-0.002	0.005	0.065	0.119^{ns}
NSPS	-0.015	0.017	0.014	0.061	-0.003	0.001	0.145	0.218^{ns}
NKPS	-0.007	0.024	0.032	0.218	-0.005	0.008	0.221	0.493^{**}
PDL	-0.004	0.012	0.019	0.172	-0.003	0.013	0.143	0.315^{*}
SL	*-0.025*	0.018	0.013	0.056	-0.002	0.004	0.087	0.140^{ns}
HW	-0.011	*0.042*	0.041	0.401	-0.006	0.018	0.246	0.737^{**}
YH	-0.007	0.037	*0.047*	4140.	-0.007	0.021	0.327	0.832^{**}
BY	-0.002	0.030	0.034	*0.572*	-0.007	0.018	0.206	0.874^{**}
HLW	-0.005	0.027	0.036	0.388	*-0.010*	0.021	0.358	0.806^{**}
TKW	-0.004	0.030	0.038	0.403	-0.008	*0.026*	0.349	0.825^{**}
HI	-0.004	0.021	0.032	0.239	-0.007	0.019	*0.491*	0.787^{**}

Residual effect=0.1657; * and ** indicates significant at (*p*=0.05) and highly significant at (*p*=0.01) probability levels respectively

(2017) who reported that days to maturity, number of tillers plant^{-1}, number of seeds spike^{-1}, biomass yield, test weight and harvest index had positive phenotypic direct effect on grain yield. Plant height, test weight, biomass yield and harvest index had positive phenotypic direct effect on grain yield (Kumar et al., 2020). On the other hand contrast to the present result plant height showed negative phenotypic direct effect on grain yield (Sharma et al., 2023). The positive direct effect of these characters on grain yield indicates that, improvement on these traits will increase grain yield. Whereas, the direct effect of days to heading (-0.041), number of effective tillers plant^{-1} (-0.012), number of spikelet spike^{-1} (-0.012), peduncle length (-0.043), spike length (-0.025) and hectoliter weight (-0.010) were observed negative. The result lined with Chimdesa et al. (2017) who reported that days to heading and number of spikelets spike^{-1} had negative phenotypic direct effect on grain yield and Mohant et al. (2016) reported that number of spikelets per spike observed negative phenotypic direct effect on grain yield. Sharma et al. (2023) Reported that spike length had negative phenotypic direct effect on grain yield. Thus indicated that the contribution of these traits for grain yield is minimum.

All traits had positive phenotypic indirect effect on grain yield through yield head^{-1}, biomass yield, test weight and harvest index except number of tillers plant^{-1} via yield head^{-1} and biomass yield. Yield head^{-1} (0.414) and test weight (0.403) imparted highest positive indirect effect on grain yield through biomass yield. However, indirect effect had highest negative via days to maturity through days to heading followed by test weight via peduncle length. Phenotypic path coefficient analyses results in the current study revealed that days to maturity, plant height, number of seeds spike^{-1}, head height, yield head^{-1}, biomass yield, test weight and harvest index are potential selection criteria for improving bread wheat grain yield.

4. CONCLUSION

Grain yield showed positive and highly significant at ($p<0.01$) genotypic and phenotypic correlation for plant height, number of seeds spike^{-1}, head weight, yield head^{-1}, biomass yield, hectoliter weight, test weight and harvest index. Genotypic and Phenotypic path analysis revealed that days to maturity, head weight, yield head^{-1}, biomass yield, test weight and harvest index exerted direct positive effect on grain yield. Therefore, these traits should be given attention for selection in wheat breeding for yield improvement.

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7. REFERENCES

Abderrahmane H., El Abidine, F.Z., Hamenna, B., Ammar, B., 2013. Correlation, path analysis and stepwise regression in durum wheat (*Triticum durum* Desf.) under rainfed conditions. Journal of Agriculture and Sustainability 3(2), 122–131.

Adugnaw, A., Dagninet, A., 2020. Wheat production and marketing in Ethiopia: Review study. Cogent Food & Agriculture, 6(1), 1778893.

Ahmed, H.M., Khan, B.M., Khan, S., Kissana, N.S., Laghari, S., 2003. Path coefficient analysis in bread wheat. Asian Journal of Plant Sciences 2(6), 491–494.

Alemu D., Firew M., Tadesse, D., 2016. Estimation of genetic and phenotypic correlation coefficients and path analysis of yield and yield contributing traits of bread wheat (*Triticum aestivum* L.) genotypes. International Journal of Natural Resource Ecology and Management 1(4), 145–154.

Anonymous, 2022. Ethiopia grain and feed annual report global agricultural information network USDA foreign agriculture service report rumber ET2022-0014. Available at https://apps.fas.usda.gov/newgainapi/api/Report/DownloadReportByFileName?fileName=Grain%20and%20Feed%20Annual_Addis%20Ababa_Ethiopia_ET2022-0014.pdf Accessed on March 10, 2024.

Ashebr, B., Berihun, B., Bantayehu, M., Derebe, B., 2020. Genotypic and phenotypic correlation and path coefficient analysis for yield and yield-related traits in advanced bread wheat (*Triticum aestivum* L.) lines. Cogent Food & Agriculture 6(1), 1752603.

Berhanu, M., Mohammed, W., Tsehaye, Y., 2017. Genetic variability, correlation and path analysis of yield and grain quality traits in bread wheat (*Tritium aestivum* L.) genotypes at Axum, Northern Ethiopia. Journal of Plant Breeding and Crop Science 9(10), 175–185.

Bhatt, G.M., 1973. Significance of path coefficient analysis in determining the nature of character association. Euphytica 22, 338–343 https://doi.org/10.1007/BF00022643

Chimdesa, O., Mohammed, W., Eticha, F., 2017. Analysis of genetic variability among bread wheat (*Triticum aestivum* L.) genotypes for growth, yield and yield components in Bore district, Oromia regional state. Agriculture, Forestry and Fisheries 6(6), 188–199.

Dewey, D.R., Lu, K.H., 1959. A correlation and path coefficient analysis of components of crested wheat grass seed production. Agronomy Journal 51(9), 515–518. https://doi.org/10.2134/agronj1959.00021962005100090002x

Dutamo, D., Alamerew, S., Eticha, F., Assefa, E., 2015. Path coefficient and correlation studies of yield and yield associated traits in bread wheat (*Triticum aestivum* L.) germplasm. World Applied Sciences Journal 33(11), 1732–1739.

Endale, H., Getaneh, W., 2015. Survey of rust and septoria leaf blotch diseases of wheat in central Ethiopia and virulence diversity of stem rust *Puccinia graminis* f. sp. *tritici.* Advances in Crop Science and Technology 3(2),166. https://DOI: 10.4172/2329-8863.1000166, https://www.omicsonline.org/peer-reviewed/survey-of-rust-and-septoria-leaf-blotch diseases-of-wheat-in-central-ethiopia-and-virulence-diversity-of-stem-rust-*puccinia-gramin*-52316.html

Falconer, D.S., Mackay, T.F.C., 1996. Introduction to quantitative genetics. 4th Edition, Addison Wesley Longman Harlow. https://vulms.vu.edu.pk/ Courses/ GEN733/ Downloads /Introduction%20to%20 Quantitative%20Genetic-DS%20Falconer.pdf

Feldmann, 2001. Origin of cultivated wheat. In: Bonjean, A.P., Angus, W.J. (Eds.), The World wheat book. A history of wheat breeding. Lavoiser Publishing, France 1, 3–56.

Fellahi, Z., Hannachi, A., Bouzerzour, H., Boutekrabt, A., 2013. Correlation between traits and path analysis coefficient for grain yield and other quantitative traits in bread wheat under semi arid conditions. Journal of Agriculture and Sustainability 3(1), 16–26.

Gadisa, A., 2019. Review on the effect of seed source and size on grain yield of bread wheat (*Tritium aestivum* L.). Journal of Ecology & Natural Resources 3(1), 1–8.

Getachew, A., Worede, F., Alamerew, S., 2021. Phenotypic variation and traits interrelationships in bread wheat (*Triticum aestivum* L.) genotypes in Northern Ethiopia. Acta Agriculturae Slovenica, 117(3), 1–9. doi:https://doi.org/10.14720/aas.2021.117.3.1291,

Haas, M., Schreiber, M., Mascher, M., 2018. Domestication and crop evolution of wheat andbarley: Genes,genomics, and future directions. Journal of Integrative Plant Biology 61(3), 204–225.

Irfan, M., Mahpara, S., Bibi, R., Ullah, R.,, Ullah, R., Abbas, S., Ihsan, M., Hassan, M., El-Shehawi, M., Brestic, M., Zivcak, M., Ifnan, M., 2021. Grain yield and correlated traits of bread wheat lines: Implications for yield improvement: Saudi Journal of Biological Science 28(10), 5714–5719. doi: 10.1016/j.sjbs.2021.06.006.

Kabir, R., Intikhab, A., Ahmed, I., Qamar, M., Hussain, M., Tajuddin, Jan, R., Ali Shah, H., Zaib-Un, N., 2017. Evaluation of bread wheat genotypes for variability and association among yield and yield related traits. International Journal of Biosciences 11(1), 7–14.

Kasa, D., Hundia, B., Dembel, W., 2015. Distribution and occurrence of wheat rusts and septoria leaf blotch in Bale and Arsi Zones, 2014 Belg season. Global Journal of Pests, Diseases and Crop Protection 3(4) 124–130.

Kashif, M., Khaliq, I., 2004. Heritability, correlation and path coefficient analysis for some metric traits in wheat. International Journal of Agriculture and Biology 6, 138–142.

Kumar, P., Solanki, Y.P.S., Singh, V., Kiran, 2020. Genetic variability and association of morphophysiological traits in bread wheat (*Triticum aestivum* L.). Current Journal of Applied Science and Technology 39(35), 95–105. Article no.CJAST.62266 ISSN: 2457-1024.

Kumar, V., Gangwar, L.K., Kumar, R., Singh, S., Anjali, Mohan, S., 2023. Study of correlation and path coefficients to emphasize grain yield and its components in bread wheat. International Journal of Plant & Soil Science 35(20), 918–925. https://doi.org/10.9734/ijpss/2023/v35i203884

Mecha, B., Alamerew, S., Assefa, A., Assefa, E., Dutamo, D., 2017. Correlation and path coefficient studies of yield and yield associated traits in bread wheat (*Triticum aestivum* L.) genotypes. Advances in plant and Agriculture Research 6(5), 128–136, https://DOI: 10.15406/apar.2017.06.00226.

Mergoum, Singh, P.K., Anderson, J.A., Peiia, R.J., Singh, R.P., Xu, S.S., Ransom, J.K., 2009. Hand book of plant breeding partly from spring wheat breeding. North Dakota State University. Fargo ND. USA, 5810–6050.

Miller, P.A., Williams, J.C., Robinson, H.F., Comstock, R.E., 1958. Estimates of genotypic and environmental variances and co-variances in upland cotton and their implications in selection 1. Agronomy Journal 50(3), 126–131.

Mohant, S., Mukherjee, S., Mukhopadhyaya, S., Dash, A., 2016. Genetic variability, correlation and path analysis of bread wheat (*Triticum aestivum* L.) genotypes under terminal heat stress. International Journal of Bio-resource and Stress Management 7(6), 1232–1238.

Reddy, M.L., Gulshanlal, N., 1999. Genetic variability and path coefficient analysis in tomato (*Lycopersicon esculentum* Mill.) under summer season. Progressive Horticultural 19(3–4), 284–288.

Robertson, G.E., 1959. The sampling variance of genotypic correlation coefficient. Biometrics 15(3), 469–485.

Sharma, J.R., 1998. Statistical and biometrical techniques in plant breeding. New AgeInternational Publishers, New Delhi, pp 432 .

Sharma, S., Tripathi, M.K., Tiwari, S., Solanki, R.S., Chauhan, S., Tripathi, N., Dwivedi, N., Kandalkar, V.S., 2023. The exploitation of genetic variability and trait association analysis for diverse quantitative traits in bread wheat (*Triticum aestivum* L.). Current

Journal of Applied Science and Technology 42(8), 19–33. https://doi.org/10.9734/cjast/2023/v42i84087

Singh, B.D., 1983. Plant breeding principles and methods. Kalyani Publisher. New Delhi, p.458.

Zeeshan, M., Arshad, W., Ali, S., 2013. Genetic diversity and trait association among some yield parameters of wheat elite lines genotypes under rainfed conditions. Journal of Renewable Agriculture 1(2), 23–26.