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RESEARCH ARTICLE

Analysis of Genetic Variability of 36 Advanced Wheat Lines and Yield-related Traits

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ABSTRACT

This experiment was carried out at the Cereal Crops Research Institute, Pirsabak Nowshera, during 2021-22. The experimental materials for this study consisted of 36 advanced wheat lines and 'GULZAR-2019' as a control. The experiment was carried out in a complete randomized block design with two replications to study genetic variability. The data were recorded following parameters, including days to heading, flag leaf area, plant height, spike length, grain yield, biological yield, 1000-grain weight, and tillers per square meter. The analysis of variance showed a significant result for all the parameters except spike length. In all of the 36 advanced lines for morphological variations, the AWL22 (113.5) was late growing genotype, AWL1 has maximum flag leaf area (59.73 cm^2), AWL23 is the tallest genotype (113.85 cm), AWL18 (283) has maximum tiller per square meter, AWL33 has more spike length (15.13 cm), AWL18 exhibited more 1000 grain weight (59.4 g), AWL22 has higher biological yield (11230 Kg/ha) and AWL32 one of the best genotype for grain yield (3545 kg/ha). In morphological and grain-related traits, genetic variation of all the parameters for advanced lines revealed better performance in all genotypes than the control 'GULZAR-2019'.

Key words: genetic variation, food security, zero hunger.

INTRODUCTION

Wheat (*Triticum aestivum* L.), a cereal grass of the family Poaceae, is one of the world's largest and important cereal crops. It has been described as the main source due to its high benefits, productivity, and prominent position in the food grain trade. It occupies an inimitable position in human life because it is one of the major sources of food and energy, with a large number of end-use products like bread, biscuits, pasta, and is also a good source for animals (Sharma et al., 2016). Wheat plays an important role in feeding the global population. In 2020, world production of wheat was 760 million tonnes (Şermet, 2021). China, Russia, and India were the three important and largest wheat producers in the world, where China contributes 80% or more of the total national wheat grains produced from the North China Plain (Zhang et al., 2021). The importance of wheat is linked to human efforts to protect themselves from hunger and gain control over their food supplies. Wheat has become the most important source of food and is growing worldwide. Historically, wheat has been the basic crop in western countries for centuries, as bread food (*Triticum aestivum*) and durum wheat (*Triticum durum*) have been cultivated to provide humans with energy and essential nutrients (Igrejas & Branlard, 2020). Today, it is the third-largest produced cereal for human consumption worldwide (FAO, 2018). As the world population grows and the demand for biofuels increases, the price of wheat has also risen dramatically. In addition, periodic bad weather conditions have resulted in a lack, shortages, and consequently, that has led to political instability in various parts of the world. Unfortunately, this variability in bad weather conditions, increases in temperature, extreme rainfall, and the presence of droughts, with a reduced adaptability capacity, tend to occur more and more frequently (Moya et al., 2021).

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Agriculture is the backbone of Pakistan's economy, and it contributes to the economic and social well-being of the nation through its influence on the gross domestic product. The total wheat production was estimated at 27.33 million tonnes in Pakistan. Nowadays, it is noted to be 27.539 million tonnes as the estimated production of K-P increased from 1.25 to 1.459 million tonnes (Gutiérrez-Moya et al., 2021; Ullah et al., 2021). Climate change is a major factor affecting agricultural productivity all over the world. This sector is the most vulnerable to weather change. The productivity of this sector is being affected by several factors, including temperature and rainfall patterns. The increase in temperature reduces agricultural production, while the rain positively affects its productivity. Climate change greatly affects agricultural productivity in Pakistan (Shafiq et al., 2021). Climate changes might also have influenced genetic variability, and all those modified traits need to be explored in breeding programs and selection of the best cultivars for future sowing. The current project was designed to evaluate the genetic variability in different advanced lines.

MATERIALS AND METHODS

Experimental Site, Materials, and Design

This experiment was carried out at Cereal Crops Research Institute Pirsabak, Nowshera, under irrigated conditions during 2021-22. The experimental materials for this study consisted of 36 advanced Wheat lines and a check cultivar (GULZAR-2019) (Tab.1). The experiments were designed in a simple partially balanced lattice 7x7 with two replications. Each plot consisted of 4 rows of 5 meters in length, and row spacing was 25 cm with a plot area of 5 m². A single row between adjacent plots was kept fallow to facilitate data recording. These advanced line seeds were sown on 29 October 2021. The agronomic practices and inputs were applied for all the entries from sowing till harvesting, and the genotypes were grown under uniform conditions to minimize environmental variations.

Table 1: Parentage of germplasm used in the experiment. A total of 36 advanced wheat lines were used with GULZAR-2019 as a check cultivar

S. No.	Parentage of germplasm	Specific Name
1	MELLAL-1/OUEDZEM-1//JOUDI	AWL1
2	NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR/5/KAUZ//ALTAR 84…..	AWL2
3	QAFZAH-33/FLORKWA-2//EXCALIBUR/3/DOUKKALA-33	AWL3
4	SW89-5124*2/FASAN/3/CAZO/KAUZ//KAUZ/4/WBLL1/5/TNMU/CBRD//MILAN/SHA7	AWL4
5	TEVEE-1/STAR'S'/3/ACHTAR*3//KANZ/KS85-8-4/4/SAKHA-93	AWL5
6	WBLL1*2/KURUKU//HEILO/3/WBLL1*2/KURUKU/4/HUBARA-3*2/SHUHA-4	AWL6
7	MAYIL	AWL7
8	VALI/5/KVZ/PPR47.89C//FRANCOLIN #1/3/2* PAURAQ/ 4/PBW343*2/KUKUNA*2//FRTL/PIFED	AWL8
9	FRANCOLIN #1/3/IWA 8600211//2* PBW343* 2/ KUKUNA/7/CHONTE*2/SOLALA/5/….	AWL9
10	DANPHE #1*2/3/T.DICOCCON PI94625/AE.SQUARROSA (372)//SHA4/CHIL/6/WBLL1/3/…..	AWL10
11	DANPHE #1*2/3/T.DICOCCON PI94625/AE.SQUARROSA (372)//SHA4/CHIL/6/WBLL1/3/………..	AWL11
12	CHONTE*2/SOLALA/5/BAV92//IRENA/KAUZ/3/HUITES*2/4/CROC_1/AE.SQUARROSA (224)//…	AWL12
13	HGO94.7.1.12/2*QUAIU #1//QUAIU #2/5/KIRITATI/4/2*BAV92//IRENA/ KAUZ/3/HUITES/6/…..	AWL13
14	COAH90.26.31/4/2*BL2064//SW89-5124*2/FASAN/3/TILHI/5/UP2338*2/KKTS*2//YANAC/6/….	AWL14
15	SHAKTI/TAITA//TAITA	AWL15
16	SERI.1B*2/3/KAUZ*2/BOW//KAUZ/4/PBW343*2/TUKURU/5/C80.1/3*BATAVIA//2*WBLL1/6/….	AWL16
17	KACHU*2/5/WBLL1*2/TUKURU/3/T.DICOCCON PI94624/AE.SQUARROSA (409)//BCN/4/…..	AWL17
18	TRAP#1/BOW/3/VEE/PJN//2*TUI/4/BAV92/RAYON/5/KACHU #1/6/TOBA97/PASTOR/3/……..	AWL18
19	BORL14/ABLEU	AWL19
20	SUP152*2/TINKIO #1/4/FRET2*2/SHAMA//KIRITATI/2*TRCH/3/BAJ #1/5/SUP152*2/TINKIO #1	AWL20
21	KACHU/SAUAL/4/ATTILA*2/PBW65//PIHA/3/ATTILA/2*PASTOR/5/KINGBIRD #1//INQALAB 91*2/TUKURU	AWL21
22	SUP152/BAJ #1*2/4/WHEAR/VIVITSI//WHEAR/3/PANDORA	AWL22
23	BAJ #1/KISKADEE #1//KACHU/KIRITATI/3/BAJ #1/KISKADEE #1	AWL23
24	MUTUS*2//TAM200/TURACO*2/3/ROLF07*2/SHORTENED SR26 TRANSLOCATION	AWL24
25	QUAIU #1/BECARD//2*BORL14	AWL25
26	SNB//CMH79A.955/3*CNO79/3/ATTILA/4/CHEN/AEGILOPSSQUARROSA(TAUS)//BCN/3/2*KAUZ/5/BAJ #1*2/HUIRIVIS #1	AWL26
27	PICUS/3/KAUZ*2/BOW//KAUZ/4/KKTS/5/T.SPELTAPI348530/6/2*FRANCOLIN 1/7/KACHU/KIRITATI	AWL27
28	CHRZ//BOW/CROW/3/WBLL1/4/CROC_1/AE.SQUARROSA (213)//PGO*2/5/KUTZ	AWL28
29	MUTUS/ROLF07//2*MUCUY	AWL29
30	VEE/MJI//2*TUI/3/PASTOR/4/BERKUT/5/BAVIS/6/BORL14	AWL30
31	KUTZ*2/3/KACHU//KIRITATI/2*TRCH	AWL31
32	WAXWING*2/KRONSTAD F2004*2//KINGBIRD #1/3/COPIO/4/COPIO	AWL32
33	WBLL1*2/4/YACO/PBW65/3/KAUZ*2/TRAP//KAUZ/5/KACHU#1*2/6/KINGBIRD#1*2/7/KFA/2*KACHU	AWL33
34	FRANCOLIN#1/3/PBW343*2/KUKUNA*2//YANAC/4/KINGBIRD#1//INQALAB91*2/TUKURU/5/BORL14	AWL34
35	KHAISTA-2017	AWL35
36	GULZAR-2019	AWL36

Selection of Plants and Parameters Analyzed

Five plants were randomly selected from each block, and the data were recorded for the following nine parameters at the applicable time, which include 1-Day to Heading, 2-Flag leaf area, 3-Spike length, 4-1000-grain weight, 5-Plant height, 7-Tiller per Square meter, 8-Biological yield per plant, and 9-Grain yield.

Statistical Analysis

Data obtained from 36 cereal genotypes were analyzed using the procedure described by Gomez and Gomez (1984) for a randomized complete block design. Further, the total sum of squares of all the genotypes was studied for a single experiment with the partition of two replications. A protected least significant difference (LSD) test was also done for mean comparison of cereal genotypes. Genetic and phenotypic correlations among traits were also computed using the procedure of Singh and Chaughry (1979).

RESULTS

Days to 50% Heading

There is a high genetic variability or variation among wheat 36 Genotypes of days to heading (Table 2). Analysis of variance showed highly significant (p 0.01) differences for days to 50 percent, heading among the tested 36 advanced wheat lines. It shows the high significance of genetic variation. The coefficient of variation for Days to 50% heading was 3.92. For 0.05 probability, 2.05 LSD is shown, and for 0.01, it shows 2.78 LSD in each block.

Among all genotypes, the maximum numbers of days to 50% were observed to be 115.0 (AWL8), followed by 114.0 (AWL20) and 113.5 (AWL22). While the minimum numbers of days to 50% heading were recorded each for 96 (AWL10) and 97.5 (AWL3). There was huge diversity within the tested genotypes for days to 50% heading.

Plant Height (cm)

There is a high genetic variability or variation among the 36 wheat genotypes of plant height (Tab. 3). Analysis of variance showed highly significant (p 0.01) differences for plant height among the tested 36 advanced wheat lines. It shows the high significance of genetic variation. The coefficient of variation for plant height was 2.49. For 0.05 probability is shown as 2.06 LSD, and for 0.01, it shows 2.79 LSD in each block.

Among all genotypes, the maximum plant heights were observed to be 13.85cm (AWL23), followed by 112.45cm (AWL25) and 111.75cm (AWL11). Minimum plant heights were recorded at 97.2cm (AWL13) and 98.95cm (AWL3).

Spike Length (cm)

There is a high genetic variability among 36 wheat genotypes of spike length (Tab. 4). Analysis of variance showed non-significant (p 0.01) differences in spike length among the tested 36 advanced wheat lines. It shows the high significance of genetic variation. The coefficient of variation for spike length was 9.36. For 0.05 probability, 2.06 LSD is shown, and for 0.01 showed 2.79 LSD is shown in each block.

Among all genotypes, maximum spike lengths were observed to be 15.13cm (AWL33) by 13.6cm (AWL17), and 13.2cm (AWL2). While a minimum spike length was recorded for each 10.8cm (AWL36) and 10.15cm (AWL32).

Biological Yield

There is a high genetic variability among 36 wheat genotypes in biological yield (Table 5). Analysis of variance showed highly significant (p 0.01) differences for biological yield among the tested 36 advanced wheat lines. It shows a highly significant genetic variation. The coefficient of variation for biological yield was 14.53. For 0.05 probability is shown as 9.27 LSD, and for 0.01, it shows 2.79 LSD in each block.

Among all genotypes, the maximum biological yield was observed to be 11230 Kg (AWK22), followed by 10650 Kg (AWL23) and 10245 Kg (AWL14). While the minimum biological yield was recorded as 5400 Kg (AWL35) and 6667.5 Kg (AWL36).

Table 2: ANOVA for days to 50% heading of 36 advanced wheat lines, including a check cultivar, estimated during the year 2021-22 at CCRI, Pirsabak Nowshera. In this table DF=Degree of freedom, SS=Sum of square, MS=Mean square, F=Fraction ratio, Prob=Probability, REPS=Replications, Trt=Treatment, RCB=Randomized complete block. CV=Coefficient of variation, LSD= Least significant difference

Source of Variance	Df	SS	MS	F-Ratio	Prob-value
REPS	1	7.347	7.347	0.414	0.525
Trt Sum of Squares (unadjusted)	35	1639.375	46.839	2.641	0.002
Blocks within Reps/ Block Sum of Squares	14	465.805	33.271		
Trt Sum of Squares (adjusted)	35	1695.535	48.443	2.73	0.005
RCB	35	909.152	25.975		
Intra-block error	25	443.347	17.733		
Total	72	2555.87			
CV %	3.92				
LSD (0.05)	2.05				
LSD (0.01)	2.78				

Table 3: ANOVA for plant height of 36 advanced wheat lines, including a check cultivar estimated during the year 2021-22 at CCRI, Pirsabak Nowshera. In this table Df= Degree of freedom, SS=Sum of square, MS=Mean square, F=Fraction ratio, Prob=Probability, REPS=Replications, Trt=Treatment, RCB=Randomized complete block. Cv=Coefficient of variation, LSD=Least significance difference

Source of Variance	Df	SS	MS	F-RATIO	Prob- value
REPS	1.00	1.56	1.56	0.226	0.639
Trt Sum of Squares (unadjusted)	35.00	1144.61	32.70	4.727	0.000
Blocks within Reps/ Block Sum of Squares	14.00	159.05	11.36	1.6421	0.135
Trt Sum of Squares (adjusted)	35.00	1145.53	32.73	4.7308	0.000
RCB	35.00	332.01	9.49	—	
Intra block error	25	172.96	6.92	—	
TOTAL	72	1478.2			
CV %	2.49				
LSD (0.05)	2.06				
LSD (0.01)	2.79				

Table 4: ANOVA for spike length of 36 advanced wheat lines, including check cultivar, estimated during the year 2021-22 at CCRI, Pirsabak Nowshera. In this table Df=Degree of freedom, SS=Sum of square, MS=Mean square, F=Fraction ratio, Prob=Probability, REPS=Replications, Trt=Treatment, RCB=Randomized complete block, Cv=Coefficient of variation, LSD= Least significance difference

Source of Variance	Df	SS	MS	F-RATIO	Prob-value
REPS	1.00	1.24	1.24	0.984	
Trt Sum of Squares (unadjusted)	35.00	57.13	1.63	1.297	0.251
Blocks within Reps/ Block Sum of Squares	14.00	6.41	0.46		
Trt Sum of Squares (adjusted)	35.00	51.78	1.48	1.175	0.341
RCB	35.00	37.87	1.08	—	
Intra block error	25	31.46	1.26	—	
Total	72	96.2			
CV%	9.36				
LSD(0.05)	2.06				
LSD(0.01)	2.79				

Table 5: ANOVA for the biological yield of 36 advanced wheat lines, including a check cultivar, was conducted during 2021-22 at CCRI, Pirsabak Nowshera. In this table Df=Degree of freedom, SS=Sum of square, MS=Mean square, F=Fraction ratio, Prob=Probability, REPS=Replications, Trt=Treatment, RCB=Randomized complete block, Cv=Coefficient of variation, LSD= Least significance difference

Source of Variance	Df	SS	MS	F-Ratio	Prob-value
REPS	1.00	1151403.13	1151403.13	0.757	0.393
Trt Sum of Squares (unadjusted)	35.00	104708612.15	2991674.63	1.966	0.008
Blocks within Reps/ Block Sum of Squares	14.00	81053454.86	5789532.49		
Trt Sum of Squares (adjusted)	35.00	122174744.89	3490707.00	2.294	0.017
RCB	35.00	119092514.24	3402643.26	—	
Intra-block error	25	38039059.38	1521562.38	—	
TOTAL	72	143899074.7			
CV%	14.53				
LSD(0.05)	9.27				
LSD(0.01)	2.79				

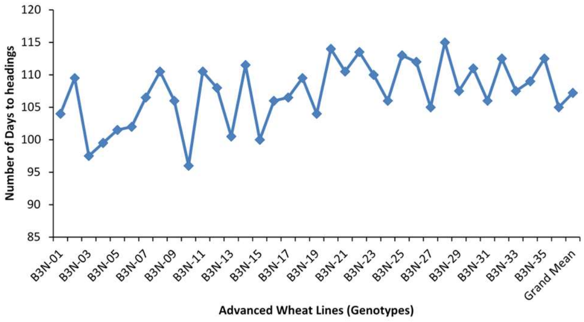

Fig. 1: Graphical representation of the mean performance of days to heading in different advanced wheat genotypes. Even numbers are missing in the wheat genotypes, but their values are shown in the graph. B3N-10 shows a minimum number of days to heading, and B3N-28 shows a maximum number of days to heading.

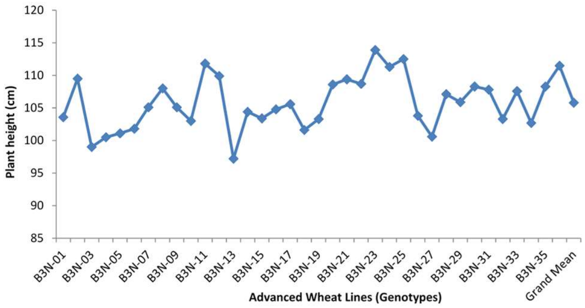

Fig. 2: Graphical representation of the mean performance of plant height in different advanced wheat genotypes. Even numbers are missing in wheat genotypes, but their values are shown in the graph. B3N-13 shows the minimum value of plant height, and B3N-23 shows the maximum value of plant height.

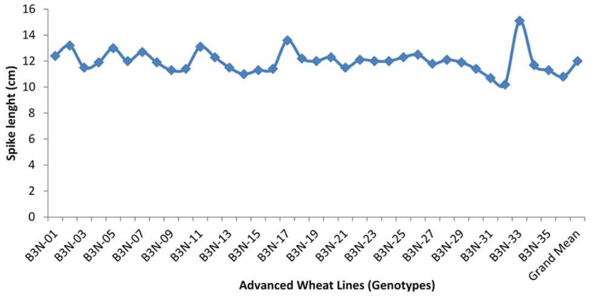

Fig. 3: Graphical representation of the mean performance of spike length in different advanced wheat genotypes. Even-numbered wheat genotypes are missing, but their values are shown in the graph. B3N-32 shows the minimum value of spike length, and B3N-33 shows the maximum value of spike length.

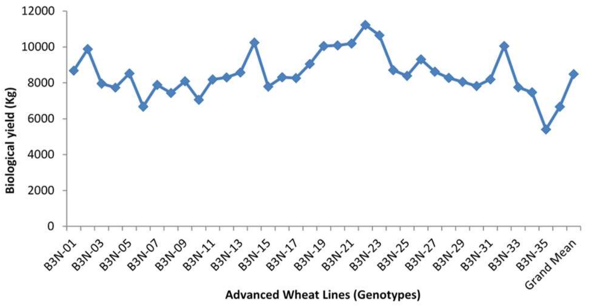

Fig. 4: Graphical representation of the mean performance of biological yield in different advanced wheat genotypes. Even-numbered wheat genotypes are not shown, but their values are shown in the graph. B3N-35 shows the minimum value of biological yield, while B3N-22 shows the maximum value of biological yield.

Table 6: ANOVA for thousand grain weight of 36 advanced wheat lines, including a check cultivar, was estimated during 2021-22 at CCRI, Pirsabak Nowshera. In this table Df= Degree of freedom, SS=Sum of square, MS=Mean square, F=Fraction ratio, Prob=Probability, REPS=Replications, Trt= Treatment, RCB=Randomized complete block, Cv=Coefficient of variation, LSD= Least significance difference

Source of Variance	Df	SS	MS	F-ratio	Prob-value
REPS	1.00	65.93	65.93	10.313	0.004
Trt Sum of Squares (unadjusted)	35.00	404.02	11.54	1.805	0.018
Blocks within Reps/ Block Sum of Squares	14.00	472.57	33.76		
Trt Sum of Squares (adjusted)	35.00	555.78	15.88	2.483	0.010
RCB	35.00	632.40	18.07	—	
Intra-block error	25	159.83	6.39	—	
TOTAL	72	1102.4			
CV%	4.66				
LSD(0.05)	2.06				
LSD(0.01)	2.79				

Table 7: ANOVA for grain yield of 36 advanced wheat lines, including a check cultivar, was estimated during 2021-22 at CCRI, Pirsabak Nowshera. In this table Df= Degree of freedom SS=Sum of square, MS=Mean square, F=Fraction ratio, Prob=Probability, REPS=Replications, Trt= Treatment, RCB=Randomized complete block, Cv=Coefficient of variation, LSD = Least significance difference

Source of Variance	df	SS	MS	F-RATIO	Prob- value
REPS	1.00	2713673.39	2713673.39	9.589	0.005
Trt Sum of Squares (unadjusted)	35.00	34336072.78	981030.65	3.466	0.000
Blocks within Reps/ Block Sum of Squares	14.00	9771771.44	697983.67		
Trt Sum of Squares (adjusted)	35.00	35401176.39	1011462.18	3.574	0.001
RCB	35.00	16846453.61	481327.25	—	
Intra block error	25	7074682.17	282987.29	—	
TOTAL	72	53896199.8			
CV%	9.19				
LSD(0.05)	2.06				
LSD(0.01)	2.79				

1000-Grain Weight

There was a high genetic variability or variation in 1000-grain weight among 36 wheat genotypes (Tab. 6). Analysis of variance showed highly significant (P 0.01) differences for thousand grain weight among the tested 36 advanced wheat lines. It shows high significance genetic variation. The coefficient of variation for thousand-grain weight was 4.66. For 0.05 probability is shown as 2.06 LSD, and for 0.01, it is 2.79 LSD in each block.

Among all genotypes, the maximum 1000-grain weights were observed to be 58.45 g (AWL31), followed by 57.425 g (AWL19) and 57.15 g (AWL24). While minimum 1000-grain weights were recorded each for 50.75g (AWL27) and 50.425g (AWL26).

Grain Yield (Kg)

There is a high genetic variability or variation among wheat 36 genotype grain yield (Tab. 7). Analysis of variance showed highly significant (p 0.01) differences for grain yield among the tested 36 advanced wheat lines. It shows high significance genetic variation. The coefficient of variation for grain yield was 9.19. For 0.05 probability is shown as 2.06

LSD, and for 0.01, it shows 2.79 LSD in each block.

Among all genotypes, maximum grain yield was observed for 3545 Kg (AWL32), followed by 3448.5 Kg (AWL14) and 3345 Kg (AWL34). While the minimum grain yields were recorded for 1990 Kg (AWL16) and 2180 Kg (AWL8).

Flag Leaf Area (cm^2)

There is a high genetic variability or variation among wheat 36 genotypes' flag leaf area (Table 8). Analysis of variance showed highly significant (p 0.01) differences for flag leaf area among the tested 36 advanced wheat lines. It shows high significance genetic variation. The coefficient of variation for flag leaf area was 4.01. For 0.05 probability is shown as 2.06 LSD, and for 0.01, it shows 2.79 LSD in each block.

Among all genotypes, maximum flag leaf area was observed for 59.73cm (AWL1) followed by 58.05cm (AWL25) and 53.89cm (AWL5). While minimum flag leaf area was recorded each for 30.0cm (AWL4) and 34.6cm (AWL9).

Tiller Per Square Meter (m)

There is a high genetic variability or variation among wheat 36 genotypes of tillers per square meter (Table 9). Analysis of variance showed highly significant (p 0.01) differences for tiller per square meter among the tested 36 advanced wheat lines. It shows high significance genetic variation. The coefficient of variation for tillers per square meter was 8.65. For 0.05 probability is shown as 2.06 LSD, and for 0.01, it is 2.79 LSD in each block.

Among all genotypes, the maximum tillers per square meter were observed to be 283 (AWL18), followed by 272 (AWL26) and 271 (AWL4). While the minimum tiller per square meter was recorded as 97 (AWL12) and 165 (AWL28).

Table 8: ANOVA for flag leaf area of 36 advanced wheat lines including check cultivar estimate during the year of 2021-22 at CCRI, Pirsabak, Nowshera. In this table Df= Degree of freedom SS=Sum of square, MS=Mean square, F=Fraction ratio, Prob=Probability, REPS=Replications, Trt=Treatment, RCB=Randomized complete block, Cv=Coefficient of variation, LSD= Least significance difference

Source of Variance	Df	SS	MS	F-Ratio	Prob-value
REPS	1.00	31.76	31.76	10.967	
Trt Sum of Squares (unadjusted)	35.00	3303.66	94.39	32.593	0.000
Blocks within Reps/ Block Sum of Squares	14.00	17.27	1.23		
Trt Sum of Squares (adjusted)	35.00	3280.92	93.74	32.369	0.000
RCB	35.00	89.67	2.56	—	
Intra block error	25	72.40	2.90	—	
Total	72	3425.1			
Cv%	4.01				
LSD(0.05)	2.06				
LSD(0.01)	2.79				

Table 9: ANOVA for tiller per square meter of 36 advanced wheat lines, including a check cultivar, was estimated during the year 2021-22 at CCRI, Pirsabak, Nowshera. In this table Df= Degree of freedom SS=Sum of square, MS=Mean square, F=Fraction ratio, Prob=Probability, REPS=Replications, Trt=Treatment, RCB=Randomized complete block, Cv=Coefficient of variation, LSD= Least significance difference

Source of Variance	Df	SS	MS	F-Ratio	Prob-value
REPS	1.00	203.35	203.35	0.623	0.437
Trt Sum of Squares (unadjusted)	35.00	84340.15	2409.72	7.379	0.00
Blocks within Reps/ Block Sum of Squares	14.00	1507.47	107.68		
Trt Sum of Squares (adjusted)	35.00	81890.08	2339.72	7.165	0.00
RCB	35.00	9670.62	276.30	—	
Intra block error	25	8163.15	326.53	—	
TOTAL	72	92706.7			
CV%	8.65				
LSD(0.05)	2.06				
LSD(0.01)	2.79				

Table 10: Mean squares performance of 36 wheat genotypes in the advanced yield trial at CCRI, Nowshera during 2021-22. CV= coefficient of variation, (**, ^{ns}) significant at 5% probability, non-significant.

Triats	Mean Squares						
	Rep (df=1)	Trt (unadj) (df = 35)	Blocks within Reps(df = 14)	Trt (adj.) (df = 35)	RCB(df = 35)	Error(df = 25)	CV%
Heading	7.35^{ns}	46.84**	33.27	48.44**	25.98	17.73	3.93
Plant height	1.56^{ns}	32.70**	11.36	32.73**	9.49	6.92	2.49
Flag Leaf Area	31.76**	94.39**	1.23	93.74**	2.56	2.90	4.01
Tillers m^{-2}	203.35^{ns}	2409.72**	107.68	2339.72**	276.30	326.53	8.65
Spike length	1.24^{ns}	1.63^{ns}	0.46	1.48^{ns}	1.08	1.26	9.36
1000-grain weight	65.93**	11.54*	33.76	15.88**	18.07	6.39	4.66
Grain Yield	2713673.39**	981030.65**	697983.67	1011462.18**	481327.25	282987.29	9.19
Biological Yield	1151403.13**	2991674.63**	5789532.49	3490707.00**	3402643.26	1521562.38	14.53

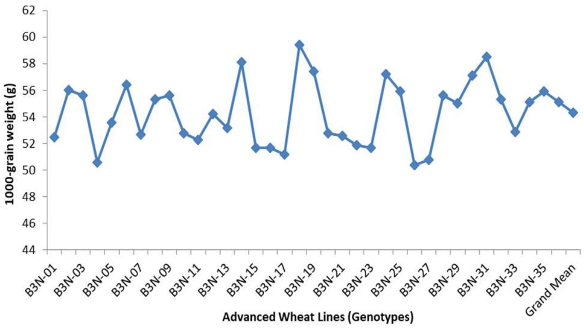

Fig. 5: Graphical representation of the mean performance of 1000-grain weight in different advanced wheat genotypes. Even numbers are missing in the wheat genotypes, but their values are shown in the graph. B3N-26 shows a minimum value of 1000-grain weight, and B3N-18 shows a maximum value of 1000-grain weight.

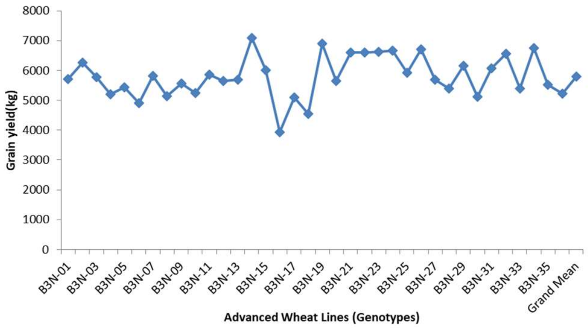

Fig. 6: Graphical representation of the mean performance of grain yield in different advanced wheat genotypes. Even numbers are missing in wheat genotypes, but their values are shown in the graph in the form of a dot. B3N-16 shows the minimum value of grain yield, and B3N-14 shows the maximum value of grain yield.

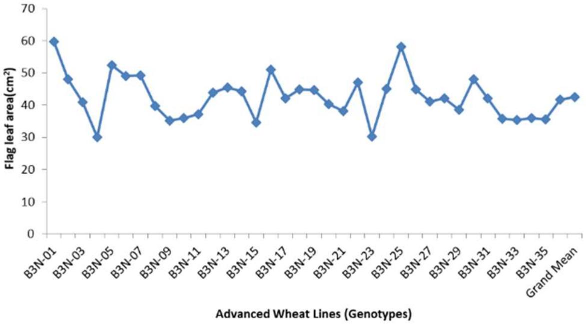

Fig. 7: Graphical representation of the mean performance of flag leaf area in different advanced wheat genotypes. Even numbers are missing in wheat genotypes, but their values are shown in the graph in the form of a dot. B3N-23 shows the minimum value of flag leaf area, and B3N-1 shows the maximum value of flag leaf area.

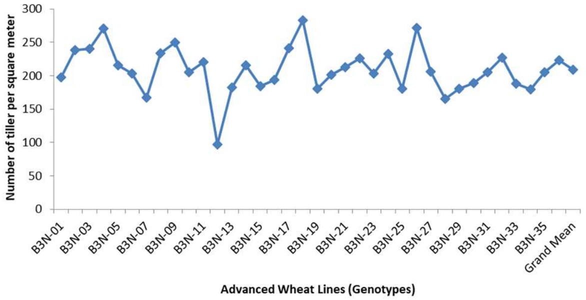

Fig. 8: Graphical representation of the mean performance of tillers per square meter in different advanced wheat genotypes. Even numbers are missing in wheat genotypes, but their values are shown in the graph in the form of a dot. B3N-12 shows the minimum value of tillers per square meter, and B3N-18 shows the maximum value of tillers per square meter.

DISCUSSION

The analysis of variance showed significance of genetic differences among the advanced wheat lines for days to heading data (Wani et al., 2018; Rauf et al., 2023) revealed a significant result for days to interval with grain-related traits in their previous findings. Arya et al. 2017 worked on mostly for all the entire grain of the morphological trait. In their past experiment, they claimed a significant result for all the morphological parameters, i.e., plant height, tiller per square meter, and spike length. In the present work, all the morphological traits were significant in their genetic variation, except spike length, which is opposite to the mentioned past finding due to the use of different wheat lines. The analysis of these parameters estimated a significant variation in their result, likely grain-related traits, i.e., 1000-grain weight, grain yield (Ali et al., 2008; Wani et al., 2018; Riaz et al., 2024). The present work was also significant for 1000-grain weight and grain yield. The same results are also exhibited by (Bhanu et al., 2018) in their past experiment. (Nukasani et al., 2013) worked on both the grain of morphological parameters, of significant in their finding for tiller per square meter and grain yield, which is estimated to yield of same result in the present work. Biological yield played an important role for animals to enhance food availability for cattle. The present study showed significant genetic diversity for biological yield. Wani et al. 2018 showed the same work on biological yield variation. The flag leaf area is one of the best morphological parameters, where it exhibits significant morphological genetic diversity, which Khaliq et al. 2008 estimated the same experimental findings. Our findings of significant genetic variation in DTH are supported by Kim et al. (2025), who conducted a GWAS on 530 Korean wheat accessions and identified specific SNPs (e.g., AX-95222044, AX-94685526) that account for up to ~8.9 days of heading variability, underscoring genetic control of heading date under autumn sowing conditions. Genetic variability for TGW and its positive correlations with yield components are documented in Sewore et al. (2024), who analyzed 196 bread wheat genotypes under drought and well-watered conditions and found significant variation and trait association of yield components. Although your spike length data

Table 11: Mean Performances of 36 wheat genotypes in the advanced yield trial at CCRI, Nowshera, during 2021-22 for days to heading, plant height, flag leaf area, and tillers per square

Genotypes	Heading	Plant height	Flag Leaf Area	Tillers m^{-2}
B3N-01	104.0	103.6	59.7	198.0
B3N-02	109.5	109.5	48.1	238.0
B3N-03	97.5	99.0	41.0	240.0
B3N-04	99.5	100.5	30.0	271.0
B3N-05	101.5	101.1	52.4	216.0
B3N-06	102.0	101.8	49.0	203.0
B3N-07	106.5	105.1	49.3	167.0
B3N-08	110.5	108.0	39.7	234.0
B3N-09	106.0	105.1	35.2	249.5
B3N-10	96.0	103.0	36.0	205.0
B3N-11	110.5	111.8	37.2	220.0
B3N-12	108.0	109.9	43.9	97.0
B3N-13	100.5	97.2	45.4	182.0
B3N-14	111.5	104.4	44.3	216.0
B3N-15	100.0	103.4	34.6	184.0
B3N-16	106.0	104.8	51.1	194.0
B3N-17	106.5	105.6	42.1	241.0
B3N-18	109.5	101.6	44.9	283.0
B3N-19	104.0	103.3	44.7	181.0
B3N-20	114.0	108.6	40.3	201.0
B3N-21	110.5	109.4	38.2	213.0
B3N-22	113.5	108.7	47.0	226.0
B3N-23	110.0	113.9	30.2	203.0
B3N-24	106.0	111.3	45.0	233.0
B3N-25	113.0	112.5	58.1	181.0
B3N-26	112.0	103.8	44.8	272.0
B3N-27	105.0	100.6	41.2	206.0
B3N-28	115.0	107.1	42.2	165.0
B3N-29	107.5	105.9	38.6	181.0
B3N-30	111.0	108.3	48.0	189.0
B3N-31	106.0	107.8	42.1	205.0
B3N-32	112.5	103.3	35.8	227.0
B3N-33	107.5	107.6	35.3	188.0
B3N-34	109.0	102.7	35.9	180.0
B3N-35	112.5	108.3	35.5	205.0
B3N-36	105.0	111.5	41.7	223.0
Grand Mean	107.2	105.8	42.5	208.8
LSD (5%)	8.7	5.4	3.5	37.2

were non-significant, several studies reveal that spike traits often depend on the germplasm diversity and environmental interactions. For example, Ahmed et al. (2023) assessed 18 Bangladeshi genotypes and observed substantial variability in spike length and other yield-related traits, especially under drought stress. The significant genotypic variance in FLA matches findings by Schierenbeck et al. (2024), who reported that flag leaf length, width, and area were significantly influenced by both genotype and environment, with identified QTNs explaining variation across multiple environments. Our results indicating significant variability in biological and grain yield are consonant with Sewore et al. (2024), which found high genetic variation and heritability for these traits, particularly under contrasting moisture regimes.

Table 12: Mean Performances of 36 wheat genotypes in the advanced yield trial at CCRI, Nowshera, during 2021-22 for spike length, thousand grain weight, biological yield, and grain yield

Genotypes	Spike length	TGWT	Biological yield	Grain Yield
B3N-01	12.4	52.5	8682.5	5705.0
B3N-02	13.2	56.0	9880.0	6255.0
B3N-03	11.5	55.6	7960.0	5785.0
B3N-04	11.9	50.6	7735.0	5207.5
B3N-05	13.0	53.6	8525.0	5430.0
B3N-06	12.0	56.4	6675.0	4905.0
B3N-07	12.7	52.7	7887.5	5815.0
B3N-08	11.9	55.3	7440.0	5145.0
B3N-09	11.3	55.6	8092.5	5565.0
B3N-10	11.4	52.8	7055.0	5250.0
B3N-11	13.1	52.3	8187.5	5870.0
B3N-12	12.3	54.2	8300.0	5645.0
B3N-13	11.5	53.2	8575.0	5700.0
B3N-14	11.0	58.1	10245.0	7083.5
B3N-15	11.3	51.7	7787.5	6000.0
B3N-16	11.4	51.7	8312.5	3930.0
B3N-17	13.6	51.2	8270.0	5090.0
B3N-18	12.2	59.4	9052.5	4545.0
B3N-19	12.0	57.4	10050.0	6890.0
B3N-20	12.3	52.8	10090.0	5645.0
B3N-21	11.5	52.6	10190.0	6610.0
B3N-22	12.1	51.9	11230.0	6595.0
B3N-23	12.0	51.7	10650.0	6615.0
B3N-24	12.0	57.2	8710.0	6665.0
B3N-25	12.3	55.9	8387.5	5925.0
B3N-26	12.5	50.4	9307.5	6700.0
B3N-27	11.8	50.8	8622.5	5700.0
B3N-28	12.1	55.6	8275.0	5405.0
B3N-29	11.9	55.0	8055.0	6150.0
B3N-30	11.4	57.1	7825.0	5125.0
B3N-31	10.7	58.5	8195.0	6080.0
B3N-32	10.2	55.3	10052.5	6555.0
B3N-33	15.1	52.9	7752.5	5400.0
B3N-34	11.7	55.1	7475.0	6745.0
B3N-35	11.3	55.9	5400.0	5530.0
B3N-36	10.8	55.1	6667.5	5235.0
Grand Mean	12.0	54.3	8488.8	5791.6
LSD (5%)	2.3	5.2	8682.5	1095.6

Conclusions

In all 36 genotypes, different parameters were studied to show their significance for the Ho hypothesis, like days to heading shows a significant result for a single degree of freedom. The average mean for days to heading was shown by 115.0 (AWL8), followed by 96 (AWL10). Flag leaf area shows a significant result with an average mean of 59.73cm (AWL1), followed by 30.0cm (AWL4). In contrast, the average mean across all the 36 genotypes, 3545 (AWL32) and 1990 (AWL16), shows a high mean for grain yield with significance of genetic variation.1000-grain weight also shows significance, with the average mean of 58.45g (AWL31) followed by 50.75g (AWL27). Plant height also shows a significant result for genetic variability, with an average mean of 13.85cm (AWL23) and 98.95cm (AWL3). For tiller per square meter, it also shows significant results, and all 36 genotypes, 283 (AWL18) and 165 (AWL28), show a high average. Spike length shows their non-significant result toward the genetic variability. High means for spike length were shown by 15.13cm (AWL33) and 10.8cm (AWL36). Biological yield also shows significance of genetic variability, with the average mean of 11230 (AWK22), followed by 5400kg (AWL35).

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