

## ESTIMATION OF HERITABILITY, GENOTYPIC VARIABILITY AND CORRELATIONS ANALYSIS FOR YIELD AND YIELD ATTRIBUTING TRAITS AMONG BREAD WHEAT (*Triticum aestivum* L.) GENOTYPES

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**ABSTRACT.** To find out genetic variability, heritability, and trait association among yield and yield-related traits among bread wheat genotypes, an alpha lattice design was used in triplicate manner where 50 wheat genotypes were evaluated at the University of Agriculture Peshawar during rabbi growing season 2021-22 along with a regional check genotype. Data were taken on ten parameters. All the genotypes showed significant variation among them, signifying the possibility of enhancing genetic improvement through breeding programs. Highly significant differences were found in days to heading, days to maturity, plant height, spike length, grain filling duration, number of grains per spike, biological yield and grain yield these traits indicating diversity in yield potential.

Moderate to low heritability values were noted for most of the traits. The study exhibits positive correlations for plant height with grain yield, spike length with biological yield and harvest index with grain yield. On the basis of high heritability and positive correlation of grain yield with other traits, it is recommended that G-41, G-3, G-12, G-37, G-34 and G-14 genotypes which have the potential to be incorporate in further breeding programs.

**Keywords:** correlation; crop improvement; heritability; quantitative genetics; variability; wheat breeding; wheat genotypes.

### INTRODUCTION

Bread wheat (*Triticum aestivum* L.), is an important cereal crop with a long



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history of cultivation dating back thousands of years. Wheat grains has been domesticated by humans approximately 10,000 years B.C during the Neolithic period and remains an important crop globally. Bread wheat is widely consumed cereal and is a staple food in worldwide.

Pakistan occupies 6<sup>th</sup> position in production of wheat worldwide. Total cultivated area with wheat crop during the 2021–2022 cropping season was 9.2 million hectares and production was recorded 27.5 million tons (PBS, 2022) It contributes 1.8% to the country's GDP and 9.2% value added in agriculture (Khan *et al.*, 2022).

In Pakistan the population growth rate is 2.4% per year, due to the increase in population a rise is occur in food demand requiring an increase in wheat production to meet the rising demand for food. However, in Pakistan, due to various factors there is a significant gap between the potential yield of wheat (7 metric tons) and the average yield (2.5 metric tons per hectare) (Kirby *et al.*, 2017).

Genetic variability plays an important role to meet the present and future crop breeding challenges such as breeding for increasing yield, wider adaptation, desirable quality, drought tolerance, pest and disease resistance (Begna, 2021). The greater the genetic variation among plants, the higher will be likelihood of achieving productive recombinants and broad heritability during genetic improvement.

Therefore, having precise knowledge of germplasm variability, heritability, genetic advance and genetic relationships among yield component traits is a prerequisite for crop

improvement programs. This knowledge can aid in the development of superior recombinants for all desired traits (Tilahun *et al.*, 2020).

Continuous processing of new genetic materials carrying various genes which are essential for enhancing cereal crops yield and productivity. To fulfill the food requirements of increasing population.

Utilization of new genetic resources in genetic improvement programs is essential for increasing wheat crop productivity (Khan *et al.*, 2013). Therefore, most plant breeding programs all over the world have main objective of developing high-yielding wheat varieties as these programs generates unique genetic material that carries high ratio of high-yielding genotypes.

Yield components plays important role for enhancing grain yield of wheat crop because these characteristics have a high genetic correlation with the yield of wheat (Bashir *et al.*, 2010). Wheat traits containing high heritability, making selection in early generations possible. To overcome the yield gap between potential and actual yield, breeders can make new crosses and develop high-yielding varieties for farmers to grow (Reynolds *et al.*, 2011).

To select desirable genotypes and identify independent traits that affect the grain yield, researchers emphasized the use of correlations and path coefficient (Chowdhury *et al.*, 2019). Correlation coefficients are crucial for determining the similarity between different traits and their dependence on grain yield.

However, analyzing correlation coefficients alone is not enough to explain the relationships between various traits, as it cannot determine the direct

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and indirect effects of independent variables on dependent variables. Therefore, path coefficient analysis tools may also be utilized to study the impact of each independent variable on the dependent variable (Alogaidi, 2018).

In light of the significance of these analytical tools, the current study was conducted to evaluate the variability of genotypes and to perform correlation analysis of yield attributing traits in bread wheat genotypes.

### MATERIALS AND METHODS

Total 50 genotypes were obtained from CIMMYT (International Wheat and Maize Improvement Center), including a regional check genotype (PS-2015) listed in (Table 1).

The experiment was conducted at The University of Agriculture Peshawar, having longitude 34.026°N, latitude 71.4814°E with altitude 359 m /1178 feet above sea level.

Annual rainfall, average temperature and day length of the area are presented in Figure 1.

Experiment was conducted using an alpha lattice design having three replications which were further divided into five sub-blocks and ten genotypes were allocated to each sub-block. Each genotype was sown in four rows, with 5 meters in length and 25 cm gap between each row. Sowing was done in November 2021.

Sampling techniques were used for recording plant height (cm), dpike length, grain filling duration, number of grains per spike, 1000-grain weight (g), biological yield, grain yield and harvest index (%) while days to heading and days to maturity were recorded on plot basis.

Seed bed preparation was done by mechanical methods. Seeds sowing was done manually.

Irrigation was applied as per the crop water demand through the flood irrigation system. Fertilizers (DAP and Urea) were applied at the time of seedbed preparation.

### Statistical Analysis

The data collected for various parameters underwent an analysis of variance (ANOVA) procedure, utilizing a suitable model for an alpha lattice design. This approach was similar to the one described by (Barreto *et al.*, 1997). Least significant test was also performed to check significance among different genotypes of wheat.

The computation of genotypic ( $r_g$ ) and phenotypic ( $r_p$ ) correlations between yield and yield attributing components involved the utilization of the formula proposed by (Singh and Chaudhary, 1985).

These correlations were derived from the analysis of phenotypic, genotypic and environmental covariance.

### Heritability

Heritability in broad sense ( $h^2$ ) was estimated by using formula suggested by (Allard, 1960) (Equation 1).

$$h^2BS = (\delta^2g)/\delta^2p \quad (1)$$

where  $\delta^2g$  = genetic variance for a specific trait;  $\delta^2p$  = phenotypic variance for a specific trait;  $h^2BS$  = heritability in broad sense for specific trait

### Correlation

The genetic correlation ( $r_g$ ) and phenotypic correlation ( $r_p$ ) between two characters,  $X_1$  and  $X_2$ , was estimated according to Kwon and Torrie (1964).

Table 1 – List of genotypes used in the experiment

S.No	Genotype	Name	Origin
1	G-1	PerSabaq 2015	PERSABAQ 2015
2	G-2	FITIS	MX11617
3	G-3	MUNAL *2/WESTONIA	MX11617
4	G-4	2*WBLL*2/KKTS/SHORTENED	MX11617
5	G-5	ATTILA/PSN/SERI/3/MILAN/4/BOW	MX11617
6	G-6	ATTILA*2/MURGA/PBW65*2	M38ES25SA16
7	G-7	FRANCOLIN#1/YANAC	M38ES25SA16
8	G-8	SHER6/PBW343*2	M38ES25SA16
9	G-9	WHEAR/2*PRL/WAXBI/4/COPOI	M38ES25SA16
10	G-10	WBLLI*2/OTUS/TUKURU/WBLLI*2	MX11617
11	G-11	WBLLI*2/4/PBW65/YACO	M38ES25SA16
12	G-12	F2001/BRAMBLING/PVN	M38ES25SA16
13	G-13	F2001/KIRITATI/C80 1/3* BATAVIA	M38ES25SA16
14	G-14	WBLLI*2/KKTS/PASTOR/KUKUNA	MX11617
15	G-15	ROLFO07/YANAC/BRAMBLING*2	M38ES25SA16
16	G-16	KIRITATI/TURKU	M38ES25SA16
17	G-17	FRET2*2/SHAMA/KUKUNA*2	MX11617
18	G-18	TRCH/SRTU/MILAN	M38ES25SA16
19	G-19	TRCH/SRTU	MX11617
20	G-20	PBW343*2/KUKUNA/KHVAKI	M38ES25SA16
21	G-21	UP2338*2/SHAMA	M38ES25SA16
22	G-22	SAUAL/YANAC/SAUL*2	M38ES25SA16
23	G-23	TACUETO F2001/SAUAL	MX11617
24	G-24	KFA/S/REH/HARE/2* BCN/PGO	MX11617
25	G-25	SAUAL/MUTUS/KUKUNA/WBLL*2	M38ES25SA16
26	G-26	SITE/MO/PASTOR/WAXWING/KIRI	MX11617
27	G-27	BOROL14/KFA/2*KACHU/2*KACHU	M38ES25SA16
28	G-28	TILILA/TURK/BOW/4/SERI.1B*2	MX11617
29	G-29	WAXWING/2*ROLF07/BORL14	MX11617
30	G-30	BECARD/FRNCLN/KACHU*1	M38ES25SA16
31	G-31	CHEWINK/CHYAK/5/UP2338*2/	MX11617
32	G-32	CHEWINK#1/CHYAK/S/UP2338*2/	M38ES25SA16
33	G-33	MUU/KBIRD/3/PRL/2*PASTOR 2	MX11617
34	G-34	BECARD/ND643/ATTILA*2/PASTOR	MX11617
35	G-35	2*ATTILA 2PASTOR/3/WBLL1*2/	MX11617
36	G-36	FRET2/TUKURU/FRET2/MUNAL#1/	MX11617
37	G-37	/4/BAV92*2/S/HAR311/6/PASTOR	MX11617
38	G-38	KIRITATI*2/3/C801/3*BATAVIA/4/	M38ES25SA16
39	G-39	2*BAV92/MUNAL#1//5/KIRITATI/4	M38ES25SA16
40	G-40	/WBLL1*2/3/COPIO/BRAMBUNG*2/	M38ES25SA16
41	G-41	PBW343*2/FRANCOLI	MX11617
42	G-42	/NADI/3/PBW343*2/KUKUNA *2/	M38ES25SA16
43	G-43	NADI/COPIO/NADI/CMSS 11B00944T	MX11617
44	G-44	WBLL1*2/KUKURI//HEILO/3/	M38ES25SA16
45	G-45	YAV3/SCO/JO69/CRA/3/YAV 79/4/AE	MX11617
46	G-46	HIGHAR/BABAX//3/ER 2000/4/	M38ES25SA16
47	G-47	PASTOR//2 *BAU/4/PANDION//FLIN/	MX11617
48	G-48	MEX94.27.1.20/3/3*BCN/5/	MX11617
49	G-49	8/BOW/VEE/5/ND/KAL/BB/3/YACO	MX11617
50	G-50	5*BORL95/CNDO/R143/ENTE/MEX1	MX11617

### Genetic correlation

(Equation 2)

$$r_g = \frac{Cov G(x_1, x_2)}{\sqrt{\sigma G(x_1) \cdot \sigma G(x_2)}} \quad (2)$$

where  $CovG(X_1 X_2)$  = Genetic covariance among trait  $X_1$  and  $X_2$ ;  $VG(X_1)$  and  $VG(X_2)$  = Genetic variance for trait  $X_1$  and  $X_2$ , respectively.

### Phenotypic correlation

(Equation 3)

$$r_p = \frac{CovP(x_1, x_2)}{\sqrt{\sigma P(x_1) \cdot \sigma P(x_2)}} \quad (3)$$

where  $COVP(X_1 X_2)$  = phenotypic covariance among traits  $X_1$  and  $X_2$ ;  $VP(X_1)$  and  $VP(X_2)$  = phenotypic variance for traits  $X_1$  and  $X_2$ , respectively.

## RESULTS AND DISCUSSION

### Days to heading and maturity

Days to heading and maturity are important agronomic traits that determine the adaptability of wheat cultivars to different environments. Different wheat genotypes exhibited significant differences for days to heading and maturity (Table 2). The data indicated that the number of days to heading ranged from 103 to 110 days, with an average of 105 days. Among the genotypes, genotype G-30 exhibited the minimum number of days to heading (103), while maximum number of days to heading (110) was noted for genotype G-50. The mean duration for days to maturity ranged from 143 to 147 days, with an average of 145.24 days. G-38 exhibited the minimum days to maturity (143 days), while G-11, G-21, and G-35 recorded the maximum days to maturity (147 days) (Table 3). The observed significant

variation among days to heading and maturity suggested that such cultivars of wheat genotypes with different heading and maturity times can be developed by breeders which are suitable for specific environments.

At genotypic level days to heading exhibited a significant positive correlation with plant height ( $r_g=0.398$ ) and grain yield ( $r_g=0.37$ ) as indicated in (Table 4). However, there was a negative correlation observed between days to heading and grain filling duration ( $r_g=-0.87$ ) at the genotypic level. Similarly, at the phenotypic level, days to heading displayed a significant negative correlation with grain filling duration ( $r_p=-0.79$ ). Similarly, at genotypic level, days to maturity displayed a significant positive correlation with grain filling duration ( $r_g=0.59$ ) and grains spike<sup>-1</sup> ( $r_g=0.589$ ), while exhibiting a negative correlation with thousand grain weight ( $r_g=-0.49$ ). Baye *et al.*, (2020) also reported a positive correlation between days to heading with plant height and grain yield. Days to heading and grain filling duration at both genotypic and phenotypic levels showed negative correlation suggested that early-heading genotypes have shorter grain filling durations, which may negatively affect grain yield of wheat genotypes (Slafer *et al.*, 2015).

The moderate broad sense heritability estimated (Table 5) for days to heading (0.46) indicated that a significant proportion of the phenotypic variation is genetically controlled and can be used for the selection of superior genotypes (Falconer and Mackay, 1996). On the other hand, the low heritability estimated for days to maturity (0.21)

indicated that environmental factors played a major role in controlling this trait, and genetic improvement may be limited (Talebi and Fayyaz, 2012).

**Plant height**

Plant height is important trait to avoid lodging in wheat genotypes, which is a major yield-limiting factor in wheat production. A thorough analysis of variance indicated noteworthy variations ( $P \leq 0.01$ ) in plant height among different wheat genotypes (Table 2). The observed plant heights ranged from 82.7 cm to 104.9 cm. Genotype G-41 exhibited shorter plants (82.8 cm), while genotype G-43 had taller plants (105.0 cm) (Table 3).

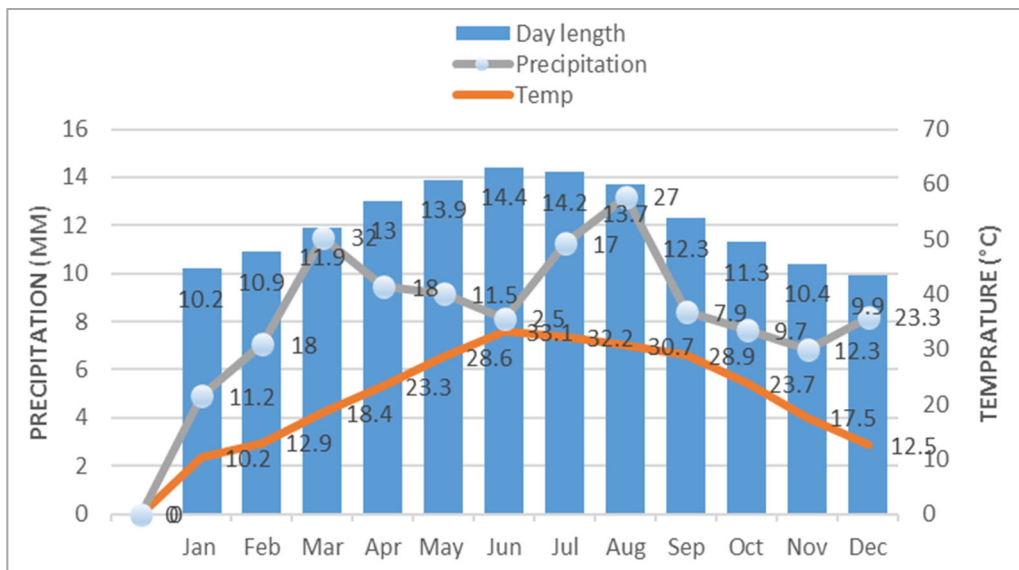
The observed significant variation for plant height among the studied genotypes suggested that there is potential for development of such cultivars with different plant height which are suitable for different environments. Our results are in line with (Khan *et al.*, 2010) who also reported

considerable disparity among wheat genotypes for plant height.

Genotypic and phenotypic correlation result showed that at the genotypic level, plant height exhibited significant positive correlations with spike length ( $r_g = 0.52$ ), biological yield ( $r_g = 0.74$ ), grain yield ( $r_g = 0.49$ ) and days to heading ( $r_g = 0.39$ ).

Plant height displayed a significant negative relationship with grain filling duration ( $r_g = -0.32$ ) (Table 4). Phenotypically, plant height demonstrated a significant positive correlation with spike length ( $r_p = 0.34$ ) and biological yield ( $r_p = 0.35$ ).

The observed positive correlation between plant height and grain yield at both genotypic and phenotypic levels is similar with previous findings of (Githinji, 2016) who reported a positive interaction between plant height and grain yield.



**Figure 1** – Precipitation and temperature in Peshawar during 2021-2022 cropping season

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Table 2 – ANOVA Table for various genotypes of bread wheat

	DH	DM	PH	GF	SL
Replication	18.621	2.541	73.7868	24.09	5.28668
Genotypes	4.115**	2.557*	68.459**	7.2699**	1.118**
Error	1.19216	1.450274	7.7937	2.647436	0.422544
<b>Total df 149</b>					
	GS	TGW	BY	GY	HI
Replication	39.5001	19.3401	17648030.3	2303344.87	47.141601
Genotypes	58.462**	70.018**	6065583.5*	994330.99**	23.593307**
Error	13.815976	10.47835	3590340.8	443114.9	12.52796
<b>Total df 149</b>					

\*, \*\* = Significant at 0.05 and 0.01 probability level, respectively.

DY=Days to heading, DM=Days to maturity, PM=Plant height, GF=Grain filling, GS=Grains spike<sup>-1</sup>, SL=Spike length, TGW=Thousand grain weight, BY= Biological yield, GY=Grain yield, HI= Harvest index

Table 3 – Average performance of wheat genotypes for various traits in bread wheat

Geno- types	DH	DM	PH	GF	GS	SL	TGW	BY	GY	HI
G-1*	105	145	90.6	41	49	10.3	36.34	17239	4918	29
G-2	106	146	98.9	40	53	10.7	37.48	19874	4858	25
G-3	106	144	96	39	40	10.8	42.67	18232	5099	28
G-4	106	146	91.8	42	44	10	40.51	18791	5324	29
G-5	105	146	97.4	42	41	10.2	41.05	20523	5121	26
G-6	106	144	96	39	49	10.6	36.19	17988	4388	25
G-7	104	146	90.8	42	48	10	36.99	18368	5353	30
G-8	109	145	103.6	37	46	9.9	40.07	19931	5384	28
G-9	107	144	103.3	39	47	10.2	40.05	18074	4607	26
G-10	105	146	85.3	42	50	9.2	38.71	16244	3703	23
G-11	106	147	90.7	42	44	9.7	35.39	15182	3662	25
G-12	105	146	94	43	58	9.5	33.8	18065	4284	24
G-13	104	144	98.1	41	49	10.3	40.47	16988	3732	22
G-14	105	145	89.8	40	49	9.6	34.55	20560	5517	27
G-15	105	146	92.7	42	47	10.2	37.27	16074	4470	28
G-16	106	144	93.5	40	41	10.3	43.07	17204	3573	22
G-17	105	145	95	41	47	9.9	39.25	18232	4578	26
G-18	107	146	93.3	39	57	10.4	36.48	19313	5110	27
G-19	106	145	94.8	40	51	9.5	39.91	17688	5435	31
G-20	105	146	94.7	43	50	9.5	38.94	18949	5254	28
G-21	106	147	92.7	41	52	10.3	37.81	18873	5502	30
G-22	106	144	93.9	40	42	10	32.77	16860	4224	25
G-23	104	144	91.6	40	41	9.6	51.1	17231	4346	26
G-24	107	145	99.6	39	53	8.9	37.24	19255	5186	28
G-25	105	145	91.2	40	49	8.6	49.22	16955	4230	25
G-26	106	144	93.9	39	42	10.2	46.22	18654	5352	29
G-27	106	144	93.4	38	48	8.6	40.25	15375	4906	33
G-28	107	144	92	39	50	9.0	49.32	15945	4343	28
G-29	104	146	86.8	43	45	8.3	40.99	17946	4534	26
G-30	103	146	85.7	43	46	10.1	42.25	17531	4495	26
G-31	105	145	94	41	52	9.8	42.62	16350	3991	25
G-32	104	145	96.2	41	53	10.4	45.11	16555	4457	27

G-33	106	145	92.8	40	39	9.8	39.6	17045	4896	29
G-34	107	146	90.8	40	52	9.7	40.0	20507	3993	21
G-35	104	147	101.1	39	56	10.0	38.28	18369	3389	19
G-36	106	145	92.4	40	44	9.0	42.49	18568	5068	28
G-37	104	145	90.9	42	45	9.9	52.97	1892	4678	25
G-38	105	143	86.9	39	46	9.2	35.51	17178	4483	27
G-39	105	145	83.2	41	40	8.5	36.82	14874	4683	32
G-40	106	146	85.8	41	47	9.5	34.41	18993	3625	20
G-41	104	146	82.8	41	43	8.7	37.92	15750	3448	22
G-42	105	146	90.0	42	48	7.9	36.41	15726	4207	28
G-43	106	144	105.0	39	48	10.3	51.30	18884	5254	29
G-44	107	146	94.7	40	47	9.4	30.63	17313	4056	24
G-45	104	146	91.7	42	49	9.1	40.04	17221	3592	21
G-46	105	144	100.6	38	47	9.2	39.52	20269	4875	25
G-47	106	146	95.4	38	46	8.6	41.67	16030	4493	28
G-48	106	146	98.9	41	47	9.1	46.19	17383	4607	27
G-49	105	146	101.6	42	53	9.3	43.49	19883	5309	27
G-50	110	145	94.5	38	40	9.4	29.18	19792	5124	26
Means	105	145.24	93.57	40.42	47.4	9.62	39.61	17875	4595	26
LSD (0.05)	1.7722	1.9547	4.53	2.641	6.033	1.06	5.254	3075.6	1080.50	5.745

DY = Days to heading, DM = Days to maturity, PM = Plant height, GF = Grain filling, GS = Grains spike<sup>-1</sup>, SL = Spike length, TGW = Thousand grain weight, BY = Biological yield, GY = Grain yield, HI = Harvest index  
\*check PS. 2015

**Table 4 – Phenotypic (rP) and Genotypic (rG) correlation coefficients for various traits in wheat**

TS	DH	DM	GF	PH	SL	GS	TGW	BY	GY	HI
<b>DH</b>	-	-0.111	-0.87**	0.398*	-0.128	-0.11	-0.28	0.239	0.37*	0.259
<b>DM</b>	-0.04	-	0.59**	-0.286	-0.129	0.589**	-0.49**	0.11	-0.29	-0.36
<b>GF</b>	-0.79**	0.67**	-	-0.6**	0.038	0.38*	-0.039	-0.19	-0.44	-0.40
<b>PH</b>	0.28	-0.18	-0.32	-	0.52**	0.312	0.18	0.74**	0.49*	0.056
<b>SL</b>	0.04	-0.06	-0.07	0.34*	-	0.115	0.162	0.35*	0.175	-0.099
<b>GS</b>	-0.09	0.109	0.14	0.17	0.034	-	-0.09	0.37*	-0.012	-0.23
<b>TGW</b>	-0.18	-0.09	0.08	0.09	0.00	-0.11	-	-0.013	0.068	0.064
<b>BY</b>	0.005	-0.09	0.02	0.35*	0.45*	0.13	-0.05	-	0.662**	0.08
<b>GY</b>	0.04	-0.10	-0.09	0.23	0.24	0.002	0.13	0.44**	-	0.788**
<b>HI</b>	0.046	-0.11	-0.11	-0.03	-0.10	-0.09	0.17	0.26	0.75**	-

\*, \*\* = significant at 0.05 and 0.01 probability level, respectively. TS = Traits, DY = Days to heading, DM = Days to maturity, PM = Plant height, GF = Grain filling, GS = Grains spike<sup>-1</sup>, SL = Spike length, TGW = Thousand grain weight, BY = Biological yield, GY = Grain yield, HI = Harvest index

However, (Slafer *et al.*, 2015) noted negative correlation between plant height and grain filling duration which indicated that taller plants have shorter grain filling durations, which may negatively affect grain yield. Genetic variance (Vg = 20.23) for plant height among the wheat genotypes exceeded environmental

variance (Ve = 7.79), resulting in a high heritability estimate (0.73) for plant height (Table 5). The high heritability estimated for plant height (0.73) suggested that genetic improvement of this trait can be effective (Falconer and Mackay, 1996).



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### Spike length

Spike length plays an important role in yield determination of wheat. Analysis of variance showed significant differences ( $P \leq 0.01$ ) in spike length among the various wheat genotypes (*Table 2*). The recorded spike length data ranged from 7.9 cm to 10.8 cm. G-42 produced shorter spikes measuring 7.9 cm, while G-3 exhibited longer spikes measuring 10.8 cm (*Table 3*). Like Thorne (1965) who also discovered a lot of variation among wheat genotypes. The observed considerable disparity for this trait among the wheat genotypes suggested the potential for genetic improvement.

There was a significant positive genetic correlation between spike length and plant height ( $r_g = 0.52$ ) as well as biological yield ( $r_g = 0.45$ ), while a phenotypic correlation was observed between spike length and plant height ( $r_p = 0.34$ ) and biological yield ( $r_p = 0.35$ ) (*Table 4*). The observed positive correlation between spike length and biological yield at both genotypic and phenotypic levels is correlated with previous finding of (Rao *et al.*, 2022) who reported a positive correlation between these two traits. The genetic variance for spike length in wheat genotypes was relatively lower in magnitude compared

to the environmental variance ( $V_g = 0.24$ ,  $V_e = 0.422$ ). Consequently, the broad sense heritability for spike length was low, amounting to 0.36 (*Table 5*).

The low heritability estimated for spike length (0.36) indicated that this trait is dominantly under the control of environmental factors. And genetic improvement may be limited (Talebi and Fayyaz, 2012).

### Grain filling duration

Grain filling duration plays a crucial role in maximizing bread wheat production as it directly influences grain size and weight. The duration of grain filling showed statistically significant variations ( $P \leq 0.01$ ) among different wheat genotypes, as presented in (*Table 2*). The data collected for grain filling duration ranged from 37 to 43 days. Among the genotypes, G-8 exhibited the shortest duration of 37 days, while G-12, G-20, G-29, and G-30 had the longest duration of 43 days (*Table 3*). The considerable disparity among wheat genotypes for grain filling duration suggested for genetic improvement. Considerable disparity for grain filling duration among wheat genotypes were also observed by (Bhushan *et al.*, 2013; Malbhage *et al.*, 2020).

**Table 5** – Heritability, genotypic and phenotypic variance estimates for various traits of bread wheat

Traits	Vg	Ve	Vp	h <sup>2</sup> (BS)
Days to heading	0.98	1.193	2.18	0.46
Days to maturity	0.38	1.451	1.83	0.21
Grain filling duration	1.55	2.648	4.20	0.38
Plant height	20.23	7.7937	28.03	0.73
Spike length	0.24	0.4226	0.66	0.36
Grains spike <sup>-1</sup>	14.89	13.816	28.71	0.53
1000 grain Wt.	19.86	10.479	30.33	0.66
Biological yield	825080.91	3590340.8	4415421.7	0.20
Grain yield	183738.73	443114.9	626853.53	0.30
Harvest index%	3.70	12.527955	16.23	0.24

Grain filling duration demonstrated significant positive genotypic and phenotypic correlations with days to maturity ( $r_g = 0.59$ ,  $r_p = 0.67$ ) and a negative genotypic correlation with days to heading ( $r_g = -0.87$ ), as shown in (Table 4). The observed positive correlation between grain filling duration and days to maturity suggested that genotypes with a longer grain filling period allowed for extended grain development and filling, leading to potentially higher grain yields. This relationship could be attributed to the availability of a longer time for resource accumulation and allocation to develop grains, resulting in increased grain weight and yield. The genetic variance for grain filling duration among wheat genotypes was relatively lower in magnitude compared to the environmental variance ( $V_g = 1.55$ ,  $V_e = 2.648$ ), resulting in a heritability of 0.38, indicating a moderate heritable component for grain filling duration. However, the low heritability estimates for grain filling duration (0.38) mentioned in (Table 5) indicated that environmental factors play a dominant role in controlling this trait, and genetic improvement may be limited (Farooq *et al.*, 2014).

### Grains spike<sup>-1</sup>

Grains spike<sup>-1</sup> is different in wheat genotypes. Statistical analysis of data showed considerable disparity ( $P \leq 0.01$ ) among wheat genotypes regarding grains spike<sup>-1</sup> (Table 2). The number of grains spike<sup>-1</sup> ranged from 39 to 58, with G-33 producing the least (39) and G-12 producing the most (58) grains spike<sup>-1</sup> (Table 3). The significant difference observed among wheat genotypes for grains spike<sup>-1</sup> suggested genetic

variations that influence this trait. Considerable disparity among wheat genotypes for grain-related traits was also reported by (Fan *et al.*, 2020; Yang *et al.*, 2020). The variation in grains spike<sup>-1</sup> could be attributed to various factors, including differences in genetic backgrounds, breeding programs, and environmental conditions during plant growth and development.

Correlation analysis results revealed significant positive correlations between grains spike<sup>-1</sup> and days to maturity ( $r_g = 0.589$ ), grain filling duration ( $r_g = 0.38$ ) at the genotypic level and a positive correlation with biological yield ( $r_p = 0.37$ ) at phenotypic level as shown in (Table 4). The positive correlation with days to maturity suggests that genotypes producing more grains spike<sup>-1</sup> tend to have a longer maturation period. (Ullah *et al.*, 2018) also observed that longer maturation periods provide more time for grain development and filling. The positive correlation with biological yield suggests that genotypes with higher grain production also exhibit greater overall biomass production. This relationship indicates the importance of a well-developed plant structure and resource allocation for achieving higher grain yield. The broad sense heritability for grains spike<sup>-1</sup> (Table 5) was estimated to be 0.53. A heritability value of 0.53 indicated that genetic factors contributed moderately to the observed variation in grains spike<sup>-1</sup>. Bhanu *et al.* (2018) also reported similar heritability estimates for other wheat traits, such as grain yield. These findings imply that selection based on grains spike<sup>-1</sup> can be effective in improving the trait in future breeding programs.

### Thousand grain weight

An investigation into the thousand grain weight among various wheat genotypes demonstrated significant variations ( $P \leq 0.01$ ) as determined by the analysis of variance (Table 2). The mean values for the thousand grain weight ranged from 29.18 to 52.97 g. G-50 exhibited the lowest recorded thousand grain weight (29.18 g), while G-37 had the highest (52.97 g) (Table 3). Previous finding of (Arya *et al.*, 2017; Kumar *et al.*, 2017; Mecha *et al.*, 2016, 2017) also reported considerable disparity among wheat genotypes in terms of thousand grain weight.

Correlation analysis indicated a genetic association between thousand grain weight and days to maturity ( $r_g = -0.49$ ) (Table 4). These results contradicted the conclusions of Rajput, (2018) and Savadi *et al.*, (2017) who reported a significant correlation between thousand grain weight and grain yield.

The genetic variance for the thousand grain weight of the wheat genotypes ( $V_g = 19.86$ ) exceeded the environmental variance ( $V_e = 10.47$ ). Consequently, the broad sense heritability for the thousand grain weight was determined to be moderate (0.66) (Table 5). Similar findings were documented by (Preeti *et al.*, 2018; Ullah *et al.*, 2018).

### Biological yield

Biological yield among different wheat genotypes showed considerable disparity among wheat genotypes (Table 2). This finding is also consistent with previous studies that have reported significant genotype differences in biological yield (Avinashe *et al.*, 2015; Singh *et al.*, 2019). The data ranged for

biological yield 14,874 kg.hac<sup>-1</sup> to 20,560 kg.hac<sup>-1</sup>. The lowest biological yield of 14874 kg ha<sup>-1</sup> was observed in G-39, while the highest yield of 20560 kg ha<sup>-1</sup> was recorded in G-14 (Table 3). Dabi *et al.*, (2016) also reported similar ranges of biological yield in other wheat studies which suggested that the observed variation is not unique to this particular study but reflects the inherent genetic variability in wheat populations.

Regarding genotype associations, biological yield exhibited significant genotypic correlations with plant height ( $r_g = 0.74$ ), grain yield ( $r_g = 0.44$ ), spike length ( $r_g = 0.35$ ), and grains per spike (0.37) (Table 4).

Similarly, phenotypically, biological yield showed correlations with plant height ( $r_p = 0.35$ ), spike length ( $r_p = 0.45$ ), and grain yield ( $r_p = 0.662$ ) (Table 4). The positive genotypic correlation between biological yield and plant height, grain yield, spike length, and grains per spike suggested that these traits contribute to higher yield potential. Similar trait correlations have been reported in previous studies by Avinashe *et al.*, (2015) supporting the robustness of these associations.

The genetic variance recorded for biological yield in wheat genotypes was lower than the environmental variance, with  $V_g = 825080$  and  $V_e = 3590340$ . Singh *et al.*, (2019) also reported higher environmental variance than genetic variance for yield-related traits in wheat. Consequently, the broad-sense heritability for biological yield was calculated to be low at 0.20 (Table 5). This implies that environmental factors, plays a significant role in influencing biological yield. It also highlights the

importance of breeding for stress tolerance and resilience to maximize yield potential under varying environmental conditions. The low broad sense heritability value of 0.20 indicated that genetic factors explain only a small proportion of the observed variation in biological yield. This study makes an agreement with the previous studies that have reported low heritability values for yield-related traits in wheat (Singh *et al.*, 2019; Jamil *et al.*, 2017).

### Grain yield

Grain yield revealed significant variation among wheat genotypes (*Table 2*). The data range from 3448 to 5517 kg ha<sup>-1</sup> for grain yield. Lowest grain yield 34478kg ha<sup>-1</sup> was reported for G-41, while highest yield of 5517 kg ha<sup>-1</sup> was reported for G-14 (*Table 3*), suggested that there are substantial differences in productivity among the tested genotypes. This finding is consistent with previous studies that have demonstrated genetic variability in grain yield among wheat varieties (Imadud *et al.*, 2018).

Correlation study revealed several significant relationships between grain yield and other agronomic traits (*Table 4*). Genotypic correlations (*rg*) indicated a strong positive association between grain yield and harvest index (*rg* = 0.75) and biological yield (*rg* = 0.662) and plant height (0.49) (*Table 4*), these findings suggested that genotypes with higher harvest index, plant height and biological yield tend to exhibit higher grain yields. This is consistent with previous research demonstrating the importance of these traits in determining grain yield potential (Fellahi *et al.*, 2013). Phenotypic correlations (*rp*) also showed significant associations between grain yield and

harvest index (*rp* = 0.788) as well as biological yield (*rp* = 0.44). These correlations indicated that phenotypic performance in terms of harvest index and biological yield can be reliable indicators of grain yield potential. However, it is important to note that phenotypic correlations can be influenced by environmental factors, whereas genotypic correlations provide a more direct measure of the underlying genetic relationships.

The genetic variance for grain yield (*V<sub>g</sub>* = 183738.73) was smaller than the environmental variance (*V<sub>e</sub>* = 443114.9), suggesting that environmental factors have a greater influence on grain yield than genetic factors. The estimated broad-sense heritability for grain yield was relatively low 0.30 (*Table 5*), implies that approximately 29% of the observed variation in grain yield can be attributed to genetic differences, while the remaining variation is influenced by environmental factors and their interactions. This suggests that improving grain yield through traditional breeding approaches may be challenging due to the relatively low heritability (Savadi *et al.*, 2017; Wang *et al.*, 2018).

### Harvest index

Considerable disparity in harvest index was observed among various wheat genotypes ( $P \leq 0.01$ ), as shown in (*Table 2*). The range of harvest index data varied from 20% to 32%, with an average of 26% (*Table 3*). Among the genotypes, G-34 had the lowest harvest index of 21%, while G-27 exhibited the highest harvest index of 33%. A correlation analysis revealed a significant correlation between harvest index and grain yield at both the phenotypic and genotypic levels (*rp* =

0.788,  $r_g = 0.75$ ) (Table 4). In a study conducted by Dabi *et al.*, (2016) was also reported that there was a strong positive correlation between harvest index and grain yield, which holds true at both the genotypic and phenotypic levels. The genetic variance ( $V_g = 3.70$ ) for harvest index in wheat genotypes was relatively lower compared to the environmental variance ( $V_e = 12.52$ ). The broad sense heritability for harvest index was determined to be low at 0.24 (Table 5).

## CONCLUSIONS

One of the main goal of wheat breeding programs is to develop high-yielding superior lines. The current study's findings indicated that there was considerable disparity among genotypes for most of the parameters studied. This suggests that there is ample opportunity for effective selection in future breeding programs. For certain traits such as plant height, there was high estimates of broad sense heritability (0.73), indicating that early generation selection would be effective in improving these traits. At the phenotypic level, grain yield showed significant correlation with days to heading, plant height, and biological yield. At the genotypic level, it exhibited a significant correlation with biological yield. Therefore, it is recommended to consider these traits in the selection process to enhance grain yield in bread wheat. Based on the current study, G-41, G-3, G-12, G-37, G-34, and G-14 are identified as potential lines for further breeding program in different ecological conditions.

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## REFERENCES

- Allard, R.W. Principles of Plant Breeding. John Wiley and Sons. Inc. New York, U.S.A., 1960, p 430.
- Alogaidi, F.F. Studying of genetic and phenotypic variances, correlation and path coefficient analysis of yield and its component in some wheat varieties. *Journal of Kerbala for Agricultural Sciences*. 2018, 5, 151-63. <https://doi.org/10.59658/jkas.v5i3.641>
- Arya, V.K.; Singh, J.; Kumar, L.; Kumar, R.; Kumar, P.; Chand, P. Genetic variability and diversity analysis for yield and its components in wheat (*Triticum aestivum* L.). *Indian Journal of Agriculture Research*. 2017, 51, 128-34. <https://doi.org/10.18805/ijare.v0i0F.7634>
- Avinashe, H.A.; Shukla, R.S.; Jaiwar, N.D.S. Correlation and path analysis for yield and yield contributing characters in bread wheat (*Triticum aestivum* L.). *Electronic Journal of Plant Breeding*. 2015, 6, 555-559.
- Barreto, H.J.; Edemeades, G.O.; Chapman, S.C.; Crossa, S. The alpha lattice design in plant breeding and agronomy: Generation and analysis. *Agricultural and Food Sciences, Computer Science*. 1997, 25, 544.
- Bashir, M.; Khalil, I.H.; Iqbal, M.; Rahman, H. Genotypic and phenotypic correlation among yield components in

- bread wheat under normal and late plantings. *Sarhad Journal of Agriculture*. **2010**, 26, 259-265.
- Begna, T.** Role and economic importance of crop genetic diversity in food security. *International Journal of Agriculture Science and Food Technology*. **2021**, 7, 164-169.  
<https://doi.org/10.17352/2455-815X.000104>
- Bhanu, A.N.; Arun, B.; Mishra, V.K.** Genetic variability, heritability and correlation study of physiological and yield traits in relation to heat tolerance in wheat (*Triticum aestivum* L.). *Biomedical Journal of Scientific and Technology Research*. **2018**, 2, 112-2116.  
<https://doi.org/10.26717/BJSTR.2018.02.000636>
- Bhushan, B.; Bharti, S.; Ojha, A.; Pandey, M.; Gourav, S.S.; Tyagi, B.S.; Singh, G.** Genetic variability, correlation coefficient and path analysis of some quantitative traits in bread wheat. *Journal of Wheat Research*. **2013**, 5, 21-26.
- Baye, A.; Berihun, B.; Bantayehu, M.; Derebe, B.** 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*. **2020**, 6, 1752603.  
<https://doi.org/10.1080/23311932.2020.1752603>
- Chowdhury, M.M.; Haque, M.A.; Malek, M.A.; Rasel, M.; Ahamed, K.U.** Genetic variability, correlation and path coefficient analysis for yield and yield components of selected lentil (M.) genotypes. *Fundamental and Applied Agriculture*. **2019**, 4, 769-776.  
<https://doi.org/10.5455/faa.21740>
- Dabi, A.; Mekbib, F.; Desalegn, T.** 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 Research. Ecology and Management*. **2016**, 1, 145-154.  
<https://doi.org/10.11648/j.ijnrem.20160104.11>
- Falconer, D.S.; Mackay, T.F.** Introduction to quantitative genetics (4th ed.). Pearson Education Limited. 1996.
- Fan, X.; Xu, Z.; Wang, F.; Feng, B.; Zhou, Q.; Cao, J.; Wang, T.** Identification of colored wheat genotypes with suitable quality and yield traits in response to low nitrogen input. *PLoS one*. **2020**, 15, e0229535.  
<https://doi.org/10.1371/journal.pone.0229535>
- Farooq, M.; Hussain, M.; Siddique, K.H.** Drought stress in wheat during flowering and grain-filling periods. *Critical reviews in plant Science*. **2014**, 33, 331-49.  
<https://doi.org/10.1080/07352689.2014.875291>
- Fellahi, Z.E.A.; Hannachi, A.; Bouzerzour, H.; Boutekratt, A.** Line × Tester mating design analysis for grain yield and yield-related traits in bread wheat (*Triticum aestivum* L.). *International Journal of Agronomy*. **2013**, 1, 9.  
<https://doi.org/10.1155/2013/201851>
- Githinji, G.G.** Effects of Mutagenesis on Drought Tolerance and Agronomic Traits of Selected Bread Wheat (*Triticum aestivum* L.). MSc Thesis, University of Eldoret, 2016.
- Imadud, D.; Fazal, M.; Irfan, A.S.; Hamayoon, K.; Fahad, U.K.; Ibrarullah, I.; Tauqir I.** Genetic variability and heritability for yield and yield associated traits of wheat genotypes in Nowshera Valley, Pakistan. *Pakistan Journal of Agriculture Research*. **2018**, 216-222.  
<http://dx.doi.org/10.17582/journal.pjar/2018/31.3.216.222>
- Jamil, A.; Khan, S.; Sayal, O.U.; Waqas, M.; Ullah, Q.; Ali, S.** Genetic

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- variability, broad sense heritability and genetic advance studies in bread wheat (*Triticum aestivum* L.) germplasm. *Pure and Applied Biology (PAB)*. **2017**, 6, 538-543.  
<http://dx.doi.org/10.19045/bspab.2017.60055>
- Khan, A.A.; Alam, M.A.; Alam, M.K.; Alam, M.J.; Sarker, Z.I.** Genotypic and phenotypic correlation and path analysis in durum wheat (*Triticum turgidum* L. var. *durum*). *Bangladesh Journal of Agriculture Research*. **2013**, 38, 219-225.  
<https://doi.org/10.3329/bjar.v38i2.15885>
- Khan, A.J.; Azam, A.; Ali, A.** Relationship of morphological traits and grain yield in recombinant inbred wheat lines grown under drought conditions. *Pakistan Journal of Botany*. **2010**, 42, 259-267.
- Khan, I.; Amanullah; Jamal, A.; Mihoub, A.; Farooq, O.; Farhan Saeed, M.; Roberto, M.; Radicetti, E.; Zia, A.; Azam, M.** Partial substitution of chemical fertilizers with organic supplements increased wheat productivity and profitability under limited and assured irrigation regimes. *Agriculture*. **2022**, 12, 1754.  
<https://doi.org/10.3390/agriculture12111754>
- Kirby, M.; Ahmad, M.U.D.; Mainuddin, M.; Khaliq, T.; Cheema, M.J.M.** Agricultural production, water use and food availability in Pakistan: historical trends, and projections to 2050. *Agriculture and Water Management*. **2017**, 179, 34-46.  
<https://doi.org/10.1016/j.agwat.2016.06.001>
- Kumar, J.; Kumar, M.; Kumar, A.; Singh, S.K.; Singh, L.** Estimation of genetic variability and heritability in bread wheat under abiotic stress. *International Journal of Pure and Applied Bioscience*. **2017**, 5, 156-163.  
<http://dx.doi.org/10.18782/2320-7051.2475>
- Kwon S.H.; Torrie, J.H.** Heritability and inter-relationship among traits of two Soybean Populations. *Crop Science*. **1964**, 4, 196-198.  
<https://doi.org/10.2135/cropsci1964.0011183X000400020023x>
- Malbhage, A.B.; Talpada, M.M.; Shekhawat, V.S.; Mehta, D.R.** Genetic variability, heritability and genetic advance in durum wheat (*Triticum durum* L.). *Journal of Pharmacognosy and Phytochemistry*. **2020**, 9, 3233-3236.
- Mecha, B.; Alamerew, S.; Assefa, A.; Dutamo, D.; Assefa, E.** Correlation and path coefficient studies of yield and yield associated traits in bread wheat (*Triticum aestivum* L.) genotypes. *Advance Plants Agriculture Research*. **2017**, 6, 128-136.  
<https://doi.org/10.15406/apar.2017.06.00226>
- Mecha, B.; Almerew, S.; Assefa, A.; Assefa, E.; Dutamo, D.** Genetic variability heritability and genetic advance for yield and yield related traits in bread wheat (*Triticum Aestivum* L.) genotypes. *Global Journal of Science Frontier Research*. **2016**, 16, 12-15.
- PBS.** Pakistan Statistical Year Book 2020, Government of Pakistan, Ministry of Planning Development & Special Initiatives, Pakistan Bureau of Statistics, Islamabad, Pakistan, 2022.
- Preeti, S.; Kamboj, M.C.; Singh, N.; Chand, M.; Yadava, R.K.** Path coefficient and correlation studies of yield and yield associated traits in advance homozygous lines of bread wheat germplasm. *International Journal of Current Microbiology and Applied Science*. **2018**, 7, 51-63.  
<https://doi.org/10.20546/ijemas.2018.7.02.008>
- Rajput, S.R.** Correlation, path analysis, heritability and genetic advance for

- morpho-physiological character in bread wheat (*Triticum aestivum* L.). *Journal of Pharmacognosy and Phytochemistry*. **2018**, 7, 107-112.
- Rao, S.D.; Raghavendra, M.; Gill, P.; Madan, S.; Munjal, R.** Effect of drought stress on phenological and yield attributes in Wheat (*Triticum aestivum* L.). *Journal of Eco-friend and Agriculture*. **2022**, 17, 65-71. <https://doi.org/10.5958/2582-2683.2022.00014.4>
- Reynolds, M.; Bonnett, D.; Chapman, S.C.; Furbank, R.T.; Mane, Y.; Mather, D.E.; Parry, M.A.J.** Raising yield potential of wheat. I. Overview of a consortium approach and breeding strategies. *Journal of Experimental Botany*. **2011**, 62, 439-452. <https://doi.org/10.1093/jxb/erq311>
- Savadi, S.; Prasad, P.; Kashyap, P.L.; Bhardwaj, S.C.** Molecular breeding technologies and strategies for rust resistance in wheat (*Triticum aestivum*) for sustained food security. *Plant pathology*. **2017**, 67, 771-791. <https://doi.org/10.1111/ppa.12802>
- Singh, R.K.; Chaudhary, B.D.** Path analysis and biometrical methods in quantitative genetic analysis, 1985, pp. 70-79.
- Singh, R.K.; Yadav, H.C.; Kumar, M.; Lal, K.; Amir, M.** Genetic variability, heritability and genetic advance analysis for seed yield and its physiological quality parameters in rice (*Oryza sativa* L.). *Journal of Pharmacognosy and Phytochemistry*. **2019**, 8, 511-513.
- Slafer, G.A.; Elia, M.; Savin, R.; García, G.A.; Terrile, I.I.; Ferrante, A.; González, F.G.** Fruiting efficiency: an alternative trait to further rise wheat yield. *Food and Energy Security*. **2015**, 4, 92-109. <https://doi.org/10.1002/fes3.59>
- Talebi, R.; Fayyaz, F.** Estimation of heritability and genetic parameters associated with agronomic traits of bread wheat (*Triticum aestivum* L.) under two constructing water regimes. *Journal of Applied Biological Science*. **2012**, 6, 35-39.
- Tilahun, B.; Habtamu, T.; Tesfaye, L.** Genetic variability, heritability and genetic advance among bread wheat genotypes at southeastern Ethiopia. *Agriculture, Forestry and Fisheries*. **2020**, 9, 128-134. <https://doi.org/10.11648/j.aff.20200904.15>
- Ullah, N.; Ullah, H.; Afridi, K.; Alam, M.; Jadoon, S.A.; Khan, W.U.; Masood, A.; Uddin, H.** Genetic variability, heritability and correlation analysis among morphological and yield traits in wheat advanced lines. *Biyolojik Çeşitlilik ve Koruma*. **2018**, 11, 166-180.
- Wang, X.; Xu, Y.; Hu, Z.; Xu, C.** Genomic selection methods for crop improvement: Current status and prospects. *The Crop Journal*. **2018**, 6, 330-340. <https://doi.org/10.1016/j.cj.2018.03.001>
- Yang, L.; Zhao, D.; Meng, Z.; Xu, K.; Yan, J.; Xia, X.; Zhang, Y.** QTL mapping for grain yield-related traits in bread wheat via SNP-based selective genotyping. *Theoretical and Applied Genetics*. **2020**, 133, 857-872. <https://doi.org/10.1007/s00122-019-03511-0>

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