



# Screening of Wheat Advanced Lines for Yield Potential in Agro-Climatic Conditions of Dera Ismail Khan

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## Abstract

Screening of wheat germplasm and developing climate-resilient wheat cultivars are crucial to ensure the growing food demand of the global population. This study was designed to evaluate nine advanced wheat lines for yield-related attributes and screen out the best-performing lines suitable for the agro-climatic conditions of Dera Ismail Khan. Nine wheat accessions, along with the check cultivar AZRC Dera, were investigated in a Randomized Complete Block Design (RCBD) with three replications at Arid Zone Research Institute (AZRI), D. I. Khan, Pakistan. Data collected for days 50% heading, days to maturity, flag leaf area, no of tillers plant-1, spike length, plant height, no of spikelet spike-1, peduncle length, no of grains spike -1, 1000-grains weight, grain yield plant -1 and spike density was subjected to Statistix v.8.1. All the characters showed highly considerable variations among genotypes ( $p < 0.01$ ). The analysis of coefficient variation revealed high magnitude for no. of grains spike-1, grain yield plant-1, 1000-grains weight, spike length, and spike density. High heritability was noticed for days to 50% heading, maturity, flag leaf area, no. of tillers per plant-1, peduncle length and spike traits. Positive association was observed for flag leaf area, spike length, no. of tillers plant -1, days to maturity, peduncle length, no of spikelet spike-1, 1000 kernels weight and no. of kernels spike - 1. Based on the mean performance of wheat genotypes under study, accession G4 showed maximum performance for most of the parameters and is recommended for further breeding purposes.

**Keywords:** Heritability, ANOVA, PCV, GCV, variance, correlation, AZRC-Deraenetic

DOI: <https://zenodo.org/records/15392740>

Journal Link: <https://jai.bwo-researches.com/index.php/iwr/index>

Paper Link: <https://jai.bwo-researches.com/index.php/iwr/article/view/123>

Publication Process Received: 04 Apr 2024/ Revised: 17 Jun 2024/ Accepted: 21 Jun 2024/ Published: 29 Jun 2024

ISSN: Online [3007-0929], Print [3007-0910]

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Indexing:



Publisher: BWO Research International (15162394 Canada Inc.) <https://www.bwo-researches.com>

## Introduction

Among cereals bread wheat is identified as the King of cereals because it can be cultivated under diverse types of soil and climate, better dough for bread making and nutrient rich food article. The world's most nutritious and easy to store food with a source of protein, mineral, dietary fiber B-group vitamins (Foulkes et al. 2009). Wheat is a good source for confectionary and is used to prepare many things like biscuits and other items like noodles (Kandel et al. 2018). Wheat provides 36% food to the whole world and 20% of energy and is a staple used almost worldwide, which accounts for approximately 240 million ha compared with other cultivated crops (Babar et al. 2022). The dependency of the global human population on wheat makes it a vital cereal crop for food and nutritional security (Zewdu et al. 2024). Wheat is the world important crop to excel other crops in the area. Production and providing about 20 percent of food calories to the world population (Nukasani et al. 2013).

The ploidy level of bread wheat is a hexaploid ( $2n=6x=42$ ) and belongs to the family Poaceae and genus Triticum (Bozzini et al. 1988). The differences among genetic materials play a critical role in providing grounds for breeding because this process primarily depends on the variation among genotypes. In this regard, description, and classification of crop germplasm, morphological characterization is considered the step of prime importance (Smith et al. 1989). The amount of differences in genetic makeup is a considerable component necessary for a successful hybridization target. Many crops such as Wheat have been genetically modified to get maximum production over the last century. Due to very narrow genetic make up most of the cereal crops including wheat has similar genetic base.

Consequently, it is crucial to create a source of new variation in breeding. Hybridization is a process where variation is created through different parental crosses. One of the chief causes of wheat yield decline is cultivating low genetic potential varieties (Prasad et al. 2021). The ongoing global climate change is expected to further aggravate the dilemma of static wheat productivity in different wheat-growing regions of the world (Mohibullah et al. 2024). Many crops such as Wheat have been genetically modified to get maximum production over the last century. Consequently, it is crucial to create a source of new variation in breeding. And a breeder is a person who can easily figure out superiority and genetic variations among materials which can easily create crossed with desirable characters. Every breeding program and its success is dependent on the available diversity & variability of the germplasm under use and more variability means more chance of improvement in crop plants (Sana et al. 2024). Genetic dissimilarities is one of the key points to carry out crosses and create genetic improvements in crops (Balkan et al. 2018). Heritability estimates provide the information on the proportion of variation that is transmissible to the progenies in subsequent generations (Bishwas & Singh, 2024) and for that the breeder should identify the variation in desired characteristics and skillfully Select the Desired crop's improvement (Ali et al. 2024). The process where comparison of various characters can be studied and improvements likely to achieve, genetically and phenotypically should be carried out (Joshi et al. 2005). A suitable breeding plan to take use of the inherent diversity of the original population, variables such as the genotypic and phenotypic coefficient of variation, heritability, and genetic advance

for the various traits are very crucial (Kumar et al. 2024).

A lot of studies have done to uncover the relationship among yield and other traits in order to achieve high yielding varieties (Singh et al. 1995, Tammam et al. 2000, Lad et al. 2003, Kashif et al. 2004). Grain production is quantitative trait with complex architecture and directly or indirectly dependent on the components of variables and their interaction. The interrelationship between two or more variables can be calculated through different ways and provide the value of their correlation. By calculating association among yield and other traits, production per capita can be improved during selection (Johnson et al. 1955). It is difficult to increase yield only through the selection of better genotypes with the naked eye. Therefore, before selection of any genotypes we have to study its phenotypic and genetic performance towards kernels yield (Preeti et al. 2018). Mostly calculation of correlation is done for yield and yield related traits to enhance performance of any crop, hence, this research work was done to reveal the difference among different genotypes, the extent of transfer of different character to offspring and their correlation to yield.

### Materials & Methods

The field experimental trial was conducted in the fields of (A.Z.R.C.) Dera Ismail Khan, Pakistan during rabbi season, December-May (2021-2022).

### Material

Nine wheat bread accessions along with one local check variety "AZRC-Dera" were used in the experiment which were different in their genetic formation. The detail of the experimental material is present in Table 1.

**Table 1** Detail of genotypes used in the experiment.

No	Source of Accessions	Annotation of Accessions
1	INESWY T 2018-19 #6	G1
2	INESWY T 2018-19 #8	G2
3	INESWY T 2018-19 #9	G3
4	INESWY T 2018-19 #10	G4
5	INESWY T 2018-19 #11	G5
6	INESWY T 2018-19 #14	G6
7	INESWY T 2018-19 #20	G7
8	INESWY T 2018-19 #23	G8
9	INESWY T 2018-19 #25	G9
10	AZRC-Dera	G10

### Research design

Germplasm for current research was planted in five-meter-long rows based on Randomized Complete Block Design (RCBD) in three replications. The space between the plants were 15 centimeters while the distance between rows were 30 centimeters.

### Parameters scored

Data on different parameters such as Days 50% heading, days to maturity, flag leaf area, no of tillers plant<sup>-1</sup>, spike length, plant height, no of spikelet spike<sup>-1</sup>, peduncle length, no of grains spike<sup>-1</sup>, 1000-grains weight, grain yield plant<sup>-1</sup> and spike density was taken from five plants in every line assisted by method outlined in Singh and Chaudhary's statistical model (1985).

### Statistical procedures

The data was obtained through variance analysis follow the method of Singh and Chaudhry (1985). Phenotypic and genetic association among all traits was calculated from range, mean, ANOVA and standard error of mean were calculated.

### Heritability

Heritability in broad sense (h<sup>2</sup>BS) was estimated with Falconer (1989) method.

$$h^2_{BS} = \frac{GV}{PV}$$

### Genetic and phenotypic coefficient of variance

Genetic analysis was estimated using mean for calculating PCV and GCV

### Genotypic coefficient of variation

$$GCV (\%) = \frac{\sqrt{GV}}{\bar{X}} \times 100$$

### Phenotypic coefficient of variation

$$PCV (\%) = \frac{\sqrt{PV}}{\bar{X}} \times 100$$

### Genetic advance

Genetic advance was obtained following Allard (1960) and Singh and Chaudhary (1979).

$$\text{Genetic advance (as percent of mean)} = k \times h \times \sqrt{\frac{\text{Phenotypic variance}}{\text{Mean value of treat}}} \times 100$$

While

GA: genetic advance.

K: constant = 2.06 at 5% selection intensity.

h<sup>2</sup>: Heritability.

GA as % of mean (GAM) = (GA/Mean Value) \*100

### Phenotypic and genetic correlation

The phenotypic and genetic association was calculated according to Kwon and Torrie (1964) to evaluate the correlation between two traits.

### Phenotypic correlation

$$(r_p) = \frac{PCov_{xy}}{\sqrt{PV_x \cdot PV_y}}$$

### Genotypic correlation

$$(r_g) = \frac{GCov_{xy}}{\sqrt{GV_x \cdot GV_y}}$$

## Results

### Analysis of variance

The mean square of all the traits studied showed the presence of highly significant differences in all traits ( $P < 0.05$ ) among the tested accessions. This suggests that the studied breeding materials have an adequate genetic variation for all of the traits. This indicates that crop improvements through selection are possible (Table 2).

**Table 2.** Mean squares of twelve agromorphological characters of nine wheat accessions

	D F	D H	D M	F L A	N T P	P H	S L	P L	N S S	N G S	G Y P	1 0 0	S D
--	--------	--------	--------	-------------	-------------	--------	--------	--------	-------------	-------------	-------------	-------------	--------

													0 G W	
R e p l i c a t i o n	2	4 . 0 3 7	4 . 7 7 8	0 . 8 7 8	1 . 3 1	0 . 5 1	0 . 6 2 7 6	3 . 1 3 6	2 . 6 5 8 1	7 . 7 7	4 . 7 3 7	6. 3 9 9 6	0 1 1 3 2	
G e n o t y p e s	8	2 3 9. 5 3 *	8 1 . 8 3 *	2 2 . 9 6 *	1 1 . 8 *	1 3 3	0 . 4 2 9 *	1 2 4. 8 5 *	1 5 . 5 1 *	2 2 5. 9 1 *	1 5 4. 1 9 *	7 0. 7 4 *	0 3 4 3 *	
E r r o r	1 6	8 . 5 7 9	1 0 . 2 7 7 8	2 . 7 3 0 2	2 . 7 9 4 8	6 5 . 4 2 7	0 . 1 4 7 2 4	6. 2 5 7	7 . 4 1 3 1	5. 3 7 6	5. 4 8 3	5. 5 3 1 9	0 . 0 0 4 8 5	
S E o f M e a n		1. 6 9	1 . 8 5	0 . 9 5	0 . 9 6	4 . 6 7	0 . 1 2	1. 4 4	1 . 5 7	1. 3 3	1. 3 5	1. 3 5	0 . 0 1	

### Days to 50% heading

Mean square for days to 50% headings depicted highly significant variation amongst genotypes. (Table 2). Range of variation for days to 50% heading according to mean data was 28 and the mean value was 103.70 (Table 3). The genotype (G9) showed maximum 115 days to 50% heading followed by two genotypes (G4) and (G8) showed same 114 days to 50% heading. On the other hand, genotype (G3) showed low value of 94 days to 50% heading. GV and PV value were 76.986 and 85.565. Values GCV and PCV for days to 50% were 3.66 and 3.86 respectively. Days to 50 % heading shown heritability of 89.97. Expected value for genetic advance was 17.14 (Table 3).

**Table 3** Range, mean, coefficients of variation and broad sense heritability estimates of various quantitative characters of nine wheat accessions and one check.

Parameters	Range	Mean	GV	PV	GCV	PCV	h <sup>2</sup> BS%	GA
Days to 50 % heading	28	103.70	76.98	85.56	3.66	3.86	89.97	17.14
Days to maturity	22	140.56	23.85	34.12	5.96	7.13	69.88	8.41
Flag leaf area	9.98	40.26	6.74	9.47	11.30	13.40	71.19	4.51

Number of tillers plant <sup>-1</sup>	8.4	8.96	2.99	5.79	14.68	20.41	51.76	2.56
Plant height	28.9	102.66	22.60	88.03	3.56	7.04	25.67	4.96
Spike length	1.4	7.84	0.12	0.17	83.53	96.53	74.87	0.63
Peduncle length	24.64	15.91	39.53	45.78	5.03	5.41	86.33	12.03
Number of spikelet spike <sup>-1</sup>	10.99	19.64	2.70	10.11	10.59	20.49	26.70	1.74
Number of grains spike <sup>-1</sup>	33.2	40.20	73.51	78.88	3.79	3.93	93.18	17.04
Grain yield plant <sup>-1</sup>	28.8	15.43	49.57	55.05	4.56	4.81	90.04	13.76
1000-grain weight	18.46	41.82	21.73	27.26	6.59	7.38	79.71	8.57
Spike density	0.95	0.77	0.11	0.11	98.32	98.75	99.12	0.69

### Days to maturity

Mean square for days to maturity depicted highly significant variation amidst genotypes (Table 2). Days to maturity showed range was 9.98 and mean value was 140.56 (Table 2). The genotype (G4) showed maximum value of days to maturity was 149 followed by genotypes (G5) which showed (145) days to maturity. On the other hand, genotype (G1) showed minimum value of days to maturity was (134). The genetic variance (GV) and phenotypic (PV) values were 23.85 and 34.12. The value of (GCV) was 5.96 and (PCV) was 7.13. Noted value of GA was 8.41 (Table 3).

### Flag leaf area

ANOVA showed highly considerable variability between genotypes for flag leaf area (Table 2). Range according to the mean data was 8.4 and the value of mean for flag leaf area was 40.26cm<sup>2</sup> (Table 2). Genotype (G9) showed maximum value of flag leaf area was 43.690 cm<sup>2</sup> followed by an genotype (G6) which showed 43.633 cm<sup>2</sup> while on the other hand genotype (G7) showed minimum 36.947 cm<sup>2</sup>. The local check gave mean values of 42.510 cm<sup>2</sup>. The genetic variance (GV) and phenotypic variance (PV) For flag leaf area was 6.74 and 9.47 respectively. The values of (GCV) and (PCV) for given parameter was (11.30) and (13.40). The heritability value and expected genetic advance for flag leaf area was (71.19) and (4.51) respectively (Table 3).

### Number of tillers plant<sup>-1</sup>

The results showed range value was 8.4 and mean value was 8.96 (Table 3). Genotype (G4) showed highest value for no. of tillers plant-1 was 11.800 followed by genotype (G9) and genotype (G2) showed 11.667 and 9.800 no. of tillers plant-1 respectively while genotype (G7) gave minimum 6.0 no. of tillers plant-1. The genetic variance (GV) and phenotypic variance (PV) for no. of tillers plant-1 was 2.99 and 5.79 respectively. The (GCV) of no. of tillers plant-1 was 14.68 and (PCV) was 20.41. The percentage of heritability was calculated 51.76 while the expected genetic advance for no. of tillers plant-1 was 2.56 (Table 3).

### Plant height

ANOVA showed huge amount of noticeable variability among genotype (Table 2). The range of variation is 28.9cm and mean for plant height was 102.66 cm (Table 2). Genotype (G8) showed maximum value of plant height 109.59 cm followed by genotype (G2) showed value (108.33) cm while genotype (G9) showed minimum value of plant height which was 108.07 cm. The local cultivar (G10) gave mean value 93.52 cm. The value of (GV) for plant height was 22.60 and phenotypic (PV) value was 88.03. The value of GCV for plant height was 3.56 and that of PCV was 7.04. The percentage of heritability was 98.27 and the value of expected genetic advance was 4.96. (Table 3)

### Spike length

Inconsiderable variation was showed by ANOVA for spike length among these genotypes (Table 2). The value of variation range was 1.4 cm and the mean for spike length was 7.84 cm (Table 3). The genotype (G6) showed maximum value spike length 8.30 cm and genotype (G3) show second great value of spike length 8.26 cm while on the other hand genotype (G1) showed 7.26 cm. Mean value of local

check for spike length was 7.26 cm. Genetic variance (GV) value was 0.12 and phenotypic variance (PV) value was 0.17. GCV and PCV 83.53 and 96.53 respectively. The percentage heritability was 74.87 and value of expected genetic advance was 0.63 (Table 3).

### **Peduncle length**

The value of range according to mean data for peduncle length was 24.64cm while mean value for peduncle length was 15.91 cm (Table 3). Genotype (G5) showed highest value peduncle length of 26.73cm among these genotypes followed genotype (G2) which showed 23.11cm while on the hand genotype (G7) showed minimum value for peduncle length 7.11cm. Genetic variance and phenotypic variance for peduncle length were 39.53 and 45.78. GCV and PCV were 5.03 and 5.41 respectively. The percentage of heritability was 86.33 and the value of expected genetic advance was 12.03 (Table 3).

### **No of spikelet spike<sup>-1</sup>**

ANOVA showed highly considerable variation were recorded among genotypes (Table 2). Range of variation according to mean data was 10.99 while mean value was 19.64 (Table 3). Genotype (G4) showed maximum 22.580 no. of spikelet spike<sup>-1</sup> followed by genotype (G6) showing 22.307 spikelet spike<sup>-1</sup> while the minimum no. of spikelet spike<sup>-1</sup> 16.700 shown by genotype (G1). Check cultivar showed mean value of (16.757). The value of (GV) and (PV) for no. of spikelet spike<sup>-1</sup> were 2.70 and 10.11 respectively. Genetic coefficient of variance value was 10.59 and that phenotypic coefficient of variance value was 20.49. The percentage of heritability was 26.70 and expected genetic advance for no. of spikelet spike<sup>-1</sup> was 1.74 (Table 3).

### **Number of grains spikes<sup>-1</sup>**

The range value was 33.2 and the value of mean notice for no. of kernels spike<sup>-1</sup> was 40.20 (Table 3). Genotype (G7) showed

maximum value of no. of kernels spike<sup>-1</sup> (48.0) having genotype (G5) on second with 47.920 no. of kernels apike<sup>-1</sup> while genotype (G5) showed minimum no. of kernels spike<sup>-1</sup> 24.100. The GV for no. of kernels spike<sup>-1</sup> was 73.51 and that of PV was 78.88. The GCV and PCV values were 3.79 and 3.93 respectively. The percentage value of heritability was 93.18. The expected genetic advance was 17.04 (Table 3)

### **Grains yield plant<sup>-1</sup>**

ANOVA showed that kernels yield plant<sup>-1</sup> possessed highly considerable variation among all the genotypes (Table 2). The value of range of variation was 28.8 and the mean value was 15.45g. Genotype (G4) showed maximum value kernels yield plant<sup>-1</sup> which was 31.237g followed by genotype with (G3) which was 17.200g while a genotype (G8) showed 5.45g which was minimum kernels yield plant<sup>-1</sup>. Mean value of check cultivar was 16. The value of (GV) and (PV) for kernels yield plant<sup>-1</sup> were 49.57 and 55.05. The value of GCV was 4.56 while the value PCV was 4.81. The percentage of heritability for kernels yield plant<sup>-1</sup> was 90.04 and expected genetic advance was 13.76 (Table 3).

### **1000-grains weight**

The range of variation for 1000 kernels weight according to mean data was noted as 18.46g and the mean value for this parameter was 41.82g (Table 3). Genotype (G2) showed maximum value of 1000-kernels weight which was 48.110g followed by genotype (G8) which showed 46.087g while a genotype (G7) possessed minimum 1000-kernels weight which was 32.833g. The value of (GV) was 21.73 and that of (PV) was 27.26 for 1000-kernels weight. The GCV and PCV were 6.59 and 7.38 respectively. Heritability percentage was 79.71 and value expected genetic advance was 8.57 (Table 3)

### **Spike density**

Range of variation according to mean data was 0.95 and mean value for this parameter was 0.77 (Table 3). The genotype (G8) indicate maximum value for spike density was 1.33 followed by genotype (G5) showing value of spike density 1.22 and genotype (G4) showed minimum value for spike density 0.42. GV and PV values were 0.114 and 0.115 for spike density respectively. The value of GCV and PCV values were 98.32 and 98.75 respectively. The heritability percentage was 98.12 and expected genetic advance was 0.69 (Table 3).

#### **Genotypic and Phenotypic Coefficients of Variation**

According to Burton and Devane (1953), GCV and PCV are classified as high (>20%), medium (10–20%), and low (<10%). In the present study, GCV ranged from 3.56 for plant height to 98.32 for spike density. PCV ranged from 3.86 for days to 50% headings to 98.75 for spike density. (Table 3).

#### **Estimation of Heritability in the Broad Sense and Genetic Advance**

The estimated heritability was studied for all traits (Table 2). Heritability values ranged from 25.67 for plant height to 99.12 for spike density. Robinson et al. 1949 classified heritability values as low (0–30%), moderate (30–60%), and high (60 and above). High heritability was observed for days to maturity (69.88), flag leaf area (71.19), spike length (74.87), 1000-grain weight (79.71), peduncle length (86.33), days to 50% headings (89.97), grains yield plant (90.04), no of grains spike (93.18) & spike density (99.12) which indicates that environment had a low influence on the expression of the traits suggesting direct selection for improvement. No of tillers plant<sup>-1</sup> showed moderate heritability value of 51.76 indicating relatively medium effect of environment on this trait. While low heritability values were found for trait no

of spikelet spike (26.70), plant height (25.67) (Table 3).

#### **Correlation Analysis**

The correlation analysis among agronomic and yield-related traits revealed predominantly weak genetic and phenotypic associations. Genetically, days to 50% heading exhibited an inconsiderable positive correlation with days to maturity, flag leaf area, peduncle length, number of tillers per plant, and spike density, while traits such as 1000-kernel weight, number of spikelets per spike, and kernel yield per plant showed weak negative associations. A highly significant positive correlation was observed between days to 50% heading and plant height, whereas a negative correlation was found with number of kernels per spike. Spike length was positively correlated with days to 50% heading but had a considerable negative association with spike density. Similarly, days to maturity demonstrated weak positive genetic correlations with several traits, including peduncle length and plant height, but showed a notable negative correlation with spike density and 1000-kernel weight (Table 4).

Phenotypic correlations followed similar trends, with most relationships being weak. Flag leaf area, number of tillers per plant, and peduncle length were positively associated with several traits, including spike length and plant height, while negative associations were recorded with 1000-kernel weight and spike density. Genetically, number of tillers per plant had a highly negative correlation with number of kernels per spike. Kernel yield per plant was positively and significantly correlated with 1000-kernel weight and negatively with spike density, both phenotypically and genetically. These findings indicate limited but relevant interactions among traits, suggesting that selection for traits with significant correlations particularly

kernel yield per plant and 1000-kernel weight may enhance yield potential in future wheat breeding programs.

**Table 4 Genotypic and Phenotypic correlation for twelve for twelve quantitative characters of nine wheat genotypes and one check.**

Parameters	DH	DM	FLA	NTP	PH	SL	PL	NSS	NGS	GYP	100 GW	SD
DH		0.45 NS	0.23 NS	0.49 NS	0.49 NS	- 0.20 NS	0.08 NS	- 0.28 NS	- 0.59 NS	- 0.05 NS	- 0.07 NS	0.13 NS
DM	0.58 NS		0.76* NS	0.16 NS	0.04 NS	0.01 NS	0.25 NS	0.17 NS	0.29 NS	0.57 NS	0.30 NS	- 0.16 NS
FLA	0.35 NS	0.91**		0.28 NS	0.05 NS	0.21 NS	0.17 NS	0.22 NS	0.18 NS	0.26 NS	- 0.25 NS	- 0.17 NS
NTP	0.55 NS	0.17 NS	0.48 NS		0.50 NS	0.20 NS	0.22 NS	0.18 NS	- 0.66*	0.26 NS	0.21 NS	- 0.41 NS
PH	0.84**	0.24 NS	0.14 NS	0.84**		0.12 NS	0.27 NS	0.10 NS	- 0.75*	- 0.10 NS	0.02 NS	0.01 NS
SL	0.04*	0.21 NS	0.30 NS	0.32 NS	0.37 NS		- 0.30 NS	0.58 NS	- 0.04 NS	0.04 NS	- 0.50 NS	- 0.66*
PL	0.18 NS	0.34 NS	0.25 NS	0.17 NS	0.41 NS	- 0.11 NS		0.05 NS	- 0.06 NS	0.36 NS	0.69* NS	0.34 NS
NSS	- 0.16 NS	0.33 NS	0.47 NS	- 0.11 NS	0.41 NS	0.93 NS	0.10 NS		0.14 NS	0.59 NS	- 0.00 NS	- 0.30 NS
NGS	- 0.62**	0.19 NS	0.14 NS	- 0.85**	- 0.99**	- 0.12 NS	- 0.11 NS	0.05 NS		0.39 NS	- 0.21 NS	- 0.06 NS
GYP	- 0.09 NS	0.50 NS	0.27 NS	0.22 NS	- 0.13 NS	0.01 NS	0.32 NS	0.58 NS	0.39 NS		0.12 NS	- 0.37 NS
GW	- 0.09 NS	- 0.37 NS	- 0.29 NS	0.21 NS	- 0.04 NS	- 0.51 NS	0.67* NS	- 0.10 NS	- 0.23 NS	0.12 NS		0.52 NS
SD	0.04 NS	- 0.24 NS	- 0.22 NS	- 0.51 NS	- 0.10 NS	- 0.68*	0.27 NS	- 0.48 NS	- 0.03 NS	- 0.36 NS	0.54 NS	

## Discussion

Parameters in this investigation presenting highly considerable variation were days to 50% headings, days to maturity, peduncle length, no. of tiller plant<sup>-1</sup>, no. of grains spike<sup>-1</sup>, 1000-grains weight and spike density. All the highly considerable traits discussed here present potential for exploration of beneficial aspects future breeding programs.

### Days to 50% heading

Highly significant variation in days to 50% headings amongst genotypes suggests

genetic diversity for this feature. Genotypes G3, G1, G2 and G6 had taken lowest days to 50% headings indicating potential for increased output. The results are consistent with the previously published results of [Elbashier et al. \(2019\)](#), & [El-Mohsen et al. \(2012\)](#).

### Days to maturity,

Days to maturity varied considerably significant between genotypes. Genotype G1 had taken lowest days to maturity and then G2, G8 and G3. These genotypes may contain genes that lead to wheat genotypes maturing earlier. The results are consistent with those of [Ashish et al. \(2020\)](#) and [Joshi et al. \(2005\)](#).

### Flag leaf area

Flag leaf area have highly considerable difference among all genotype. Genotype G9 had largest value for flag leaf area followed by G6 and G4. Flag leaf area showed high value of heritability and low value for genetic advance which indicate non additive gene action and findings of [Aliyu Usman Ibrahim et al. \(2019\)](#) support this result.

### Number of tillers plant<sup>-1</sup>

No of tillers plant<sup>-1</sup> significantly affects yield. There was highly significant heterogeneity across genotypes for this characteristic. Genotype G4 had the highest no of tillers plant followed by G9 and G2. These genotypes might provide valuable genes for enhancing tillers hence grain yield of wheat germplasm. Results found were in accordance with the reported findings of [Arega et al. \(2010\)](#) & [Vichitra Kumar Arya et al. \(2017\)](#).

### Plant height

Mean squares of plant height show high considerable difference among all genotypes. Higher plant is considering well due to good amount of straw but taller plant always has problems of lodging. therefore, dwarf plant is considering good to prevent from this issue. Genotype G3

had lowest value for plant height followed by G1 and G7. [Arega et al. \(2010\)](#), [Matkovic et al. \(2018\)](#) and depicted same findings in their results.

### **Spike length**

Mean squares of spike length have inconsiderable difference among genotypes. Genotypes G6 had highest value for spike length followed by G9 and G3. [Nukasani et al. \(2013\)](#) found similar result. [Bhushan et al. \(2013\)](#) calculated similar amount of genetic advance

### **Peduncle length**

Peduncle length is another crucial factor in yield. This characteristic exhibited significant variation among genotypes. Genotype G7 had smallest value for peduncle length followed by G6 and G1. These genotypes might provide useful genes for short stature plants. Similar findings were reported by [Ashfaq et al. \(2014\)](#), & [Safi et al. \(2017\)](#).

### **Number of spikelet spike<sup>-1</sup>**

Mean square show high considerable difference among genotypes for no. of spikelet spike<sup>-1</sup>. Spikelet spike<sup>-1</sup> is a yield relevant trait because higher the no. of spikelet in spike higher will be the no. of kernels and automatically yield will be increased. Genotypes G6 had largest value for this trait followed by G6 and G5. [Jamil et al. \(2017\)](#) and [Bhushan et al. \(2013\)](#). [Zeeshan et al. \(2013\)](#) witnessed similar estimates for this trait.

### **Number of grains spikes<sup>-1</sup>**

The quantity grains spike is another crucial factor in yield. There was also highly significant diversity across the genotypes for this characteristic. Genotype G7 exhibited the most no of grains per spike, followed by G5 and G3. These genotypes may contain genes that promote grain growth and enhancing yield per plant. These results were supported by studies of [NIKKHAHKOUC HAKSARAEI and Martirosyan \(2017\)](#), [Sachan & Singh](#)

[\(2003\)](#), [Bayisa et al. \(2020\)](#), [Tsegaye et al. 2012](#) and [Gerema et al. \(2021\)](#).

### **Grain yield plant<sup>-1</sup>**

Mean square of kernels yield per plant possessed highly considerable variation among all genotypes suggests for breeders to manipulate this trait in said genotypes. Genotypes G4 showed promising results for this trait followed by G3 and G1. [Arega et al. \(2010\)](#) found similar result

### **1000-grain weight**

Wheat breeding focusses on maximizing grain production hence focusing on weight of the grains. The genotypes showed significant variance for this characteristic. G2 produced the largest grain weight followed by G8 and G5. These genotypes have the potential to provide great yields and healthy grains. Similar estimates were revealed by the reported outcomes from studies of [Preeti et al. \(2018\)](#) and [Nukasani et al. \(2013\)](#).

### **Spike density**

Spike density is an important component in determining yield. This character depicted strong significant heterogeneity across genotypes. Genotype G8 had the highest spike density, followed by G5 and G1. These genotypes might provide valuable genes for enhancing spike density. Similar findings were reported by [Nasir et al. \(2024\)](#), [Kalimullah et al. \(2012\)](#) and [Kumar et al. \(2017\)](#).

### **Heritability Estimates**

Estimating heritability can reveal the genetic basis of characteristics and provide areas for improvement via Selective breeding. The study found that heritability values varied across variables, indicating different levels of genetic influence. Traits with high heritability, such as days to maturity, flag leaf area, spike length, 1000-grain weight, peduncle length, days to 50% headings, grains yield plant<sup>-1</sup>, no of grains spike<sup>-1</sup> & spike density have a significant genetic component. This indicates that

genetic factors influence the manifestation of these features comparatively higher. Direct selection for these features is expected to enhance crop performance. Traits with moderate heritability, including tillers per plant had a moderate genetic effect. Traits vary due to both hereditary and environmental causes. Optimizing these features may need a combination of genetic selection and proper environmental management.

In support of this study, high heritability estimates were also recorded by Alemu et al. (2017), Dabi et al. (2019), Din et al. (2018), Balkan et al. (2018), Bayisa et al. (2020), Gerema et al. (2020), Hossain et al. (2021), Ullah et al. (2011), El-Mohsen et al. (2012), Joshi et al. (2004), Arega et al. (2010), Safi et al. (2017), Sachan & Singh (2003), Nukasani et al. (2013), Kalimullah et al. (2012), Kumar et al. (2017). Zewda et al. (2024), and Dabi et al. (2019) found modest heritability for no of tillers per plant, which aligns with our findings. By comparison, Ullah et al. (2021) and Din et al. (2018) reported high heritability values for no of tillers plant<sup>-1</sup>. The high heritability estimates for most characteristics suggest that selecting for them might improve wheat output. Identifying high-yielding genotypes with suitable agronomic features can enhance wheat breeding operations. Additional research is needed to corroborate these findings and generate high-yielding wheat cultivars.

## Conclusions

This study identified significant variation among wheat genotypes for key agronomic traits such as days to 50% heading, days to maturity, flag leaf area, peduncle length, number of tillers per plant, number of kernels per spike, kernel yield per plant, 1000-kernel weight, and spike density.. Genotypic mean performance highlighted G4 and G9 as top performers across multiple traits, with G4

excelling in grain yield per plant and other yield-contributing characteristics.

Heritability estimates were high for most traits, suggesting strong genetic control and potential for selection. Traits such as days to 50% heading, peduncle length, number of kernels per spike, and kernel yield per plant showed moderate genetic advance, indicating their suitability for selection in early breeding generations.

Correlation analysis revealed minimal direct association between most traits and kernel yield per plant, although traits like number of kernels per spike were influenced by factors such as days to 50% heading and plant height. These interactions should be considered in future selection strategies. Overall, genotype G4 demonstrated superior performance and is recommended for use in wheat breeding programs aimed at yield improvement.

## Acknowledgement

Maham Jamshed and Jamal Abdul Nasir conceived the idea and designed the research. Rizwan Ahmed, Muhammad Muddasir and Umer Mustafa conducted the experiments, collected and analyzed the data, and drafted the manuscript. All authors cross-checked the manuscript.

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