



Research Article

Performance of Different Wheat Cultivars in Semi-arid Ecological Conditions

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Abstract | A field trial of 49 wheat genotypes was performed in an alpha lattice design to evaluate the phenological and morphological traits. The data analysis revealed considerable variations among genotypes for traits like days to heading (81–97), days to maturity (152–157), plant height (80.7–97 cm), flag leaf area (16.2–31.7 cm²), peduncle length (23.0–33.3 cm), tillers per square meter (116–440), spike length (8.0–12.4 cm), spikelet's per spike (14.8–20.8), thousand-grain weight (27.0–49.2 gm), biological yield (5375–13250 Kg/ha), grain yield (1375–5290 Kg/ha), and harvest index (23.5–53.1%). The genotypes, PR-156 had the earliest maturity, Nia Zarkhaize with the highest tillers per square meter, while PR-153 recorded the highest 1000-grain weight. Pirsabak-15 and Pirsabak-23 had the highest grain and biological yields, respectively. Highly significant positive correlations, such as days to heading with maturity ($rP = 0.89^{**}$), tillers and grain yield with biological yield ($rP = 0.35^{**}$ & $rP = 0.87^{**}$), and harvest index with 1000-grain weight ($rG = 0.50^{**}$), highlighted the coordinated genetic control. These correlations indicate that the selection could simultaneously enhance the given traits in breeding programs. On the other hand, the genotype Pirsabak-15 is a candidate line for grain yield increase and may be considered for future wheat breeding programs.

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Keywords | Bread wheat, Cultivars, Heritability, Genetic advance, Phenotypic Coefficient of variation, Genotypic Coefficient of variation



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Introduction

Wheat (*Triticum aestivum* L.), a member of the family Poaceae, is a staple grain crop grown worldwide, primarily for human consumption (Ahmad *et al.*, 2020). As a self-pollinated, long-day crop, wheat ranks first among cereal crops in terms of cultivation and grain yield in regions like Uruguay, Aus-

tralia, Argentina, Syria, and Morocco (Arzadun *et al.*, 2006). Globally, wheat is cultivated from sea level to altitudes exceeding 3000 meters.

The wheat cropping system is pivotal to Pakistan's agriculture-dependent economy. It ensures food security for the rapidly growing population and contributes significantly to foreign exchange (Amin *et al.*,

2017). The main wheat-growing regions are in the Indus plains across Pakistan, approximately 900 meters above sea level (PARC, 2009), while Pakistan ranks 9th in wheat cultivation area and 7th in production globally (MINFAL, 2022-23). Deploying high-yield, rust-resistant spring wheat cultivars is crucial to meet the country's increasing food demands (Muhammad *et al.*, 2017; Sadiq *et al.*, 2025). Selection for yield components, aided by traits with high heritability and genetic advancement, is essential for enhancing yield potential (Balkan, 2018). However, negative correlations among yield attributes can hinder breeding programs, emphasizing the importance of breaking unfavorable linkages (Abdulhamed *et al.*, 2021). The development of new spring wheat cultivars has led to significant increases worldwide (Rauf *et al.*, 2023). Farmers favor cultivars with stable performance across diverse environments (Hancock, 2004).

Genetic diversity is vital for developing novel genotypes and can be measured through morphological traits, molecular markers, or pedigree analysis (Habash *et al.*, 2009; Rauf *et al.*, 2023). Traits like plant height, grain number, and spikes per unit area exhibit significant genetic variation, aiding selection for higher yields. Genotypic associations among yield-contributing traits play a crucial role in determining their influence on grain production (Salman *et al.*, 2014; Rauf *et al.*, 2023). The genetic architecture of yield-related traits is fundamental to wheat improvement. Correlation studies between quantitative traits and their direct and indirect effects on grain yield are indispensable for breeding programs (Khan *et al.*, 2010; Sadiq *et al.*, 2025). Wheat breeders focus on developing resilient cultivars with enhanced grain yield to meet the needs of the growing population (Mangova and Rachovska, 2004).

Bread wheat is highly adaptable, thriving in diverse climatic conditions. Climate change poses significant challenges to Pakistan's agriculture, with rising greenhouse gas emissions exacerbating temperature increases and affecting crop growth. Developing wheat cultivars that can withstand adverse environmental conditions is vital. The interaction between genotype and environment (GEI) plays a key role in determining the stability and performance of wheat genotypes across diverse conditions (Sadiq *et al.*, 2025; Khan *et al.*, 2023). Multi-environment trials assess genotype adaptability and help identify superior cultivars (Piepho *et al.*, 2012). Soil, climate, and management

practices are critical factors influencing wheat genotype performance. Temperature changes, particularly terminal heat stress above 22–24 °C, adversely affect wheat grain yield. Heat-tolerant cultivars with broad adaptability are essential for increasing productivity (Shafi *et al.*, 2013; Khan *et al.*, 2023).

Correlation coefficients help determine the relationship between grain yield and yield components. Days to maturity and thousand-grain weight are highly positively correlated with grain yield (Gelalcha and Hanchinal, 2013). The path coefficient analysis would go deeper into yield components' direct and indirect effects (Del-Moral *et al.*, 2003). Such analyses guide breeders to identify traits critical for yield improvement. Genetic heritability and variability provide essential information for crop improvement. Traits with high heritability and genetic advancement are crucial for selecting superior genotypes (Ibrahim *et al.*, 2020). Mutagenic trait inheritance, assessed through heritability, supports efficient breeding strategies (Bhargava *et al.*, 2003). Global wheat production must rise significantly to meet the increasing demand driven by population growth, necessitating the development of robust cultivars (FAO, 2018).

Greater genetic diversity in base populations increases the likelihood of developing desirable plant types. This study analyzed 49 wheat genotypes to estimate genetic diversity, heritability, and genetic gain for traits related to productivity and quality, providing insights for future crop improvement efforts. The current project was designed to identify the high-yielding wheat varieties with genetic diversity, adaptability, and yield potentials suitable for the semi-arid to sub-humid agroecological conditions of Peshawar Valley, KP.

Materials and Methods

Experimental Materials and Resources

A total of 49 wheat genotypes, which include 11 advanced lines and 38 potential cultivars, were cultivated in two repetitions in a seven-by-seven Alpha lattice square configuration at the Cereal Crop Research Institute (CCRI), Pirsabak Nowshera, Pakistan (Table 1). The agronomic cultural methods were used in the field trial, where four rows, two meters long and 25 centimeters apart, were used for sowing seeds.

These 49 wheat lines were analyzed for different parameters, including days to heading, days to ma-

turity, plant height, flag leaf area (width $\times$ length $\times$ 0.75), peduncle length, tiller per square meter (Total Number of Tillers/Number of Rows $\times$ R-R space $\times$ Row length), Spike Length, Spikelets spike⁻¹, Thousand-grain weight, Biological yield, Grain yield, Harvest Index (Grain yield/Biological Yield $\times$ 100).

Table 1: Details of 49 different wheat genotypes used in the field trial.

S.N.	Genotypes	S.N.	Genotypes	S.N.	Genotypes
1	PR.138	18	Pirsabak-19	35	Zincol-16
2	PR.139	19	Gulzar-19	36	Pakistan-13
3	PR.141	20	Abaseen-21	37	MA-20
4	PR.142	21	Zarghoona-21	38	Akbar-19
5	PR.146	22	Pirsabak-21	39	Subhani-21
6	PR.147	23	Taskeen-22	40	M.H-21
7	PR.148	24	Fahim-19	41	Dilkash-21
8	PR.149	25	Kohat-17	42	V-19347
9	PR.150	26	Kt-22	43	Ghazi19
10	PR.151	27	Swabi-1	44	Nawab-21
11	PR.152	28	NIFA Lubna	45	NIA Shaheen
12	Pirsabak-13	29	S.N-005	46	NIA Sunhari
13	Shahkar-13	30	TRB-2-103	47	NIA Zarkhaize
14	pirsabak-15	31	Wafaq-23	48	Fakhar-e-Bakkar
15	paseena-17	32	NAKC Super	49	Bakkar star
16	wadan-17	33	Makaf-19		
17	Khaista-17	34	Borlaug-16		

Statistical Analysis

The variance data were analyzed using Steel and Torri (1980) for the Alpha lattice design (Table 2). The least significant difference (LSD) was used to differentiate between means. The computer software MSTAT-C and TUANSTAT were utilized to analyze variance (ANOVA) and correlation among various traits.

Table 2: Anova for Alpha Lattice Design.

Source of Variations	DF	SS
Envi	e-1	SS _e
Geno (unadjusted)	g-1	SS _g
Blocks (within replications)	rs-r	SS _b
Geno (Adjusted)	g-1	SS _g
RCB	(g-1) b(r-1)	SS _{rb}
Geno x Envi.	(g-1)(e-1)	SS _{ge}
Intra Block Error	e(g-1)(r-1)	Sse
Total	egr-1	SS _T

Correlation analysis

Genotypic and phenotypic correlations for various morphological, physiological, and biochemical traits were computed for both genotypic and phenotypic correlations using TNAUSTAT software (Manivannan, 2014).

Results and Discussion

We have analyzed several variables, including days to heading, days to maturity, plant height, flag leaf area, peduncle length, tillers meter⁻², spikelets per spike, spike length, thousand-grain weight, biological yield, grain yield, and harvest index. This was designed to estimate genetic diversity, heritability, genetic advance, and correlation analysis of 49 genotypes of bread wheat related to the important above-mentioned traits. The statistical analyses of the mean square, mean values, LSD, heritability, genetic advance, genotypic, and phenotypic correlation values are shown (Tables 3, 4, 5, 6, 7 and 8).

Days to heading

Analysis of variance revealed a significant difference in the heading ($P \leq 0.01$) among the tested genotypes. The coefficient variation for days to heading was 0.70%. The mean heading interval was 117.0 days for the 49-genotype set, with a range from 81 to 97 days (Table 5). The maximum (97) and minimum (81) days heading were reported for GULZAR-19 and PIRSABAK-21, respectively (Figure 1 and Table 5). The three days were the least significant change (LDS) of 5% for the direction. The heritability estimate of heading was 0.98, while genetic advance was 6.12 (Table 7). Moderate genetic advancement combined with a high heritability is shown for heading (Table 7).

Results for heading were also supported by Chauhan *et al.* (2022), who found highly significant differences for a set of 40 genotypes evaluated in a randomized complete block design in 2021. Likewise, Iqbal *et al.* (2017) evaluated 16 wheat genotypes and found a CV of 0.98% for heading. Gerema *et al.* (2020) evaluated 180 genotypes during 2017-18, where they noted a CV of 1.60% for days to heading. Tefera (2022) also supports the current mean range for maturity interval, which varied between 48-80 days for 81 genotypes evaluated. Early studies by Dabi *et al.* (2017) found a high heritability of 86.4% with very low genetic gain

Table 3: Mean squares for days to heading, days to maturity, plant height, flag leaf area, peduncle length, and tillers per meter square at CCRI during 2022–23.

SOV	DF	DH	DM	PH	FLA	PL	TM
REPS	1	2.78**	0.26	4.50*	2.30	0.65	4.08
Geno.(unadjusted)	48	39.36**	2.91**	37.99**	15.92**	9.14**	15379.90**
Blocks within Reps/ Block	14	9.60	0.49	10.57	2.09	0.56	5.54
Geno. (adjusted)	48	38.87**	2.99**	37.83**	15.45**	9.14**	15162.31**
RCB	48	3.14	1.42	3.95	1.59	0.65	4.08
Intra block error	42	0.39	1.46	1.00	1.12	0.56	2.82
CV	--	0.70	0.78	1.13	4.60	1.50	3.39

**, * significant at 1% and 5% respectively.

Table 4: Mean squares for spike length, Spikelets spike⁻¹, 1000 grain weight, grain yield, biological yield, and harvest index at CCRI during 2022–23.

SOV	Df	SL	SPS	TGW	GY	BY	HI
REPS	1	0.84*	0.02	0.16	1493979.59**	5739.795918	0.826530612
Geno (unadjusted)	48	1.88**	4.04**	40.89**	924014.58**	6060958.759**	52.43275248**
Blocks within Reps/ Block	14	1.07	0.64	0.22	1330706.49	7789.723032	1.121720117
Geno (adjusted)	48	1.89**	4.07**	39.31**	888121.17**	5540442.471**	49.81130822**
RCB	48	0.43	0.81	0.16	456981.68	5739.795918	0.826530612
Intra block error	42	0.14	0.71	0.11	78695.94	3963.19242	0.570699708
CV	98	3.75	4.67	0.85	7.63	0.64	2.08

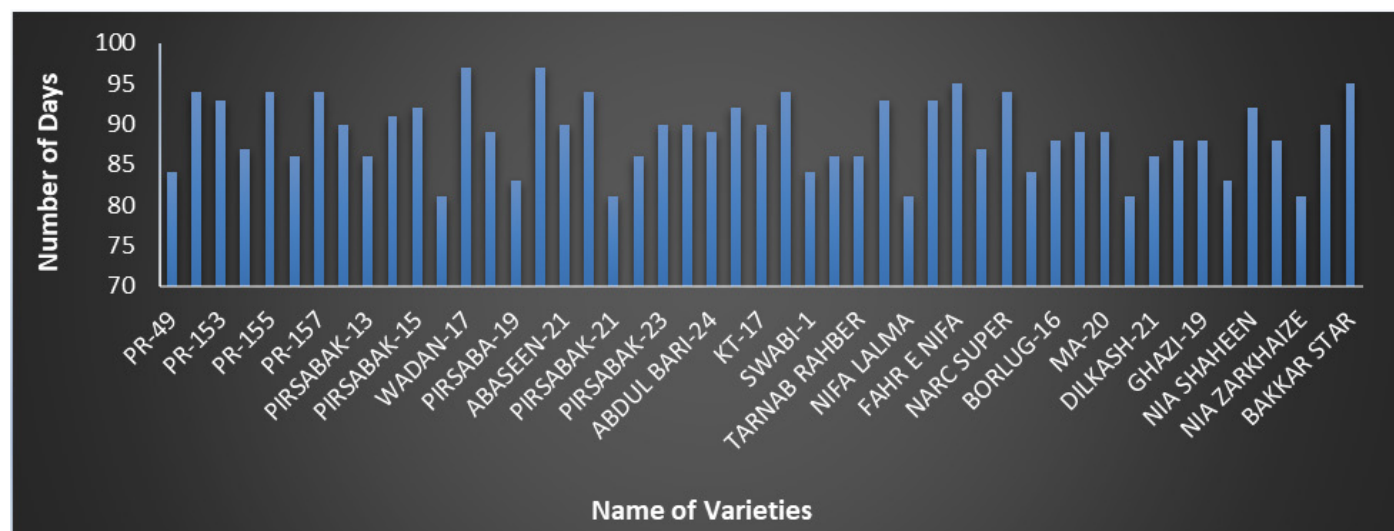


Figure 1: The number of days to heading in 49 different varieties of bread wheat.

for heading and supported these findings regarding heritability. These differences in results about genetic gain may be related to the genetic materials used in the experiments.

Days to maturity

Analysis of variance across maturity revealed highly significant differences between the genotypes ($P \leq 0.01$) (Table 3). The coefficient of variation for days to maturity was 2.41%. The general mean for the ma-

turity period among the 64 genotypes in the collection was 154 days, while the minimum and maximum ranges were from 152 to 157 days. The shortest period of 152 days was obtained in PR-156, and the longest period of 157 days was obtained in SWABI-1 (Table 3). The LSD 5% took two days for maturity. Mature genes had a heritability value of 0.34 and genetic advances of 0.74. Low genetic progress was observed for maturity, and moderate heritability was fixed (Table 5).

Table 5: Means performances of wheat advanced lines for days to heading, days to maturity, plant height, flag leaf area, peduncle length, and tillers per square meter at CCRI during 2022-23.

Varieties	Days to heading	Days to maturity	Plant height (cm)	Flag leaf area(cm ²)	Peduncle length(cm)	Tiller meter (m ⁻²)
PR-49	84	156	83.8	23.3	32.7	116.0
PR-152	94	155	92.5	19.9	27.3	240.0
PR-153	93	153	92.5	21.5	27.1	260.0
PR-154	87	156	87.0	20.8	29.3	360.0
PR-155	94	153	93.3	21.9	28.1	400.0
PR-156	86	152	85.3	21.0	29.0	200.0
PR-157	94	155	89.0	23.1	30.0	160.0
PR-158	90	154	89.5	25.7	31.0	230.0
PIRSABAK-13	86	154	86.2	20.4	30.0	200.1
SHAHKAR-13	91	155	91.3	16.2	26.3	300.0
PIRSABAK-15	92	156	92.0	18.9	30.0	400.1
PASEENA-17	81	153	81.3	25.2	29.7	360.0
WADAN-17	97	154	96.5	25.2	33.3	140.1
KHAISTA-17	89	154	89.3	26.0	27.7	200.0
PIRSABA-19	83	156	83.0	22.5	31.3	204.1
GULZAR-19	97	156	97.0	25.0	30.3	136.0
ABASEEN-21	90	156	90.0	22.4	27.7	200.1
ZARGHOON-21	94	155	93.8	26.3	33.3	300.0
PIRSABAK-21	81	153	80.7	31.7	31.0	240.1
TASKEEN-22	86	153	86.3	26.0	32.3	160.0
PIRSABAK-23	90	154	90.0	23.4	32.3	300.1
KHYBER-23	90	154	90.0	21.7	32.0	156.0
ABDUL BARI-24	89	155	89.2	25.0	29.0	160.1
FAHIM-19	92	156	91.8	20.4	30.3	280.0
KT-17	90	155	89.0	22.1	32.4	280.1
TANDA-23	94	155	93.8	24.6	32.3	300.0
SWABI-1	84	157	84.2	28.9	29.3	180.1
NAURANG-23	86	154	86.3	20.7	32.7	372.0
TARNAB RAHBER	86	153	84.7	23.8	32.3	128.1
TARNAB GANAM	93	155	93.0	23.1	29.7	176.0
NIFA LALMA	81	152	80.7	23.5	32.8	200.1
NIFA NIJAT	93	154	92.5	24.0	30.7	180.0
FAHR E NIFA	95	155	94.5	19.8	28.7	400.1
WAFaq-23	87	156	88.3	19.6	30.3	240.0
NARC SUPER	94	155	93.7	21.1	31.7	276.1
MARKAZ-19	84	154	83.5	23.0	31.7	180.0
BORLUG-16	88	153	87.7	27.7	31.3	200.1
ZINCOL16	89	153	89.3	24.5	32.8	300.0
MA-20	89	155	88.5	22.7	28.3	420.1
AKBAR-19	81	156	81.0	19.7	30.0	200.0
DILKASH-21	86	153	85.7	25.2	27.7	350.1
UROOJ-2022	88	155	88.3	27.5	27.3	220.0
GHAZI-19	88	154	86.5	24.5	32.7	300.1
NAWAB-21	83	154	82.5	22.1	29.7	260.0

NIA SHAHEEN	92	152	92.2	21.8	31.0	190.1
NIA SUNHERI	88	155	88.3	21.5	31.0	300.0
NIA ZARKHAIZE	81	154	81.2	20.3	23.0	420.1
F.BAKKAR	90	156	90.0	20.6	30.4	440.0
BAKKAR STAR	95	156	95.0	22.2	32.4	196.1
GM	88.8	154.4	88.6	23.0	30.3	253.3
LSD	1.25	2.44	2.01	2.14	1.5	3.4

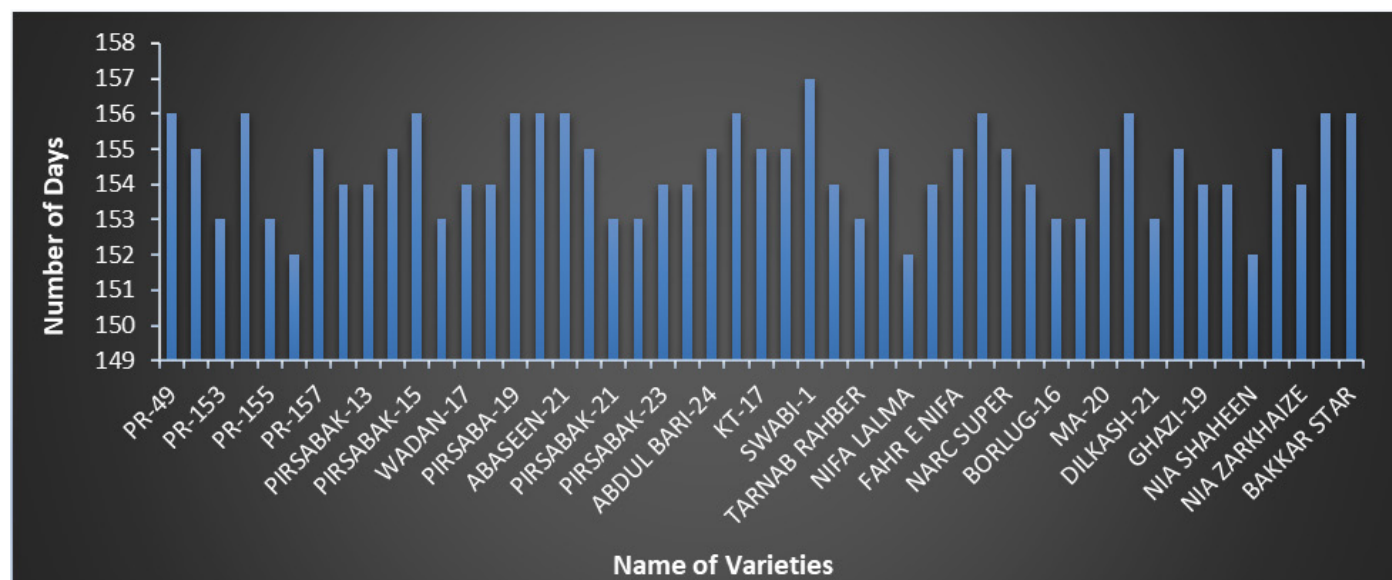


Figure 2: The number of days to maturity in the 49 varieties of bread wheat.

Our results for maturity agree with Kanwar *et al.* (2020), who found highly significant differences for a set of 25 genotypes evaluated in a Latin square design. Likewise, Dabi *et al.* (2017) evaluated 12 wheat genotypes and found a CV of 1.98% for maturity interval. Rana *et al.* (2023) also support the current mean range for maturity interval, which varied between 146-153 days for 40 genotypes. The heritability estimates disagree with the previously obtained results by Arya *et al.* (2017), who found that 17% was low in heritability for the maturity interval. Further results were drawn by Bhushan *et al.* (2013), whereby a set of 40 wheat genotypes in a randomized full-block design emerged with a high heritability of 77.5% for days to maturity. Experimental results may be inconsistent because of variations in the genetic material under experimentation.

Plant Height (cm)

The results of the analysis of variance showed that changes from genotype to genotype, for this parameter, were highly significant ($P \leq 0.01$) (Table 3). The CV was 2.02% for plant height. The overall mean plant height of the genotypes was 88.6 cm, with a minimum value of 80.7 cm and a maximum of 97.0 cm. PIRSABAK-21 showed the shortest plant height

of 80.7 cm, while GULZAR-19 and DILKASH-21 showed the highest plant height of 97.0 cm (Table 5 and Figure 3). In the case of plant height, the LSD 5% was 2.0 cm. Heritability estimated for plant height was 0.90, and genetic advancement was 5.75. Low genetic improvement and high heritability were noticed for plant height.

Likewise, Gerema *et al.* (2020) evaluated 10 wheat genotypes and reported a CV of 6.6% for plant height. Kanwar *et al.* (2020) also confirmed that the mean range for plant height varied between 71-95 cm for 25 genotypes. Current means for plant height are supported by Kanwar *et al.* (2020), who found highly significant differences in the evaluation of 25 genotypes using a Latin square design. Furthermore, heritability results were confirmed by early researchers like Nukasani *et al.* (2019) found high heritability (92%) for plant height. Likewise, Bhushan *et al.* (2013) reported high heritability (97.6%) for plant height during the evaluation of 40 wheat genotypes in a randomized complete block design. Similarly, Din *et al.* (2018) reported a genetic advance of about 11.81 for plant height observed in the screening of 23 genotypes.

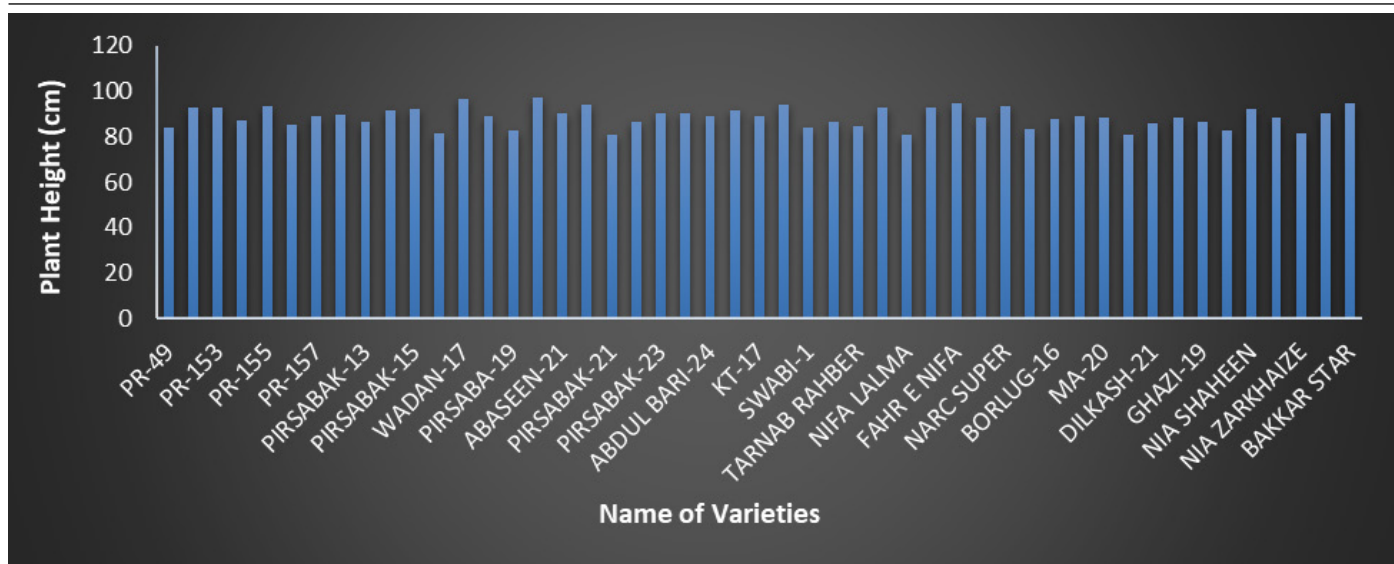


Figure 3: Data on the plant height of the 49 varieties of bread wheat.

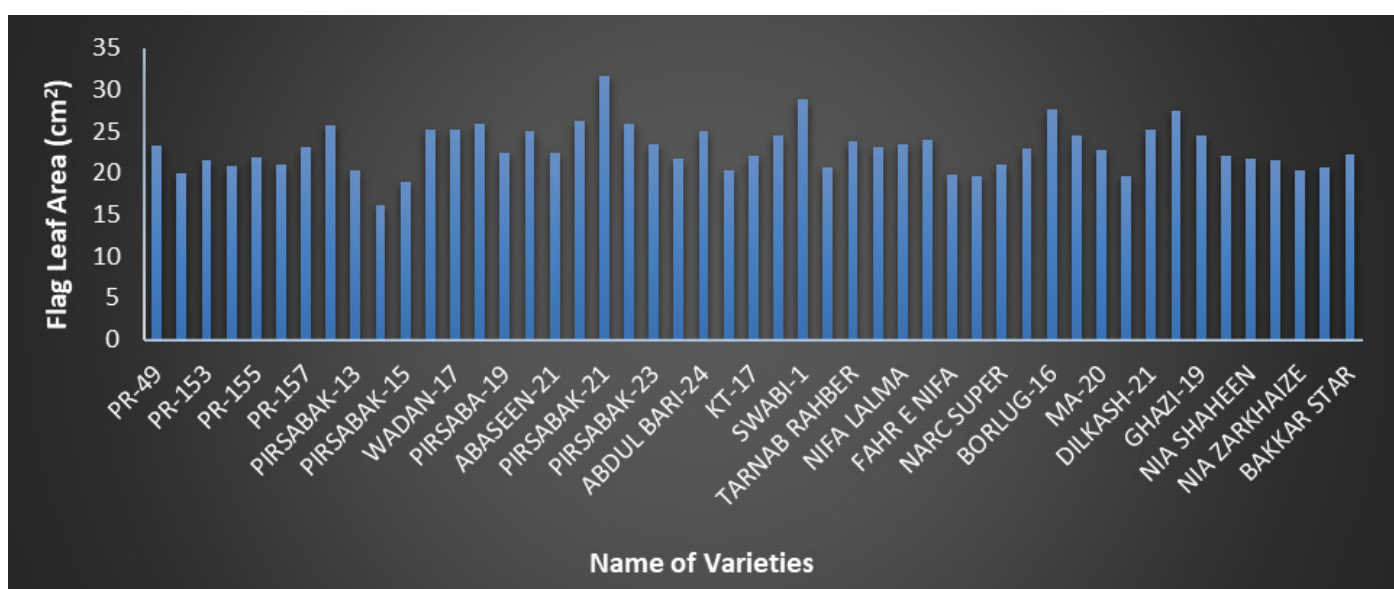


Figure 4: Details of the flag leaf area of 49 varieties of bread wheat, used for analysis.

Flag leaf area (cm²)

Analysis of variance conducted on the flag leaf area showed very significant differences between genotypes at $P \leq 0.01$ (Table 3). The coefficient of variation for this parameter was 2.10%. Means ranged from 16.2 to 31.7 cm² for the genotypes, with a value of 17.6 cm². The smallest flag leaf area, 16.2 cm², was recorded for SHAHKAR-13, and the largest, 31.7 cm², for PIRSABAK-21 (Figure 4/Table 3). LSD at 5% for the flag leaf area was 2.1 cm², and 0.86 was the heritability estimate of the flag leaf, while genetic progress was 3.51 (Table 7). The flag leaf area showed low genetic progress accompanied by high heritability (Table 7).

Our results for the flag leaf area agree with Kanwar *et al.* (2020), who found highly significant differ-

ences for a set of 25 genotypes evaluated in a Latin square design. Likewise, Dabi *et al.* (2017) evaluated 12 wheat genotypes and found a CV of 1.98 % for the flag leaf area. Ahmad *et al.* (2023) also confirmed mean range for flag leaf area varied between 21.29–36.41 cm² for 10 genotypes. A high heritability of 92% has been reported for plant height by Arya *et al.* (2017). Likewise, Bhushan *et al.* (2013) observed high heritability (97.6%) for plant height during the evaluation of 40 wheat genotypes in a randomized complete block design. Similarly, Iqbal *et al.* (2017) reported a genetic advance of about 2.63 for flag leaf screening in 16 genotypes (Table 4).

Peduncle length (cm)

According to the results of the analysis of variance (Table 3), the difference in genotypes demonstrated

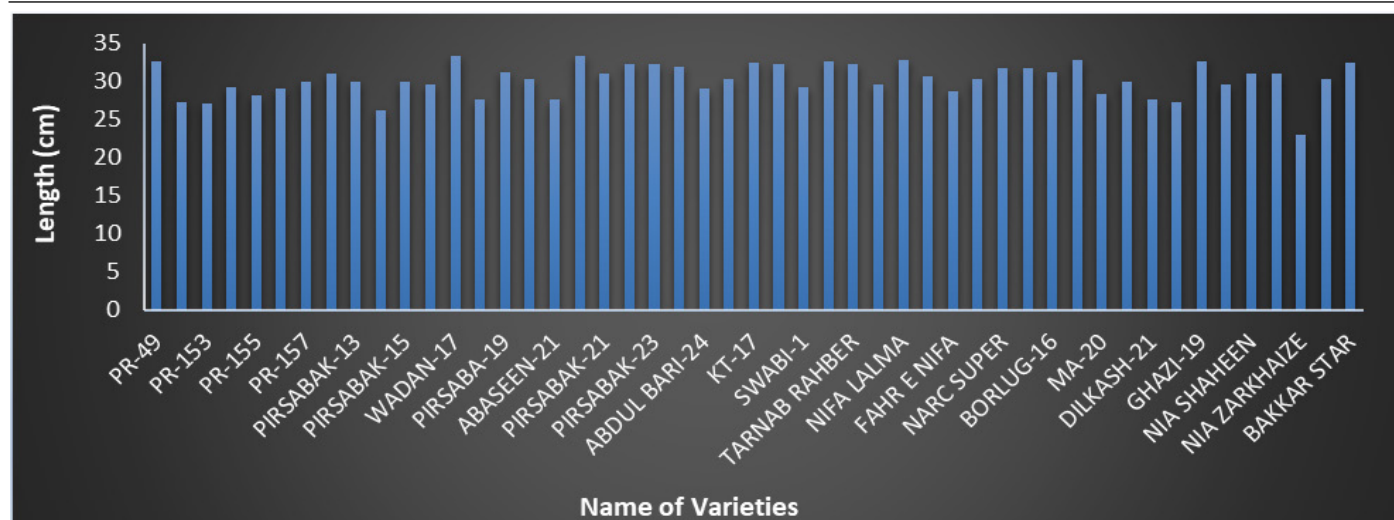


Figure 5: Peduncle length data of 49 varieties of bread wheat.

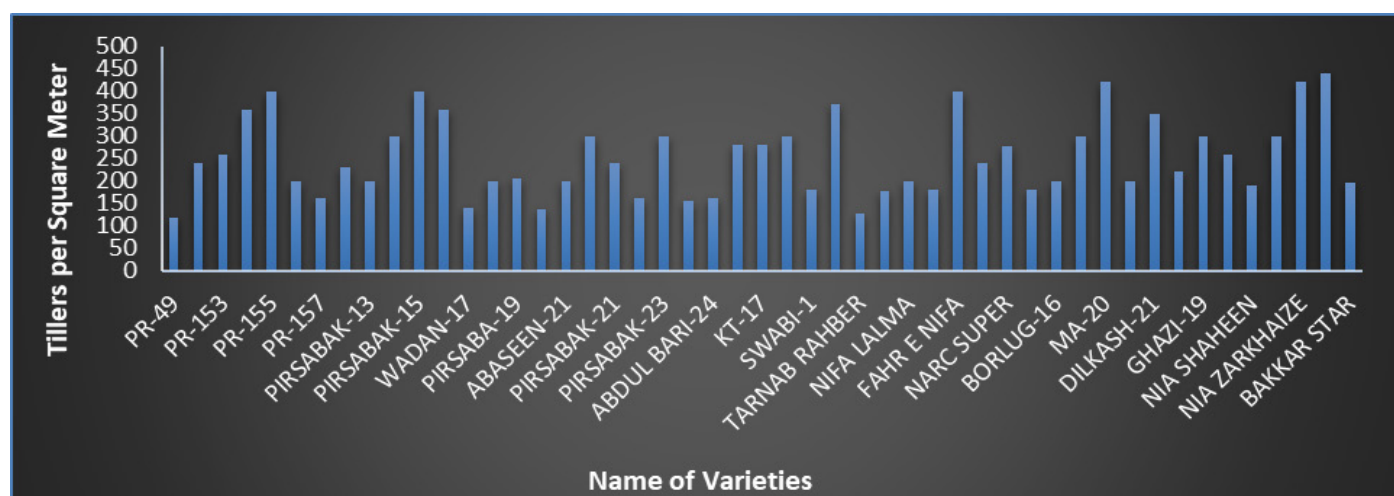


Figure 6: Number of tillers per square meter in the reported 49 varieties of bread wheat.

a highly significant effect on peduncle length ($P \leq 0.01$). The CV of peduncle length was 1.50%. The mean pedicle length of the genotypes was 30.27 cm, ranging between 23.00 to 33.33 cm. The NIA ZARKHAIZE had the least peduncle length of 23.00 cm, and ZARGHOON-21 had the maximum peduncle length of 33.33 cm (Figure 5/Table 5). The 5% LSD was 1.5 cm for peduncle length, the heritability of a peduncle was 0.88, and the genetic advance was 2.75. Low genetic advance is predicted for peduncle length, and high heritability (Table 7).

Our results for peduncle length are supported by Gerema *et al.* (2020), who found highly significant differences in the evaluation of 180 genotypes using an alpha lattice design. The results of Rana *et al.* (2023) also support the current mean range for peduncle length varied between 37 to 67 cm for 40 genotypes. Heritability value is also in agreement with the early researchers like Bishwas *et al.* (2024), who found a high

heritability of 78% for peduncle length. Adhikari *et al.* (2019) reported a genetic advance of about 1.53% for peduncle length in the screening of 26 genotypes.

Tillers m^{-2}

Significant differences were observed at $P \leq 0.01$ among the genotypes for tillers m^{-2} (Table 3). Correspondingly, the CV was 3.39 for tillers per square meter. Average tiller m^{-2} was 253.31 with a range between 116.00 and 440.00. A maximum number of tillers m^{-2} (440.00) was recorded on F. BAKKAR, whereas PR-49 had the least number of tillers m^{-2} (116.00) (Figure 6/Table 7). More specifically, an LSD of 5% for tillers m^{-2} was 3.39 with the smallest significant difference. The heritability value of tillers m^{-2} was 0.88, and the genetic advance was equal to 2.75. Tillers have low genetic advancement and considerably high heritability (Table 7).

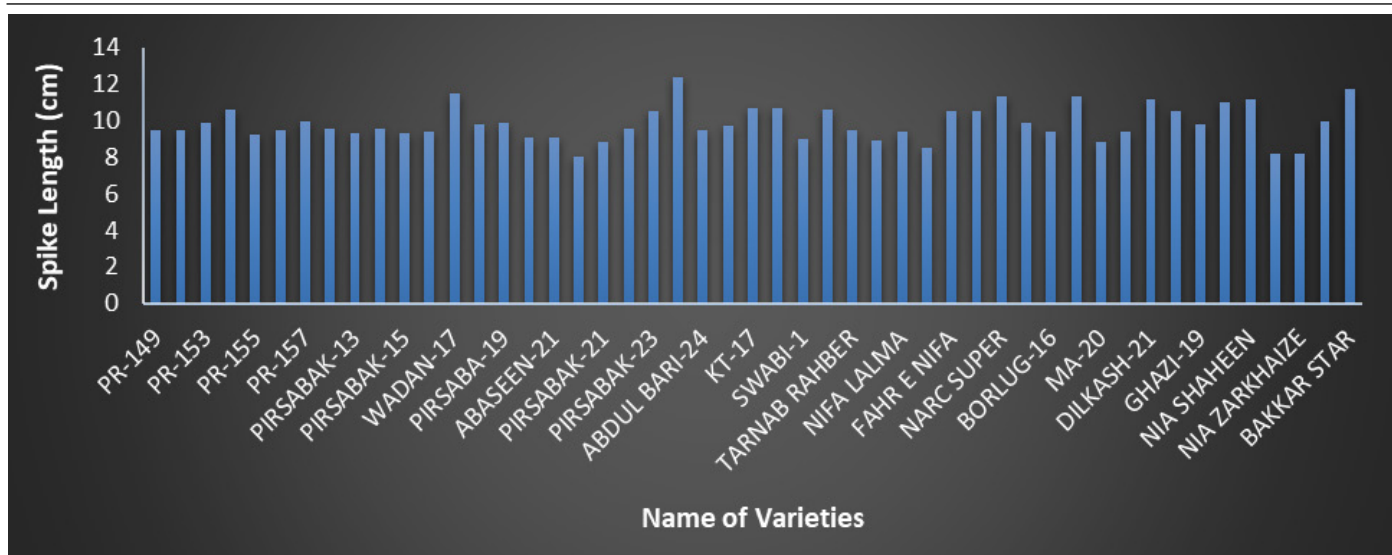


Figure 7: Data on the spike length of 49 varieties of bread wheat.

Present results for tillers m^{-2} are recorded by Prasad *et al.* (2021), where they found highly significant differences in the evaluation of 50 genotypes using a randomized complete block design. The findings of Varsha *et al.* (2019) also support the current mean range for tillers m^{-2} varied between 94.00 to 115.00 cm for 98 genotypes. Chauhan *et al.* (2023) reported a high heritability (83.6%) for tillers in the evaluation of 40 wheat genotypes in a randomized complete block design. Similarly, Ahmad and Gupta (2023) reported a genetic advance of about 1.76 for tiller screening of 10 genotypes.

Spike length (cm)

The length of spikes showed highly significant ($P \leq 0.01$) variations among genotypes for spike emergence (Table 4). The CV for spike length was 3.75%, while the mean spike length was 9.86 cm, with a range of 7.98 to 12.48 cm among the genotypes. The minimum spike length was recorded for KHYBER-23 (12.48cm), while the maximum was noted for ZARGHOON-21 (7.98 cm) (Figure 7/Table 5). The least significant difference (LSD 5%) for spike length was 0.75 cm. The heritability estimate of spike length was 0.86, while genetic advance was 1.23. A high heritability coupled with low genetic advance was recorded for spike length (Table 7).

Kyosev and Desheva (2015) also supported the current mean range for spike length varied between 9.20-17.60cm for 32 genotypes evaluated during 2014. The heritability result is also confirmed by early researchers like Desheva and Kyosev (2015), who found a high value of 83% for spike length. Rana *et*

al. (2023) found lower genetic progress at 2.64, with a high heritability of 74% in the screening of 40 wheat genotypes in a randomized complete block design.

Spikelet spike⁻¹

Genotype differences for spikelet spike⁻¹ were highly significant with $P \leq 0.01$ based on the value of the mean squares (Table 4). The coefficient of variation computed for spikelet spike⁻¹ was 4.67%. The spikelet counts ranged from 14.83 to 20.83, with an average of 18.08 spikelets spike⁻¹. The lowest spikelet spike⁻¹ was recorded for ZARGHOON-21, and the highest was found in MARKAZ-19, which had 20.83 (Figure 8/Table 6). A 1.70 was the least significant difference with an LSD of 5% for spikelets spike⁻¹. The heritability value of 0.70 was obtained for the spikelets spike⁻¹, and the genetic advance was 1.53. A minimum genetic advance with high heritability was observed for the spikelets (Table 7).

Our results on the number of spikelets per spike agree with the very significant differences Dragove *et al.* (2022) reported. Tefera *et al.* (2022) estimated a CV of 5.3% on a set of 81 genotypes tested in a triple lattice design in the same year. In the evaluation of 50 genotypes by Prasad *et al.* (2021), the range for spikelets per spike was confirmed to average between 14.10 to 21.23. In addition, for 180 wheat genotypes evaluated under alpha lattice design, Gerema *et al.* (2020) reported high heritability (60%) coupled with low genetic gain (21.1) in spikelets spike⁻¹. This difference in findings might be attributed to variations in the genetic material used in experiments.

Table 6: Mean performances of wheat advanced lines for Spike length Spikelets spike⁻¹, thousand-grain weight, grain yield, biological yield, and harvest index at CCRI during 2022-23.

Varieties	Spike length(cm)	Spikeletsspike ⁻¹	Thousand-grain-weight(g)	Biological yield (Kg ha ⁻¹)	Grain yield (Kg ha ⁻¹)	Harvest index
PR-149	9.5	20.7	38.9	10000	3440	36.5
PR-152	9.5	18.3	42.9	9750	3775	36.4
PR-153	9.9	18.5	49.2	8500	4365	40.4
PR-154	10.6	17.5	38.3	9500	3435	30.0
PR-155	9.2	17.5	47.8	8000	4745	43.4
PR-156	9.5	17.3	40.0	7750	4100	44.0
PR-157	10.0	19.7	43.6	11500	4340	40.1
PR-158	9.6	16.8	42.1	12000	4020	35.8
PIRSABAK-13	9.3	17.5	44.2	10500	4320	38.3
SHAHKAR-13	9.6	18.2	36.9	10500	3735	32.8
PIRSABAK-15	9.3	17.7	40.1	11000	5290	41.7
PASEENA-17	9.4	18.5	41.0	11500	4010	40.0
WADAN-17	11.5	16.7	39.1	11750	3665	32.4
KHAISTA-17	9.8	20.3	44.3	11000	4675	37.8
PIRSABA-19	9.9	18.3	33.8	13000	3995	34.1
GULZAR-19	9.1	17.3	40.2	11250	3890	37.2
ABASEEN-21	9.1	15.7	38.1	12000	3800	33.8
ZARGHOON-21	8.0	14.8	42.1	11000	4375	35.2
PIRSABAK-21	8.8	20.5	41.0	10000	3770	37.2
TASKEEN-22	9.6	17.3	37.2	12500	4020	36.1
PIRSABAK-23	10.5	16.2	42.9	13250	4315	37.1
KHYBER-23	12.4	17.3	45.9	10500	3455	37.7
ABDUL BARI-24	9.5	17.0	43.2	9500	3875	41.6
FAHIM-19	9.7	18.7	41.6	9750	4070	38.5
KT-17	10.7	18.5	34.8	10750	4010	36.5
TANDA-23	10.7	18.0	42.7	7500	3970	52.1
SWABI-1	9.0	17.0	38.9	8750	4235	46.4
NAURANG-23	10.6	16.3	41.1	9750	3465	35.4
TARNAB RAHBER	9.5	18.0	43.2	11750	3495	33.6
TARNAB GANAM	8.9	15.7	40.3	9000	3320	32.3
NIFA LALMA	9.4	16.7	44.5	10500	4550	36.6
NIFA NIJAT	8.5	18.5	31.6	8750	2870	32.9
FAHR E NIFA	10.5	16.3	34.7	9500	3655	34.7
WFAQ-23	10.5	19.2	43.7	7250	3000	37.2
NARC SUPER	11.3	19.3	39.0	11500	4170	36.9
MARKAZ-19	9.9	20.8	35.7	9500	2745	33.7
BORLUG-16	9.4	18.3	38.5	9500	3480	25.6
ZINCOL16	11.3	16.3	40.2	8250	3465	35.3
MA-20	8.8	19.3	29.5	5375	3160	46.3
AKBAR-19	9.4	17.7	27.0	7000	1375	23.5
DILKASH-21	11.2	17.7	40.5	7500	2665	36.4
UROOJ-2022	10.5	20.5	42.4	9000	3935	29.4
GHAZI-19	9.8	19.3	39.4	8750	3200	33.4
NAWAB-21	11.0	18.0	39.6	10750	3730	37.6

NIA SHAHEEN	11.2	18.7	38.8	8500	2750	36.0
NIA SUNHERI	8.2	18.7	35.6	8500	3315	34.5
NIA ZARKHAIZE	8.2	19.3	29.1	6250	2100	27.5
F.BAKKAR	10.0	20.7	36.6	9000	3490	32.2
BAKKAR STAR	11.7	18.8	43.6	11250	3600	31.9
GM	9.9	18.1	39.7	9798.5	3698.4	36.2
LSD	0.8	1.7	0.7	127.1	566.1	1.5

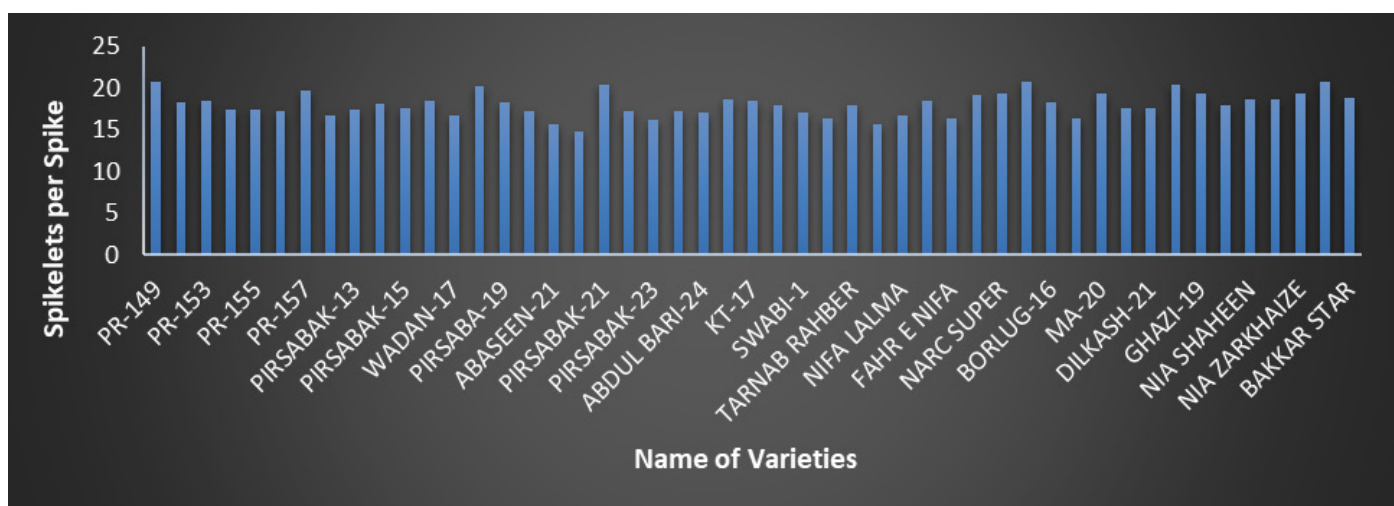


Figure 8: Number of Spikelets per spike in 49 different varieties of bread wheat.

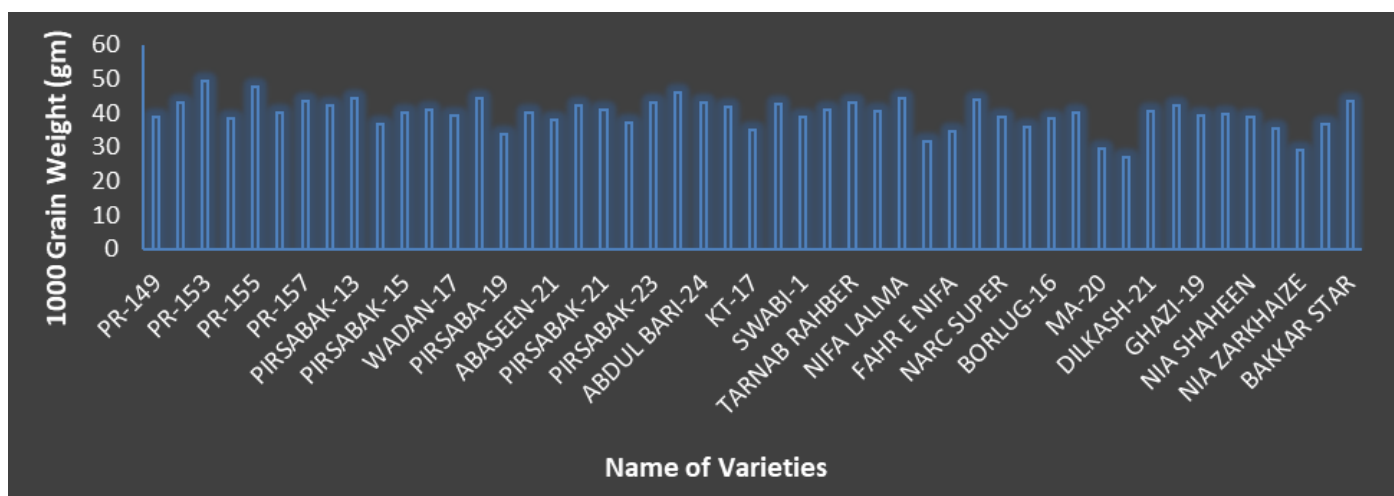


Figure 9: The 1000-grain weight of 49 varieties of bread wheat.

1000-grain weight (gm)

The means squares of different genotypes differ in 1000-grain weight very significantly ($P \leq 0.01$) (Table 4). The coefficient of variation calculated for 1000 grains was 0.85%. The average value for 1000-grain weight for each genotype was 18.50 g, having a range of 27.00–49.20 g. The maximum weight for 1000 grains (49.20 g) was recorded for PR-153, while AK-BAR-19 has the least weight for 1000 grains (27.00g) (Figure 9/Table 5). A 2.21 g was the least significant difference (LSD 5%) for 1000-grain weight. At 1000 grain weight, the heritability estimate was 0.99, and

genetic progress was 6.13. High heritability with very low genetic progress was observed for the predicted thousand-grain weight (Table 7).

Our results for the 1000-grain weight were following Varsha *et al.* (2019), in which significant differences were found for the set of 98 genotypes evaluated in a randomized block design in the year 2019. Likewise, Wani *et al.* (2018) evaluated 24 wheat genotypes and found a CV of 0.57 % for 1000-grain weight. Din *et al.* (2018) also supported the current mean range for thousand-grain weight varied between 34.3–41.7cm

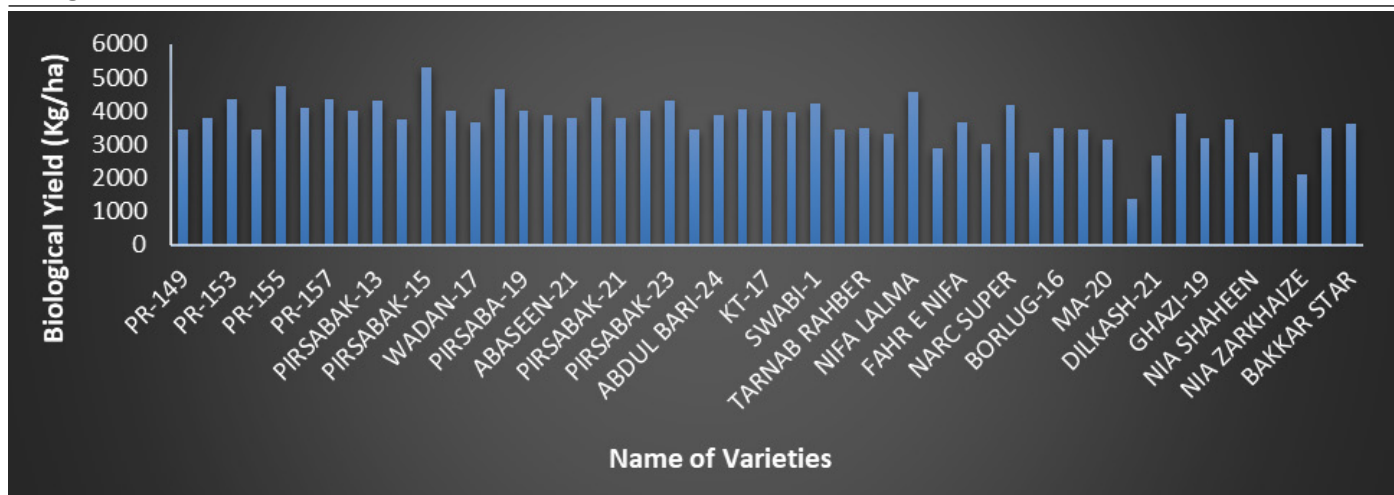


Figure 10: The biological yield data of 49 varieties of bread wheat.

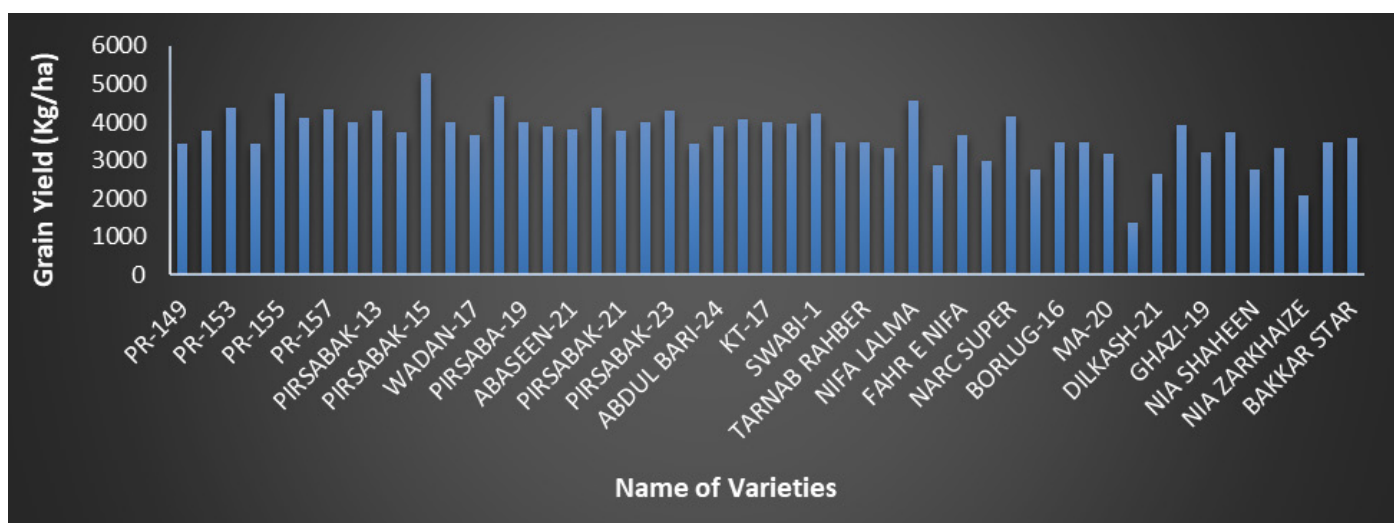


Figure 11: The grain yield data of 49 varieties of bread wheat.

for 23 genotypes. The estimate for thousand-grain weight had a heritability value of 95%, matching that of previous early researchers, [Chauhan et al. \(2022\)](#). In subsequent works, [Nukasani et al. \(2011\)](#) obtained 114 genotypes in an RFB design with three replications, resulting in a high heritability of 96 %, which disagrees with that of [Ahmad et al. \(2023\)](#), conforming to the current 4.89% genetic advance (Table 7).

Biological yield ($Kg\ ha^{-1}$)

Variance analysis of biological yield showed significant changes from genotype to genotype at $P \leq 0.01$ (Table 4). The coefficient of variation (CV) estimated for biological yield was 0.64%. The mean values for biological yield ranged from 13250.00 to 5375.00 with an average of 9798.47 (Table 6). The minimum biological yield (13250.00) was documented for PIR-SABAK-23, whereas the maximum biological yield (5375.00) was recorded for MA-20 (Figure 10/Table 6). The least significant difference (LSD 5%) for bi-

ological yield is 127.05. The heritability estimate of biological yield was 0.998, while genetic advance was 2257.43 (Table 7).

Our results for biological yield are in agreement with [Bishwas et al. \(2024\)](#), who found highly significant differences for a set of 20 genotypes evaluated in a randomized block design. [Rana et al. \(2023\)](#) also observed mean range for bio yield varied between 20 and 52 for 40 genotypes. These results are supported by an estimated significant heritability of 93% for bio-yield ([Arya et al., 2017](#)). Moreover, [Bhushan et al. 2012](#) observed a high heritability of 92% in 30 genotypes in a randomized block design with three replications. On the other hand, [Iqbal et al. \(2017\)](#) reported a genetic gain of 19.28%.

Grain yield ($Kg\ ha^{-1}$)

There was a significant variation in grain yield ($P \leq 0.01$) among genotypes (Table 4). Coefficients of var-

iation computed for grain yield were 8.98%. Grain yield ranged from 2916 to 5784 Kg ha⁻¹, averaging 4457.13 Kg ha⁻¹. PIRSABAK-13 had the highest grain yield, while SWABI-1 had the lowest grain yield with 2916.19 Kg ha⁻¹ (Figure 11/Table 6). In the case of grain yield, the LSD 5% was 802.18 Kg ha⁻¹. The heritability for grain yield was estimated at 0.84, and the genetic progress was 820.75. The grain yields manifested significant genetic progress with high heritability (Table 7).

In the grain yield, our results agree with [Chauhan et al. \(2022\)](#), who found highly significant differences for the set of 40 genotypes tested in a randomized whole-block design. [Iqbal et al. \(2017\)](#) reported a CV of 11.50% for grain yield by evaluating 16 wheat genotypes. The heritability value is also similar in magnitude to the findings of [Bhushan et al. \(2009\)](#), with a high heritability of 78% for grain yield. Likewise, [Bhushan et al. \(2009\)](#) also reported a high heritability (92%) by observing 30 genotypes in an RBD with three replications. A heritability value as high as 79% and genetic advance of 103.79 for genotype 114 were also recorded in an RBD design with three replications by [Nukasani et al. \(2011\)](#). In contrast, [Bayisa et al. \(2020\)](#) reported about 10.38% genetic gain. Contradictions in genetic advancement may be the case due to variations in the genetic material used in those experiments.

Harvest index

On the harvest index, ANOVA showed genotype significant differences at ($P \leq 0.01$) (Table 4). The coefficient of variation (CV) estimated for the harvest index was 2.08%. Mean values for the harvest index ranged from 23.50 to 52.13 Kg ha⁻¹ with an average

of 36.24 Kg ha⁻¹ (Table 6). The minimum harvest index (23.50 Kg ha⁻¹) was documented for AKBAR-19, whereas the maximum harvest index (52.13 Kg ha⁻¹) was recorded for TANDA-23 (Figure 12/Table 7). The least significant difference (LSD 5%) for harvest index (Kg ha⁻¹) was 1.52 Kg ha⁻¹. The heritability estimate of harvest index was 0.98, while genetic advance was 6.92. The harvest index presents rather low genetic progress associated with high heritability (Table 7).

Our results for the harvest index are in agreement with those of [Prasad et al. \(2021\)](#), who found highly significant differences for a set of 50 genotypes evaluated in a randomized block design. Likewise, [Dabi et al. \(2017\)](#) evaluated 12 wheat genotypes with a CV of 10.1 % for the harvest index. [Kanwar et al. \(2018\)](#) also observed mean range for the harvest index varied between 30.0–64% for 98 genotypes. These outcomes concur with those of other research, including [Varsha et al. \(2019\)](#), who found that the harvest index had a high heritability value of 96%. A related study by [Bhushan et al. \(2009\)](#) also detected a high heritability of 92%, using 30 genotypes and three replications in a randomized block design. While [Rajput et al. \(2019\)](#) observed a genetic advance of about 8.73%.

Phenotypic and genotypic correlation

Days to heading and days to maturity expressed a highly significant positive phenotypic relationship, $rP = 0.89$, $P = 0.01$, about the harvest index, $P = 0.01$, and $rP = 0.64$. On the other hand, days to heading showed a strongly negative phenotypic connection with the biological yield ($rP = 0.35$, $P = 0.05$) and tillers meter⁻² ($rP = -0.42$, $P = 0.01$) (Table 8). Similar correlations between heading and bio-yield ($rp = -0.19^*$) were

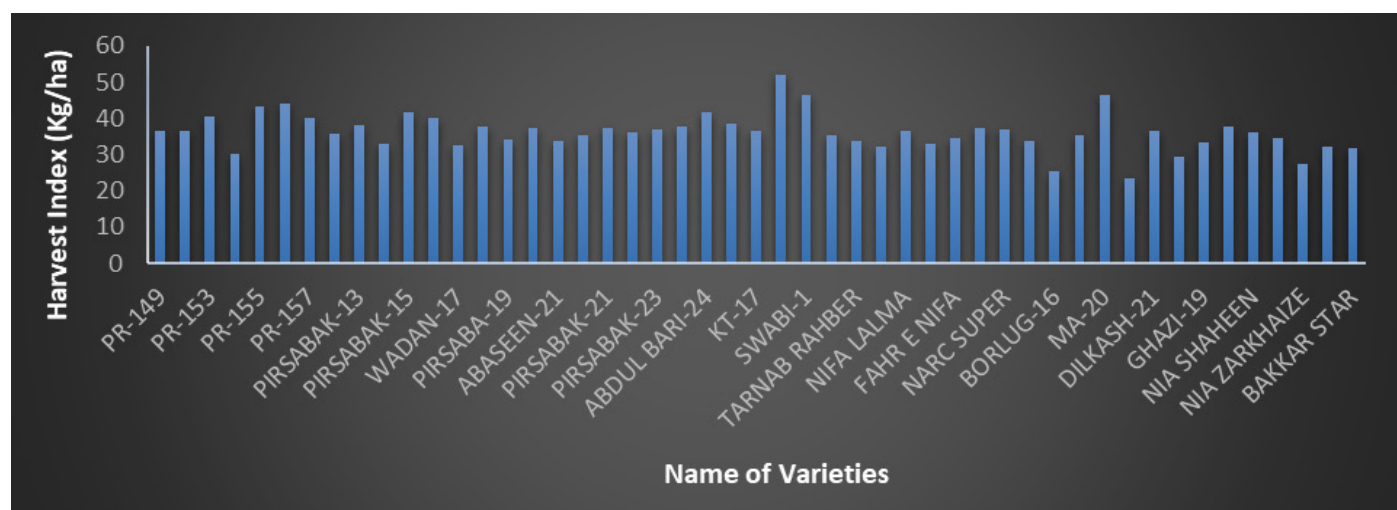


Figure 12: Harvest index data of 49 varieties of bread wheat.

Table 7: Estimation of genetic, environmental and phenotypic variance with their respective heritability and genetic advance for various traits.

Name of Traits	Genetic Variance (V_g)	Environmental Variance (V_e)	Phenotypic Variance (V_p)	Heritability (h^2)	Genetic Advance (GA)
Days to heading	19.24	0.39	19.63	0.98	6.12
Days to Maturity	0.76	1.46	2.22	0.34	0.72
Plant Height	18.42	1.98	20.39	0.90	5.75
Flag Leaf Area	7.16	1.12	8.28	0.86	3.51
Peduncle Length	4.29	0.57	4.86	0.88	2.75
Tillers metre ⁻²	7579.75	2.82	7582.57	0.98	122.73
Spike Length	0.88	0.14	1.02	0.86	1.23
Spikelets Spike ⁻¹	1.68	0.71	2.39	0.70	1.53
Thousand Grain weight	19.02	0.11	19.13	0.99	6.13
Grain Yield	404712.61	78695.94	483408.55	0.84	820.75
Biological Yield	2768239.64	3963.19	2772202.83	0.98	2344.28
Harvest Index	24.62	0.57	25.19	0.98	6.92

Table 8: Phenotypic Correlation (above Diagonal) and Genotypic Correlation (below Diagonal) for various traits.

	DH	DM	PH	FLA	PDL	SL	SPK	TM	GY	BY	TGW	HI
DH	--	0.89**	0.20	-0.12	-0.10	-0.25	-0.19	-0.42**	-0.22	-0.35*	-0.08	0.64**
DM	0.68**	--	0.25	-0.17	-0.37**	-0.29*	-0.61**	-0.34*	-0.50**	-0.15	0.29*	0.43**
PH	0.02	0.30*	--	0.35*	0.83**	-0.26	-0.29*	-0.62**	-0.36*	-0.48**	-0.13	-0.35*
FLA	0.01	0.02	0.37**	--	0.80**	0.45**	-0.17	-0.41**	-0.23	-0.32*	-0.08	-0.25
PDL	0.03	0.00	0.07	0.45**	--	0.78**	0.04	-0.24	-0.24	-0.35*	-0.10	-0.25
SL	-0.10	-0.09	-0.01	0.05	0.35*	--	0.47**	0.59**	-0.39**	-0.56**	-0.19	-0.45**
SPK	-0.12	-0.29*	-0.40**	-0.03	0.00	0.71**	--	0.72**	-0.22	-0.38**	-0.13	-0.35*
TM	-0.25	-0.23	-0.09	-0.12	-0.42**	0.26	0.59**	--	0.83	0.35*	-0.34*	-0.72**
GY	-0.14	-0.14	-0.04	-0.06	-0.08	-0.29*	-0.19	0.55**	--	0.87*	-0.15	-0.40**
BY	-0.20	-0.29*	-0.36*	-0.08	-0.11	-0.2	-0.26	0.22	0.73**	--	0.60**	0.22
TGW	-0.04	-0.04	0.04	0.02	0.00	-0.08	-0.09	-0.22	-0.13	0.43**	--	0.54**
HI	0.44**	0.26	0.00	-0.01	-0.03	-0.14	-0.15	-0.33*	-0.20	0.00	0.50**	--

**, * significance at 1% and 5%, respectively. DH = days to heading, DM = days to maturity, PH = plant height, FLA = flag leaf area, PDL = Peduncle length, SL = spike length, SPKS = spikelets spike⁻¹, TM = tiller meter², GY = grain yield and BY = biological yield.

also recorded by Rana *et al.* 2023 in their research. Mecha *et al.* (2017) and Gerema *et al.* (2020) observed the same relationship between heading and maturity in their respective experiments ($r_G=0.42^{**}$ and $r_G=0.39^{**}$), respectively. Days to maturity showed a positive phenotypic association with harvest index ($r_P = 0.43$, $P = 0.01$), and thousand-grain weight ($r_P = 0.29$, $P = 0.05$). The same relationship between plant height and maturity, $r_G=0.53^*$, was reported by Abinasa *et al.* (2011) for a set of 16 durum genotypes. Plant height and peduncle length showed significant positive phenotypic relationships ($r_P=0.83$, $P = 0.01$; flag leaf area, $r_P=0.35$, $P = 0.05$). Moreover, a signif-

icant negative correlation between the plant height and the harvest index, tillers meter⁻², grain yield, bio yield, and spikelets spike⁻¹, with corresponding r_P values of -0.35, $P = 0.05$, -0.52, $P = 0.01$, -0.36, $P = 0.05$, -0.48, $P = 0.01$, and r_P values of -0.29 and $P = 0.05$ (Table 8). Ibrahim *et al.* (2010) demonstrated a strong positive phenotypic correlation between plant height and 1000-grain weight ($r_P=0.31^*$) and flag leaf area ($r_P=0.50^{**}$), further validating the current association. In this regard, Khaliq *et al.* (2004) reported a high positive phenotypic association $r_P = 0.82^{**}$ between plant height and spikelets spike⁻¹.

Flag leaf area and plant height were strongly positively genotypically associated $rG = 0.37$, $P = 0.05$. On the other hand, spikelets spike^{-1} and biological yield had a strong negative genotypic association with the plant height (Table 6). Upadhyay *et al.* (2020) observed almost similar associations, viz., a positive significant genotypic correlation between plant height and peduncle length, $rG = 0.88^{**}$; and Rahman *et al.* (2017) showed a similar correlation between plant height and spikelets spike^{-1} , $rG = 0.79^{**}$. Similarly, Khaliq *et al.* (2004) found a significant positive genotypic association of $Q = 0.76^*$ existing between plant height and flag leaf area. More recently, Ibrahim *et al.* (2020) revealed a positive genotypic correlation $rp = 0.52^{**}$, between plant height and 1000-grain weight.

On the other hand, flag leaf area and spike length, $rP = 0.45$, $P = 0.01$, peduncle length, $rP = 0.80$, $P = 0.01$, indicated a strong positive phenotypic relationship. According to this, there was a highly significant negative association ($rP = -0.41$ at $P = 0.01$) and positive relationship ($rP = 0.32$ at $P = 0.05$) between the tillers meter^{-2} and bio-yield and leaf area, respectively (Table 8). In contrast, flag leaf area and peduncle length were highly significantly positively associated on a genotypic basis, $rG = 0.45$ at $P = 0.01$. Iqbal *et al.* (2017), tested 16 genotypes in a randomized complete block design and established the same relationship of flag leaf area with bio-yield, $rG = 0.30^*$.

The peduncle length correlated significantly negatively with biological yield, while it correlated positively with spike length with $rP = -0.35$ and $rP = 0.78$, respectively at $P = 0.01$. The peduncle length correlated significantly positively with spike length and negatively with tillers meter^{-2} , with $rG = 0.35$ and $rG = -0.42$, respectively, at $P = 0.05$ (Table 7). Ullah *et al.* (2021) reported the same magnitude of peduncle length with spikelets per spike, $rG = 0.78^{**}$.

The spikelets, however, recorded negative phenotypic association with harvest index, $rP = -0.35$, $P = 0.05$, and with bio-yield, $rP = -0.72$, $P = 0.01$. Similarly, spikelets spike^{-1} and tillers meter^{-2} also recorded a positive association, $rP = 0.59$, $P = 0.01$ (Table 7). Bishwas and Singh (2024) led to the same conclusion about the association of spikelets spike^{-1} and bio-yield with $rG = 0.9345^{**}$ from their experiments, consisting of 20 genotypes in a block design. Chauhan *et al.* (2022) reported the morphological and genotypic association between spikelets and bio-yield as $rG = 0.440^{**}$ and

$rP = 0.395^{**}$. The phenotypic association between tillers and bio-yield showed a strong positive association with $rP = 0.35$, $P = 0.05$.

The tillers, however, were negatively correlated to the harvest index with $rP = -0.72$ at $P = 0.01$ and thousand-grain weight with $rP = -0.34$ at $P = 0.05$. However, a strong positive genotypic association, $rG = 0.55$ at $P = 0.01$, was found to exist between tiller meter^{-2} and grain yield. However, a significant negative genotypic association was observed between tiller meter^{-2} and harvest index with $rG = -0.33$ at $P = 0.05$. Gao *et al.* (2024) revealed the presence of a negative relationship between tiller meter^{-2} and chlorophyll content, $rG = 0.36^*$. Kiss *et al.* (2021) reported an identical finding of a strong negative genotypic association between tiller meter^{-2} with 1000-grain weight; $rG = -0.60^{**}$. Similarly, 1000-grain weight and tiller meter^{-2} showed a strong negative phenotypic association $rP = -0.44^{**}$. The phenotypic relation of grain yield and biological yield was highly significant, $rP = 0.87$, $P = 0.01$, while the harvest index showed a negative relationship, $rP = 0.40$, $P = 0.01$.

Furthermore, the biological yield and grain yield exhibited a highly positive genotypic relationship, $rG = 0.73$, $P = 0.01$ (Table 8). According to Bayisa *et al.* (2020), there was a high positive genotypic association between grain yield and biological yield, $rG = 0.62^{**}$. Furthermore, Din *et al.* (2018), indicated that there existed a positive genotypic correlation between grain yield and bio-yield, $rG = 0.961^{**}$. A high positive phenotypic and genotypic correlation between the thousand-grain weight and harvest index, with $rP = 0.54$, $P = 0.01$, and $rG = 0.50$, $P = 0.01$, respectively (Table 8). Chauhan *et al.* (2022) estimated the correlations of genotype and phenotype with the harvest index to be $rG = 0.378^{**}$ and 0.384^{**} , respectively.

Conclusion and Recommendations

Our analysis of the 49 different wheat genotypes revealed significant variations across various phenological and morphological traits. Among these genotypes, some of them were identified for specific traits, like PR-156 for early maturity, NIA ZARKHAIZE for the highest tillers per square meter, PR-153 for the highest 1000-grain weight, PIRSABAK-15 for the highest grain yield, and PIRSABAK-23 for the highest biological yield. Significant positive genotypic correlations were observed among various key traits

including days to heading with maturity and harvest index, maturity with plant height, plant height relative to the flag leaf area, spike length relative to spike⁻¹, tillers relative to grain yield, and grain yield with biological yield and 1,000-grain weight relative to the harvest index. These are the indicators of the possibility of charting improvement at the same time in the right proportion through the breeder's effort and coordination in genetic management. All these correlations show coordinated potential for simultaneous improvement through breeding efforts.

We recommend that some of the enhancing traits, such as early maturity, tillering capacity, grain yield, 1000-grain weight, and biological yield, can be considered for future breeding programs, as well as efforts need to utilize advanced techniques for more efficient trait improvement. Further research can help in understanding the trait relationships, and leveraging advanced breeding technologies will be crucial for developing high-yielding and resilient wheat varieties to address agricultural challenges.

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Novelty Statement

The field trial of 49 different wheat genotypes revealed that genotypes PR-156, Nia Zarkhaize, and PR-153 had the earliest maturity, the highest tillers per square meter, and 1000-grain weight, respectively. Furthermore, Pirsabak-15 and Pirsabak-23 had the highest grain and biological yields, respectively.

Author's Contribution

Zarghoona: Research experiment executed/MS drafting

Khilwat Afridi: Field trial supervision

Ruby Wali Khan, Rahmat Elahi, Nadia, Kashmala Jabbar, Guleena Khan, Haleema Bibi and Haseeba: Data collection

Ikramullah Khan: Proofreading

Abdur Rauf: Research Supervision/MS drafting and proofreading.

Generative AI and AI-assisted technology statement

The author(s) declare that no Generative AI was used in the creation of this manuscript.

Conflict of interest

The authors have declared no conflict of interest.

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