

EVALUATION OF VARIOUS WHEAT GENOTYPES IN THE ENVIRONMENTAL CONDITIONS OF DISTRICT NOWSHERA

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Abstract

In the district Nowshera, Khyber Pakhtunkhwa, Pakistan, an experiment was conducted during the 2019-2020 period to assess twenty wheat genotypes based on morphological traits. The study employed a randomized complete block design under normal growing conditions. Significant differences ($P \le 0.05$) were observed among the genotypes for days to heading, thousand grain weight, plant height, grain yield, spike length, spikelets per spike, biological yield, and harvest index. Days to heading ranged from 108.66 to 114.66 days, while plant height varied between 84.01 and 100.66 cm. Spike length ranged from 8.42 to 10.62 cm, and spikelets per spike ranged from 15.92 to 20.42. The 1000-grain weight varied from 58.29 to 70.79 g, biological yield from 4333.32 to 8666.66 kg ha⁻¹, grain yield from 2043.01 to 3713.32 kg ha⁻¹, and harvest index from 18.63 to 29.29%. The genotype CT-13052 exhibited the earliest heading at 108.66 days, while DN-120 showed the shortest plant height at 84.01 cm. Genotype DN-122 displayed the longest spike length at 10.62 cm, and Pakhtunkhwa-2015 had the highest spikelets per spike at 20.42. The genotype AUP-07014 recorded the highest 1000-grain weight at 70.79 g, and PS-35 achieved the maximum grain yield of 3713.32 kg ha⁻¹, followed by CDRI-SA-12, CT-13052, PS-28, and DN-120. This study plays a crucial role in ensuring food security and providing resistant genotypes for future breeding programs. The genotypes AUP-07014, PS-35, CT-13052, and Pirsabak-13 were

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recommended for their superior performance in yield and related attributes. They hold promise for future breeding initiatives aimed at enhancing grain production in bread wheat.

Keywords: Grain yield, Heritability, Morphological characters Wheat

Introduction

Hexaploid wheat, a member of the grass family Poaceae and tribe triticae, has undergone several classifications since Linnaeus's original classification in 1753. Debate continues as to whether the genus Aegilops, closely related to wheat, should be combined with Triticum (Athwal). 1968). Triticum covers diploid, tetraploid and hexaploid species, highlighting the important influence of polyploidy on wheat evolution. Hexaploid wheat occupies an important place in cereal crops in most regions of the world. It serves as a staple diet for about 36% of the world's population, which equates to 2 billion people, sustaining civilizations for over 8,000 years. Its versatile uses include breads, chapatis, cakes, cookies and confectionery items. In Pakistan, wheat is an important crop, contributing 13.7 percent to agricultural value addition and 3 percent to GDP (Pakistan, 2017-18). Globally, wheat accounts for approximately 55% of carbohydrate and 20% of dietary calories and protein consumption (Breman, 1995). In 2018, global wheat production reached 757.9 million tonnes, Pakistan ranked eighth globally and fourth in Asia (Food, 2017). Other leading wheat producers include China, India, Russia, USA, France and Canada. In Pakistan, hexaploid wheat is grown on 8.73 million hectares, yielding 25.4 million metric tons with an average yield of 2919 kg/ha. There are regional variations, such as in Khyber Pakhtunkhwa, where wheat is grown on 0.76 million hectares, producing 1.4 million tonnes with an average vield of 1860 kg/ha. Variation in yield is also observed between irrigated and non-irrigated areas (Laghari et al., 2016). Enhancing germplasm and genetic diversity is critical to ensure stable and sustainable food production. It is important to estimate genetic diversity in winter wheat using genetic information and morphological traits. Genetic variation, as measured by heritability, plays an important role in breeding programs, assisting in the selection of parental genotypes for hybridization and subsequent crop improvement efforts (Zeven and Schachl, 1989; Roy, 2014; Chimdesa, 2014; Tewolde *et al.*, 2006). Advances in agriculture, including the use of effective fertilizers and the development of high-yielding varieties such as semi-dwarf wheat, have significantly increased wheat production in diverse agro-ecological settings over the past three decades. The objective of this research is to evaluate wheat genotypes based on their performance and morphological



characteristics, estimate genetic variation and heritability and identify promising genotypes for future breeding programs.

Material and Methods

The research conducted between 2019-2020 in farmer Field at district Nowshera, Pakistan, under irrigated conditions focused on evaluating twenty wheat genotypes using a randomized complete block design with three replications. Here's a summary of the methodology and statistical analysis used in the study:

Experimental Setup:

Genotypes: Twenty wheat genotypes were studied, including eighteen advanced lines and two control cultivars (Pakhtunkhwa-2015, Pirsabak-13).

Design: Randomized complete block design (RCBD) was employed with each genotype planted in three replications.

Planting Details: Each genotype was sown with a row-to-row distance of 25 centimeters and a row length of 5 meters. To facilitate data collection, an empty row was left between adjacent plots.

Data Collection: Data on various agronomic traits were collected at appropriate times:

1. Days to Heading: Counted from the first sowing date until 50% of plants achieved heading.

2. Plant Height: Measured in centimeters at physiological maturity.

3. Spike Length: Measured as the distance from the first spikelet to the top of the spike, excluding awns.

4. Number of Spikelets per Spike: Counted on eight randomly selected spikes from each plot.

5. Thousand Grain Weight: Randomly selected grains (1000 g) were weighed from each plot's bulk grain production.

6. Biological Yield: Calculated using the formula: (Biological yield plot-1 / plot area m²) \times 10,000 m² = biological yield (kg ha⁻¹).



7. Grain Yield: Estimated using the formula: (Grain yield plot-1 / plot area m^2) × 10,000 m^2
= grain yield (kg ha^-1).

8. Harvest Index: Calculated as: [Grain yield plot-1 / Biological yield plot-1] × 100 (%).

Statistical Analysis:

The study was subjected statistical analysis using SAS (2009). Differences among means were tested using the LSD test at a 5% probability level, as per Steel and Torrie (1980).



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Results and Discussion

Number of days to heading

Mean squares for days to heading revealed highly significant (p < 0.01) differences. Important trait days to heading show genetic diversity amongst wheat genotypes. Days to heading productivity of wheat cultivars varied from 108.67 to 114.67 days, with genotype CT-13052 having the lowest days to heading (108.67 days) and CDRI-SA-12 (109.01 days) followed by PS-28 (109.33 days) and PS-33 (110 days) while late heading genotypes were AUP-07014 (114.67 days), CDRI-PV-1 and PS-35 (113.33 days each). In (Table 1) average value for overall days to heading was 111.93. Plant breeders are actively engaged in developing novel genotypes that exhibit early heading, a highly desirable trait. Early-heading genotypes offer distinct advantages over their late-heading counterparts. They benefit from an extended grain-filling period, enabling them to achieve higher grain yields earlier in the season when temperatures are cooler and more conducive (Memon et al., 2007). Estimating heritability is crucial in plant breeding, as it assesses the transferability of traits from one generation to the next. This estimation serves as a valuable tool, particularly when combined with other parameters, for predicting genetic progress in various traits (Khan et al., 2007).

Plant height (cm)

There were significant differences (p<0.01) found among the plant height for each genotypes. The presence of genetic change amongst cultivars for plant height was shown to have a significant effect. Plant height mean values varied from 84.01 cm to 100.66 cm, where maximum plant height was recorded for genotypes DN-120 (84.01cm) followed by other genotypes PS-28(85.66cm) and AUP-05814 (86.32 cm) while maximum plant height was recorded in CT-13169 (100.66 cm). Average plant heights of 20 genotypes were (91.80 cm) (Table 1). Plant height holds significant importance in breeding programs due to its correlation with lodging resistance and responsiveness to fertilizer applications (Donald and Hamblin, 1976). It is a crucial parameter in wheat breeding efforts as it impacts lodging susceptibility, seedling vigor, economic productivity, and weed management strategies (Akhtar et al., 2001). The experimental findings underscored substantial differences in plant height among genotypes, consistent with earlier research demonstrating notable variation in wheat genotype heights (Khan et al., 2010).



Spike length (cm)

The investigation into spike length highlighted its significant role (p < 0.05) in influencing final grain yield, thereby revealing considerable genetic diversity among the studied wheat genotypes. Spike length exhibited a range from 8.42 cm to 10.62 cm across the genotypes, with genotype DN-122 displaying the maximum spike length at 10.62 cm, whereas genotype AUP-07014 exhibited the shortest spike length at 8.42 cm. Notably, several other genotypes, including CDRI-PV-1 (10.59 cm), CDRI-SA-12 (10.42 cm), SRN-13121 (10.15 cm), and PS-23 (10.15 cm), also demonstrated noteworthy spike lengths. These findings underscore the importance of spike length variability in wheat genotypes, underscoring its pivotal role in determining grain yield outcomes (Table 1). Long spikes are highly prized by plant breeders due to their potential to enhance yield per unit area (Sharma et al., 2003). Spike length exhibits a strong positive correlation with grain weight per spike and ultimately contributes to higher grain yields. Additionally, spikes with awns contribute to an extended photosynthetic duration, keeping them functional and green for an extended period (Hamam and Khalid, 2009). Significant differences in spike length were observed according to the ANOVA table, reinforcing earlier findings of considerable variation among wheat genotypes (Thorne, 1965). On average, spikes can account for 20-30% of the dry matter accumulated in seeds (Akram et al., 2008).

Spikelet's spike

Significant differences (p < 0.05) were observed among all genotypes regarding spikelets per spike, emphasizing the genetic variability for this trait. The mean number of spikelets per spike ranged from 15.92 to 20.42 across the studied genotypes. Genotype Pakhtunkhwa-2015 recorded the highest number of spikelets per spike at 20.42, followed closely by PS-33 (19.92), Pirsabak-2013 (19.86), PS-28 (19.56), and DN-123 (19.12). In contrast, genotype AUP-07014 exhibited the fewest spikelets per spike at 15.92. The overall average mean for spikelets per spike was 19.86, highlighting the diversity in this trait among the genotypes. These findings underscore the significance of spikelet number variation in wheat genotypes, which plays a crucial role in determining potential grain yield outcomes. Such insights are essential for breeding programs aiming to enhance wheat productivity by selecting genotypes with optimal spikelet characteristics (Table 1). Wheat genotypes with longer spikes tend to exhibit a greater abundance of spikelets per spike to increased grain yield due to the higher spikelet number



per spike (Mohammadi *et al.*, 2011; Kashi and Ihsan, 2004). The study highlighted significant variations in flag leaf area among the genotypes, aligning with previous research that also reported significant differences in this trait among wheat genotypes (Abbasi *et al.*, 2003).

Table 1: Means data of Twenty wheat genotypes examined for number of days to heading,

Genotypes	Days to heading	Plant height	Spike length	Spikelet's spike
Inq-91/FS(f8)	110.66	93.66	9.02	17.92
SRN-13121	113.01	89.66	10.42	16.42
CT-13052	108.66	91.01	9.06	17.22
CT-13169	112.32	100.66	9.62	17.93
DN-120	112.32	84.01	10.12	17.79
DN-122	112.32	94.01	10.62	17.52
DN-123	112.66	96.01	10.09	19.12
PS-22	112.66	94.66	8.69	17.36
PS-23	112.01	87.01	10.16	16.36
PS-28	109.32	85.66	9.56	19.56
PS-33	110.01	91.66	9.09	19.92
PS-34	113.01	93.66	8.96	18.62
PS-35	113.32	92.66	9.36	17.12
AUP-05814	113.32	86.32	9.92	18.22
AUP-07014	114.66	100.01	8.42	15.92
CDRI-PV-1	113.32	91.01	10.59	18.02
CDRI-PV-2	111.66	88.32	9.42	18.82
CDRI-SA-12	109.01	89.66	10.42	18.49
Pakhtunkhwa-	111.32	90.32	10.01	20.42
2015				
Pirsabak-13	113.01	96.01	8.89	19.86
Means	111.92	91.79	9.62	19.86
LSD (0.05)	2.83	7.62	1.33	2.33



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Thousand grains weight (g)

Analysis of variance (ANOVA) revealed significant differences ($p \le 0.05$) in 1000-grain weight (Table 2), indicating substantial genetic variation among genotypes for this important trait. The mean values of 1000 grain weight ranged from 58.3 g to 70.8 g. Specifically, genotypes such as AUP-07014 (70.8 g), Parsabak-2013 (69.8 g), CT-13169 (69.1 g), and PS-34 (67.2 g) showed the highest weight, while genotype DN-123, PS-35, and PS-22 exhibited weights of 67.0 g, 66.9 g, and 66.6 g, respectively. In contrast, genotype DN-120 showed the lowest 1000-grain weight of 58.3 g. On average, the average 1000-grain weight of the genotypes was 64.90 g (Table 2). The 1000-grain weight is a crucial factor in wheat production, directly influencing yield potential. This parameter serves as a valuable criterion for selecting high-yielding varieties. Grain yield is positively correlated with the weight of 1000 seeds, which reflects the accumulation of dry matter in the grains. Our experiment identified significant variation in this critical 1000-grain weight parameter. Interestingly, our findings contrast with earlier studies by Ahmad et al. (2006) and Kamal *et al.* (2003), which reported conflicting results regarding thousand grain weight.

Biological yield

The analysis of variance (ANOVA) technique revealed highly significant variations (p < 0.01) in biological yield (Table 2). Biological yield ranged widely from 4333.3 to 8666.7 kg ha⁻¹, with the highest yields observed in genotypes AUP-07014 and PS-22, each yielding 8666.7 kg ha⁻¹, followed by SRN-13121 (6266.7 kg ha⁻¹), Pirsabak-2013 (6200 kg ha⁻¹), CDRI-PV-2 (6133.3 kg ha⁻¹), and Inq-91/FS(f8) (6600.0 kg ha⁻¹). In contrast, the lowest biological yields were recorded for genotypes DN-123 and CT-13169, both yielding 4333.3 kg ha⁻¹. Additionally, Pakhtunkhwa-2015 and PS-34 also exhibited similar biological yields of 5533.3 kg ha⁻¹ each. Overall, the average biological yield across all 20 wheat cultivars was 5653.3 kg ha⁻¹ (Table 2). Significant differences were observed among genotypes in terms of biological yield. Similar findings were reported by Mecha et al. (2016), who also found significant differences in biological yield among cultivars. The high heritability observed for biological yield indicates that this trait is predominantly controlled by genetics rather than environmental factors. These findings align with previous research by Bhushan et al. (2013), which similarly concluded that biological yield exhibits considerable heritability.



Grain yield

The analysis in Table 2 indicated highly significant differences in mean square due to grain yield. Grain yield varied from 2043.0 to 3713.3 kg ha⁻¹, with genotype PS-35 achieving the highest yield at 3713.3 kg ha⁻¹. Following closely were other genotypes like CDRI-SA-12, CT-13052, PS-28, and DN-120, yielding 3180.0 kg ha⁻¹, 3066.7 kg ha⁻¹, 3000.0 kg ha⁻¹, and 2949.3 kg ha⁻¹, respectively. Conversely, the lowest grain yield was recorded by genotype CT-13169 at 2043.0 kg ha⁻¹. On average, across all 20 wheat genotypes, the mean grain yield was 2849.5 kg ha⁻¹ (Table 2). Grain yield stands as the foremost and pivotal characteristic in wheat cultivation, commanding significant attention from breeders striving for improvements. This parameter exhibits strong correlations with other traits such as spike length, grain weight, and spikelets per spike, either through direct or indirect influence. In a recent experiment, substantial differences in grain yield among wheat genotypes were notably significant. This aligns with earlier findings by Khayatnezhad (2010), who similarly observed significant variations between wheat genotypes in terms of grain yield.

Harvest Index

Table 2 indicates that the mean square due to harvest index (%) exhibited significant differences across all studied genotypes. Harvest index varied from 18.63% to 29.30%. The genotype DN-120 displayed the highest harvest index at 29.30%, while genotype DN-123 had the lowest at 18.63%. Additionally, genotype CT-13169 showed a high harvest index of 26.23%, followed by CT-13052 at 24.80% and CDRI-PV-2 at 24.73%. Genotypes SRN-13121 and AUP-05814 both exhibited a harvest index of 24.67%. On average, across the 20 wheat genotypes studied, the mean harvest index was 23.28%.



Table 2: Means data for twenty wheat genotypes evaluated for thousand grain weight,biological yield, harvest index and final grain yield

Genotypes	Thousand grain	Biological yield	Grain yield	Harvest index
	weight			
Inq-91/FS(f8)	64.76	6600.01	2606.66	23.09
SRN-13121	61.06	6266.66	2460.01	24.64
CT-13052	62.46	5466.66	3066.66	24.82
CT-13169	69.12	4333.32	2043.01	26.20
DN-120	58.29	4600.01	2949.32	29.29
DN-122	65.42	5466.66	2726.66	20.46
DN-123	67.01	4333.32	2813.32	18.63
PS-22	66.59	8666.66	2562.66	23.05
PS-23	61.69	5000.01	2606.66	23.27
PS-28	61.22	5733.32	3000.01	23.46
PS-33	65.76	5000.01	2496.01	22.56
PS-34	67.22	5533.32	2273.32	22.46
PS-35	66.92	5200.01	3713.32	21.74
AUP-05814	60.96	4666.66	2674.66	24.67
AUP-07014	70.79	8666.66	2358.66	22.18
CDRI-PV-1	64.82	4933.32	2946.66	22.87
CDRI-PV-2	63.56	6133.32	2306.66	24.72
CDRI-SA-12	64.92	4933.32	3180.01	22.77
Pakhtunkhwa-	65.52	5333.32	2647.32	22.15
2015				
Pirsabak-13	69.86	6200.01	2429.66	22.39
Means	64.89	5653.32	2693.06	23.27
LSD (0.05)	5.97	983.08	20.89	4.45



Conclusion

Based on our study findings, significant variations were observed in days to heading, plant height, biological yield, spike length, spikelets per spike, thousand-seed weight, grain yield, and harvest index among the studied wheat genotypes. Most traits exhibited moderate to high heritability, indicating strong genetic control. Genotypes CT-13052 and CDRI-SA-12 demonstrated the shortest days to heading, while genotype DN-122 exhibited the longest spike length. The highest spikelets per spike were found in genotype Pakhtunkhwa-2015. Grain yield showed robust correlations with spike length, biological yield, spikelets per meter, and number of grains per spike in both environments. Genotypes AUP-07014, Pirsabak-13, PS-35, and CT-13169 displayed the highest 1000-grain weights, with PS-35, CDRI-SA-12, and PS-28 yielding the highest grain yields overall. These genotypes, particularly AUP-07014, PS-35, CT-13052, and Pirsabak-13, are recommended for their favorable morphological and yield-related traits, highlighting their potential in future breeding programs aimed at enhancing bread wheat grain production.



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