



Research Article

Genetic Variability Among Advanced Wheat Lines for Yield and Yield Related Traits

Aizaz Akbar^{1*}, Ijaz Ahmad², Aftab Jehan³, Imtiaz Ali⁴ and Muhammad Haris⁵

¹Department of Plant Breeding and Genetics, Faculty of Crop Production, The University of Agriculture, Peshawar, Pakistan; ²Department of Plant Breeding and Genetics, Faculty of Crop Production, Amir Muhammad Khan Campus, Mardan, The University of Agriculture, Peshawar, Pakistan; ³Department of Agriculture Extension, District Kohat, Pakistan; ⁴Department of Agriculture research, District Swabi, Pakistan; ⁵Department of Plant Breeding and Genetics, Faculty of Crop Production, The University of Agriculture, Peshawar, Pakistan.

Abstract | Wheat, a staple crop in Pakistan is vital for food security and economic stability. A set of 49 advanced wheat lines and one commercial cultivar (Swabi-1) were tested for the estimation of different genetic parameters and association of yield with yield components. Randomized complete block design with triple replications was conducted at the Agriculture Research Station, Swabi during 2021-22. Mean Square values showed substantial variation ($p \leq 0.01$) among genotypes for the studied traits. Genotype CIM-47 was observed for early heading, while CIM-39 showed early maturity. Genotype CIM-37 had the longest grain filling duration, while CIM-18 showed the shortest plants. Genotype CIM-10 produced the most productive tillers plant⁻¹, while CIM-36 revealed the longest spikes. Genotype CIM-48 had the highest 1000-grain weight, while CIM-10 and CIM-36 showed the highest grain yield. Heritability and genetic advance as a percentage of the mean were observed to be high for grain filling duration ($h^2 = 0.76$, $GAM\% = 29.20$) and grain yield ($h^2 = 0.80$, $GAM\% = 30.21$). Grain yield showed substantial positive phenotypic and genotypic association with productive tillers plant⁻¹ and a significant positive phenotypic relationship with days to heading. Wheat genotypes CIM-10 and CIM-36 performed well for grain yield and recommended for future breeding programs.

Received | June 07, 2024; **Accepted** | November 4, 2024; **Published** | January 24, 2025

***Correspondence** | Aizaz Akbar, Department of Plant Breeding and Genetics, Faculty of Crop Production, The University of Agriculture, Peshawar, Pakistan; **Email:** aizazakbar503@gmail.com

Citation | Akbar, A., I. Ahmad, A. Jehan, I. Ali. and M. Haris. 2025. Genetic variability among advanced wheat lines for yield and yield related traits. *Sarhad Journal of Agriculture*, 41(1): 154-164.

DOI | <https://dx.doi.org/10.17582/journal.sja/2025/41.1.154.164>

Keywords | CIMMYT, Correlation, Genetic advance, Genetic variability, Heritability, Yield



Copyright: 2025 by the authors. Licensee ResearchersLinks Ltd, England, UK.

This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<https://creativecommons.org/licenses/by/4.0/>).

Introduction

Triticum aestivum, a leading species within the Poaceae family, occupies a preeminent position as the most extensively cultivated and economically dominant crop globally, having a profound impact on

worldwide food systems, agricultural economies, and ecosystem services (Gurvinder *et al.*, 2024). Wheat's contribution to global food security is manifold, as evidenced by its share (28%) of the world's edible crop biomass. Moreover, in resource-constrained regions, this crop serves as a vital caloric source, providing up

to 60% of daily energy requirements, thus highlighting its significance in addressing the persistent issue of global food insecurity (Shoib *et al.*, 2024).

Globally, 2022-23 wheat production was 788 million tons from 220.60 million hectares, while achieving an average yield of 3574 kg ha⁻¹ (USDA, 2023). In Pakistan, during cropping season 2022-23, wheat production was 27.634 million tons from 9.04 million hectares with an average yield of 3056 kg ha⁻¹ (GoP, 2023).

Selection by breeders that only favors high yield and early maturation in wheat genotypes has limited genetic diversity found in the current wheat cultivar. Therefore, the productivity of this essential crop is impacted by a number of stresses (Singh *et al.*, 2024). It is therefore desperately needed to expand this important crop's genetic base by introducing genes from other sources. For successful breeding programs, the presence of genetic variability is of prime importance to overcome this problem. More variability governed by genetic makeup serve as a gene pool for selecting genotypes with desirable traits from the population (Tanveer *et al.*, 2022). Breeding for new genotypes is based upon the existing genetic variability or induced variations. These variations are quantified in terms of heritability which provides a quantitative measure of the genetic contribution of parental lines to the phenotypic expression of their hybrid offspring (Demeke *et al.*, 2024).

Correlation reveals the direction and extent of association between two traits. Understanding these relationships is crucial for combining desirable characteristics to boost yield (Baye *et al.*, 2020). Yield is a polygenic trait that depends upon component variables and their interaction with environment (Sumit *et al.*, 2024). Therefore, direct selection may not be fruitful, rather breeders have to go for indirect selection via contributing traits to get high yielding genotypes. So, the knowledge of correlation will enable precise breeding, improving yield and speeding genetic progress (Meyari *et al.*, 2013).

Pakistan's wheat production is significantly impacted by challenges related to climate change, mainly erratic rainfall and temperature variations (Belay *et al.*, 2017; Senbeta and Worku 2023). These factors have led to fluctuating wheat yields, making it difficult to meet the rising demand of this staple crop for the inhabitants of Pakistan. The changing climate has

intensified the need for adaptive strategies in agricultural practices to ensure food security in the region (Barma *et al.*, 2019). Additionally, outdated agricultural practices and poor farm management contribute to lower yields per hectare compared to other major wheat-producing nations.

This research focused on breeding program to determine genetic variability among advanced wheat lines for yield components, and to identify yield associated traits for indirect enhancement in wheat productivity to contribute to food security.

Materials and Methods

Experimental Site, Materials and Design

This experiment was carried out at Agriculture Research Station, (ARS) of Swabi, Khyber Pakhtunkhwa, Pakistan during the growing season 2021-22. The experiment was located at 72° 30' 22" E and 34° 07' 30" N longitude and latitude, elevation is 370 meter while it has sub-tropical humid climate. Summers are hot and humid while winters are too cold. A set of 49 wheat advanced lines were tested against one commercial check 'Swabi-1'. Details of advanced lines are given in (Table 1). The experiment was designed in randomized complete block design with three replications. Each plot comprised six rows and each row was three meters long. The space between two rows and plants were 30 cm and 15 cm, respectively. Irrigation was limited to sustain the normal growth of wheat plants. Other cultural practices were meticulously implemented throughout the crop cycle to minimize experimental variability and ensure the overall health and vigor of crop, thereby maximizing the accuracy and reliability of the results of experiment.

Data collection

The observations were recorded on days to heading (DH), maturity (DM), grain filling duration (GFD), plant height (PH), productive tillers plant⁻¹ (PTP), spike length (SL), thousand seed weight (TSW) and grain yield (GY).

Statistical analysis

The collected data for different parameters were subjected to statistical Software Statistix 8.1 (2006) as outlined for randomized complete block design (RCBD). The ANOVA procedure of Gomez and Gomez (1984) was used for the computation of all studied traits. Significance differences among geno

Table 1: Summary of CIMMYT wheat lines used in the research.

S.NO	PARENTAGE
CIM- 1	NADI# 1
CIM- 2	WADDER# 1
CIM- 3	BORIL14*2 // BEACARD/QAUAIU/ #1
CIM- 4	NDI63/2*/WBL1//VILLAJUAREZ /F209/KACHU//KARITAI/2*TRACH
CIM- 5	KAURD/BORLA14
CIM- 6	KAKURU// SUP15//BAJ #1
CIM- 7	KACHUA*2/ SUPA152/ 3/WABLL1*2/BRAMB//LING*2//BAVIS
CIM- 8	FRANCOLIN #1//NELOKI//3//PRL//2*PASTOR// KACHU
CIM- 9	KACHUWHEAR/SHARMA/3//C801//3*WBALL1/5/CIRIO16/WBLA1*2//BRAMB//LING*2//BAVISA
CIM- 10	TOHA # 1//2//KFAA/2/*KACHA
CIM- 11	HARTOG/SUMAI3/2*NAVAJ07/4/MUTAUS//KIRITA/2*TRACH/3/WHEAI/KRON/2/STAD/F2004
CIM- 12	BEARAD/2//FRNCLAN//BAJA2/#1//TECUEI #1
CIM- 13	BORLA14*2/3//WBLA1*2//BRAMBDA//LAING*2//BAVIS
CIM- 14	KACHUA//DAN/PHE*2//MATUS*2//HARILA#1
CIM- 15	BAJI#1/3//KIRATATI//HUWA234+LR34//PRINIA/4//KIRATI//HUWA24+LRA34//PRINIA/2//MATUS*2//HARILA#1/6//BAJI#1*2//TINAKIO#1
CIM- 16	BAJI#1/3//KIRAITATI//HUWA234+LR34//PARINIA2/4//KIRIA/TATIA.//HUWA24/LRA
CIM- 17	BAJI#1/3//KIRATATI//HUWA234//LR34//PRINIA/4//KIRIATATI//HARILA#1
CIM- 18	BAJI#1/3//KIRATATI//HUWA234//LR34//PRINIA/4//KIRIATATI//HUWA34+LRA34//PRINIAK
CIM- 19	WBL1A*2//BRAMBA/LING//BAVIAS*2/3//SUPER152//BAJI #1
CIM- 20	PFAU/MILANA/3//BABAZ. /LRA42//BABAZ/1//CROCA/1//AESQUARA//ROSAL//PGO/10//ATTILLA*2/9//KAT/BAGEI//FNA/U/3//BZAR
CIM- 21	WHEARI//KUKUNAI#1/5//KACHUA//KIRITATI//2*TRACH/6//KACHUI//KIRA/2*TRC
CIM- 22	PFAU//WEAVERI*2//TRANSFERI#//12P8/3//WHEARI//2*PRL/2*PASTORI/4/2*WBL1A*2//BRAMBA/LING
CIM- 23	SUPER152//BAJI #1//KIDEADI
CIM- 24	SUPER152//KENYA//SUNBIRD/3//KAHUI//KIRITATI/2*TRCHA
CIM- 25	SOKOL/3//PASTORI/2//HXL75/2*BAURI/4//SOKOLIA/WBL1A/5//MUCYI
CIM- 26	KISKA#1/5//KAZ*2//MNVI//KAUZI/3//MILANA/WHEAR//2*PRL/2*PASTORI//KACHUA//2*TRCHA
CIM- 27	DANPHEE/3//ROLF07//YANACIA//TACUPETOFR2001//BRAMBA/LING/4//ROBINKA
CIM- 28	TOH#1/2//MUTUS*2//TECUEA #1
CIM- 29	PFAU//MILANA/3//BA/BAZI/LR42//BABAX*2/4//PASTI//2*TUI/3/2*PASTOR//4//BERKUT/5//PFAU//MILANA
CIM- 30	HDT29673//SWASR/2//TBA//2*BLOCK /#1//WBL1A*2//KURUKUI
CIM- 31	KACHUA//BECARDI//WBL1A*2//BRAMA//BALING*2/3//ABLEUI
CIM- 32	WBL1A*2//KIRAITATI//FRNCLNI/3//BECARDI/4/2*KACHUA/DANPHER(MXIA2021\M42EAS2\9\SA20H\162)
CIM- 33	WBL1A*2//KIRAITATI//FRNCLNI/3//BECARDI/4/2*KACHUA/DANPHEI(MXIA2021\M42EI\S29S\A20H\163)
CIM- 34	WBL1A*2//KIRAITATI//FRNCZCXZ/3//BECARDI/4/2*KACHU/DANPHE(MXI20H21\BNM42ES-29SA20H\164)
CIM- 35	TAM20//PAISTOR//TOBAI97/3//HEILLO/4//PAURAI/5//BRBTI/1*2//KIRAITATI*2//KINGBIRD#1
CIM- 36	BAJ#1//KISKADEEI#1/3//WBL1A*2//BRAMBALING*2//BAVISA//4//BAJ#1//KISKADEE#1/ (MXI2021//M42ES/29SA20H/171)
CIM- 37	BAJ#1//KISKADEEI#1/3//WBL1A*2//BRAMABLING*2//BAVISA
CIM- 38	PRL/2*PASTORI/4//CHOIX/STAR/3//HEA/3//CNOA79//2*SERIA/5/2*PAURIAQUE#1
CIM- 39	SHORTI//ENEDSRI2/6//TRANSLOCATIONS//2*WBL1A*2//KAKATS/3//BECARDIA/4/2*BORLA14(MXI2021\M142ES29SA20H\179)

CIM- 40	SHORT/ENDSR/2/1/6TRANSLOCATIONS//2*WBL1A*2/KAKTS/3/BECARDI/4//2*BORLIA14(MXI2021\M142ES29SA20H\180)
CIM- 41	MUTUSI//KIRAITATI/2*TRCHI/3/WHEARI/KRONI/1/STADFI/2004/4/2*WBL1A*2//BRAMBLINGS*2//BAVISA
CIM- 42	MUNAL*2/CHONTE*2/3/SAWSR/22TB/2*BLOUK#1
CIM- 43	MUNALIA#1*2/4/HUWA24+LR341//PRIANIA//PBW343*2/KUKUNAI/3/ROLF07*2/5/WBL1A1
CIM- 44	KACHU#1*2/6/KINGBIRD#1/7/COPIOA/8/WBL1A1*2/4/YACOI/PBW65/3/KAUZI*2/TRAPA//KAUZI/5//KACHU#1
CIM- 45	ORION. / 5/2*FRNCLNI/4/WHEARI//KUKUNAI/3/C801/3*BATI//AVIA
CIM- 46	ESTOC/7/2*KISKADEEL#1/5/KLAUZ*2/MINV//KAUZ/3/MIHLAN/4/BAV92/WHEARI/2*PRLA/2*PAS-TORI
CIM- 47	CROC1/AESQAROSAI(205)//BORLI95/3/PRLA//SARAI//TSIA/VEE#5/4/FRETA2/5//CIROI16*2/6/SUPA152*2//TECUE #1
CIM- 48	NADI#2/MUACUY
CIM- 49	MUNAL #1/SUJATA//CHIPAKI
Local	Swabi-1
Check	

CIMMYT = *International Maize and Wheat Improvement Center.*

types justified genetic analysis. The means for individual traits were additionally separated and related by using the least significant difference (LSD) test 5% probability. Heritability was calculated from the variance components derived from the ANOVA mean squares, providing insights into the genetic and environmental contributions to trait variation. Additionally, genotypic and phenotypic associations among all traits were calculated using the method described by [Kwon and Torrie \(1964\)](#).

Heritability (h^2) was estimated by the method described by [Singh and Chaudhary \(1985\)](#). The formula for calculating h^2 in broad sense is:

$$h^2(b.s) = \frac{Vg}{Vp}$$

$$\text{Genotypic variance } (Vg) = \frac{GMS - EMS}{r}$$

$$\begin{aligned} \text{Environmental variance } (Ve) &= EMS \\ \text{Phenotypic variance } (Vp) &= Vg + Ve \end{aligned}$$

According to [Allard \(1964\)](#), Heritability estimates were grouped as follow:

Low: up to 30%, moderate: from 30 to 60%, high: equal to or above 60%.

Genetic advance (GA) and genetic advance as percentage of mean (GAM %), as described by [Khan et al. \(2001\)](#).

$$\text{Genetic advance } (GA) = k \times h^2 \times \sqrt{Vp}$$

Where;

k = Selection Intensity, Vp = Phenotypic variances, h^2 (b.s) = Broad sense heritability

$$GAM = \frac{GA}{\bar{x}} \times 100$$

Where;

\bar{x} = Mean value of trait.

[Johnson et al. \(1955\)](#) classified genetic advance (as percent of mean) into groups as mentioned below:

Low = up to 10%, moderate = from 10 to 20%, high = equal to or above 20%.

Phenotypic and genotypic correlations were computed by formula of [Kwon and Torrie \(1964\)](#).

$$\text{Phenotypic correlation} = \frac{COVp(x_1, x_2)}{\sqrt{Vp(x_1) \cdot Vp(x_2)}}$$

Where;

$COVp(x_1, x_2)$ is phenotypic covariance between traits x_1 and x_2

$Vp(x_1)$ and $Vp(x_2)$ are the phenotypic variances of trait x_1 and x_2 , respectively.

$$\text{Genotypic correlation} = \frac{COVG(x_1, x_2)}{\sqrt{VG(x_1) \cdot VG(x_2)}}$$

Where,

$COVG(x_1, x_2)$ is genotypic covariance between traits x_1 and x_2

$VG(x_1)$ and $VG(x_2)$ are the genotypic variances of trait x_1 and x_2 , respectively.

Table 2: ANOVA for agro morphological traits in wheat lines.

Traits	Replications	Genotypes	Error	CV (%)
	2	49	98	
DH	4.17	23.14**	1.07	0.859
DM	31.94	77.39**	3.23	1.26
GFD	14.61	43.02**	3.95	8.90
PH	40.26	90.86**	26.27	6.21
PTP	0.72	1.74**	0.61	13.97
SL	1.50	4.77**	1.34	11.15
TSW	20.60	47.16**	5.84	5.90
GY	75617.3	866604.3**	68294.9	8.32

** = Significant at 1% probability level; Note: DH: Days to heading; DM: Days to maturity; GFD: Grain filling duration; PH: Plant height; PTP: Productive tiller plant⁻¹; SL: Spike length; TSW: 1000-seed weight; GY: Grain yield

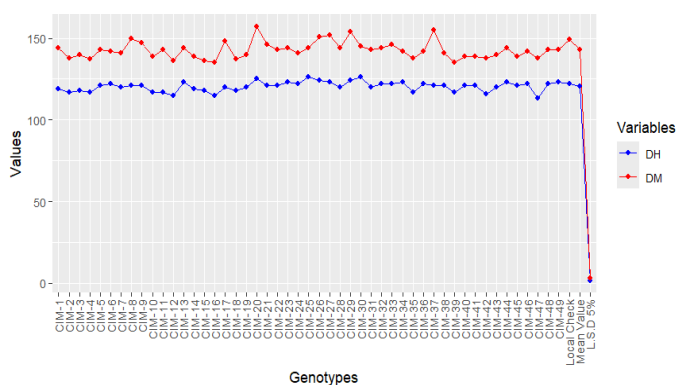


Figure 1: Mean values for days to heading (DH) and days to maturity (DM) at ARS Swabi, during 2021-22.

Results and Discussion

Analysis of variance, range values, heritability and genetic advance (%)

Days to heading (DH): DH is main physiological phenotype directly related to maturity, grain filling duration and strongly dependent upon day length and light (Salma et al., 2022). Analysis of variance revealed highly significant ($P \leq 0.01$) differences among advanced wheat lines for DH (Table 2). This indicates the existence of genetic differences among wheat genotypes for heading. Early DH (113 days) was noted for genotype CIM-47 followed by CIM-12 and CIM-16 (115 days). Earliness can be exploited by selecting early heading genotypes. Genotypes CIM-25 and CIM-30 were found late for DH (126 days), while mean across genotypes for DH was 120.5 days (Figure 1). Heritability estimates were observed high (0.87) while genetic advance as percent of mean was low (4.34%) in case of DH, which indicates the

role of non-additive gene action in controlling the expression of the trait (Table 3). Previously, Hassani et al. (2022) also reported highly significant differences among 44 wheat genotypes during 2020-21. Similarly, Sheera et al. (2022) reported high heritability and low genetic advance for DH.

Days to maturity (DM): DM is important trait as early maturity helps to create room for the next crop, residual moisture and may escape biotic and abiotic stresses at harvest maturity (Charan et al., 2024). Wheat genotypes showed differential in performance ($P \leq 0.01$) for DM shown by mean square values for DM (Table 2). Genotypes CIM-39 and CIM-16 were noticed early maturing (135 days), while late maturity was recorded for genotype CIM-20 (157 days) followed by genotype CIM-37 (155 days). Mean of 142.8 days were recorded across wheat genotypes for DM (Figure 1). Heritability estimate for DM was high (0.88) as evidenced by significant genetic differences for maturity, while genetic advance as percent of mean was low (6.76) (Table 3). High heritability indicates strong genetic influence with non-additive gene action. Sugandh et al. (2022) in their previous study also reported highly significant differences among 49 wheat genotypes for DM during 2019-20. Results of heritability for DM are in accordance with Sawant et al. (2023), who also reported high heritability with low genetic advance (%).

Grain filling duration (GFD): GFD is a key determinant of cereal yield affected by days to heading and maturity, availability of water and nutrients (Zhenning et al., 2023). Analysis of variance showed significant ($P \leq 0.01$) differences among advanced wheat lines for GFD (Table 2). Longest GFD was recorded for genotype, CIM-37 (34 days), followed by genotype, CIM-20 (32 days). Shortest GFD of 18 days was recorded for wheat genotypes, CIM-45, CIM-15 and CIM-39. Majority of the genotypes were at par for GFD by taking 22.3 days for the period of grains filling (Figure 2). High heritability and genetic advance of 0.76 and of 29.20%, respectively was noticed for GFD (Table 3). It indicates that the trait controlled by additive gene action, could be substantially considered for making selection. In the previous study, Sharma et al. (2023) also reported significant variation among 102 wheat genotypes for grain filling duration. High heritability (0.89) coupled with low genetic advance (10.56%) was noticed for aforementioned trait and confirm genetic role in regulation of variation for GFD.

Table 3: Estimation of genetic parameters for traits of wheat lines.

Traits.	V_g	V_e	V_p	h^2	G.A	G.A.M%
Days to heading	7.36	1.07	8.42	0.87	5.22	4.34
Days to maturity	24.72	3.23	27.95	0.88	9.65	6.76
Grain filling duration.	13.02	3.95	16.97	0.76	6.52	29.20
Plant height	21.53	26.27	47.80	0.45	6.42	7.79
Productive tiller plant ⁻¹	0.37	0.61	0.99	0.38	0.78	13.89
Spike length	1.14	1.34	2.48	0.46	1.49	14.38
1000-seed weight	13.77	5.84	19.65	0.70	6.41	15.66
Grain yield	266103.1	68294.9	334398.0	0.80	947.33	30.21

V_g : Genetic variance; V_e : Environmental variance; V_p : Phenotypic Variance; h^2 : Heritability; GA: Genetic Advance; GAM: Genetic advance as percent of mean.

Table 4: Phenotypic (above) and genotypic (below) correlation among traits of different advanced wheat lines.

	DH	DM	GFD	PH	PTP	SL	TSW	GY
DH	-	0.63**	0.11	-0.22**	0.04	-0.13	-0.1	0.16*
DM	0.71**	-	0.84**	-0.18*	0.08	-0.06	0.01	0.07
GFD	0.22	0.85**	-	-0.07	0.07	0.01	0.09	-0.03
PH	-0.31*	0.28*	-0.16	-	-0.03	0.35**	0.13	0.03
PTP ⁻¹	0.13	0.17	0.14	-0.02	-	-0.07	-0.01	0.21**
SL	-0.17	-0.09	-0.002	0.40**	-0.03	-	0.04	-0.001
TSW	-0.13	-0.01	0.08	0.31*	-0.04	0.13	-	0.03
GY	0.15	0.09	0.01	0.1	0.44**	0.03	0.12	-

*** = Significant at 1% and 5% probability level; Note: DH: Days to heading; DM: Days to maturity; GFD: Grain filling duration; PH: Plant height; PTP: Productive tiller plant⁻¹; SL: Spike length; TSW: 1000-seed weight; GY: Grain yield.

Plant height (PH): PH express the performance of a crop related to vertical growth followed by plant biomass. Desirability for plant height in wheat depends upon the area of plantation as tallness is preferred in rainfed areas, while semi dwarf and short stature plants are the key feature of irrigated varieties (Hong et al., 2022). Analysis of variance revealed significant ($P \leq 0.01$) differences for PH among genotypes of wheat (Table 3). Short stature plants were noticed in genotypes, CIM-18 and CIM-25 (each with 72 cm), while tallest genotype was CIM-39 (93 cm) followed by CIM-43 (92 cm), CIM-7 and CIM-47 (both 91 cm). Mean across 50 wheat genotypes for the aforementioned trait was 82.5 cm (Figure 2). Moderate heritability estimate and low genetic advance of 0.45 and 7.79%, respectively was discerned for PH (Table 3). Highly significant variations among 21 wheat genotypes were previously reported by Tanveer et al. (2022) for plant height. Moderate heritability and

low genetic advance (0.32 and 3.78%, respectively) was also reported by Amitava et al. (2021) for PH.

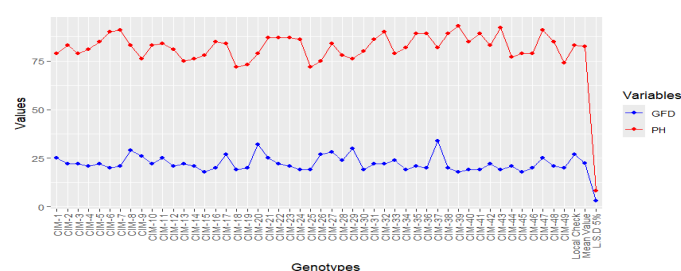


Figure 2: Mean values for grain filling duration (GFD) and plant height (PH) at ARS Swabi, during 2021-22.

Productive tiller plant⁻¹ (PTP): PTP is a key yield determinant, directly linked to spike density and ultimately with grains per plant and grain yield per unit area. More tillering variety is the prime goal of any wheat breeding program (Yundong et al., 2024). Mean square of the data showed significant ($P \leq 0.01$) differential in performance among wheat genotypes for PTP (Table 2). This revealed considerable inherent variation for PTP. Maximum PTP were recorded for genotypes CIM-10 and CIM-36 (8 and 7 tillers, respectively), while least PTP were observed for genotypes CIM-4, CIM-13, CIM-16, CIM-20 and CIM-35 (each with 4 tillers). Grand mean of genotypes for PTP among genotypes was 5.6 (Figure 2). PTP exhibited moderate heritability (0.38) and genetic advance (13.89%) indicating non-additive gene regulation for this trait (Table 3). Additive genes moderately control the trait making simple selection not a viable breeding strategy. The results of Chethan and Gurjar (2023) and Patil et al. (2023) showing highly significant differences among wheat genotypes are coherent with our research findings. Similarly, Patil et al. (2023) also reported moderate heritability and low genetic advance as percent of mean for PTP.

Spike length (SL): SL is an important trait for wheat breeders to be considered as it contribute to yield via grains per spike and grains per plant (Mingxiu *et al.*, 2023). However, this may not be true for all genotypes. Long spike with more and heavy grains are desirable. Data analysis for spike length displayed significant ($P \leq 0.01$) genetic differences among 50 wheat genotypes (Table 3). Genotypes CIM-36 and CIM-39 produced long spikes (each with 12.9 cm), followed by CIM-41 (12.7 cm). Genotype CIM-20 had shortest spikes (8.4 cm), while average across the studied wheat lines was 10.4 cm (Figure 3). Moderate heritability and genetic advance of 0.46 and 14.38%, respectively was noticed for SL (Table 3). Results of the current study are supported by Sugandh *et al.* (2022) who had also reported significant difference with moderate heritability (0.59) and genetic advance (11.66%) estimates for SL in their study.

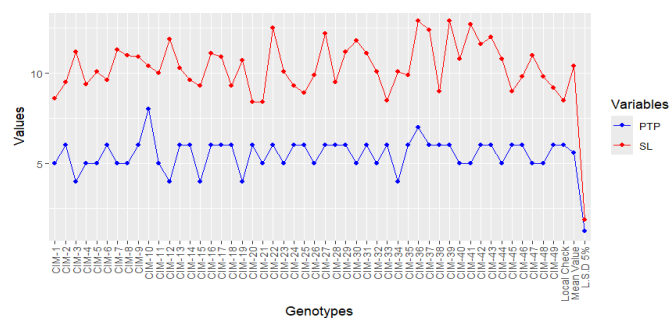


Figure 3: Mean values for productive tillers plant⁻¹ (PTP) and spike length (SL) at ARS Swabi, during 2021-22.

Thousand seed weight (TSW): TSW is a critical yield determinant as it contribute to yield directly and depends upon proper grain filling duration, spike length and plant height (Tao *et al.*, 2022). Mean square value showed significant ($P \leq 0.01$) differences among wheat genotypes for TSW (Table 3). Maximum TSW was recorded for genotype CIM-48 (51.4 g) followed CIM-31 (49.9 g) and CIM-1 (47.2 g). Least TSW was recorded for line CIM-11 (33.6 g), while mean across genotypes was 41.0 g (Figure 4). TSW revealed high heritability of 0.70 and moderate genetic advance of 15.66%. (Table 3). This indicated that additive genes control the trait and can go for direct selection for improvement. Considerable variations among wheat genotypes for TSW were observed by Choudhary *et al.* (2020). Likewise, Sawant *et al.* (2023) also reported high heritability coupled with low genetic advance as percent of mean for TSW.

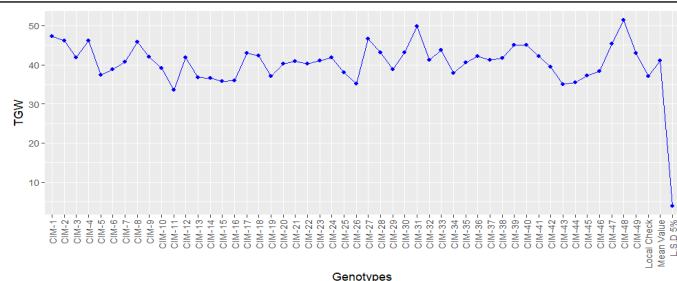


Figure 4: Mean values for thousand seed weight (TSW) at ARS Swabi, during 2021-22.

Grain yield (GY): GY is the key target on which all breeding strategies are focused to drive food security in terms of quantity and quality (Philomin *et al.*, 2020). Analysis of data displayed significance ($P \leq 0.01$) differences among wheat genotypes for GY (Table 3). Highest GY was noted for genotypes CIM-10, CIM-36 and CIM-25 (3930.6, 3916.7 and 3888.9 kg ha⁻¹, respectively) with average GY of 3142.2 kg ha⁻¹ among 50 wheat genotypes (Figure 5). High heritability (0.80) and high genetic advance (30.21%) were observed for GY (Table 3). It indicated that the trait controlled by non-additive genes is less responsive to selection. Sharma *et al.* (2023) supported our results by reporting highly significant variations in wheat genotypes, high heritability (0.98) and genetic advance (27.68%) for GY.

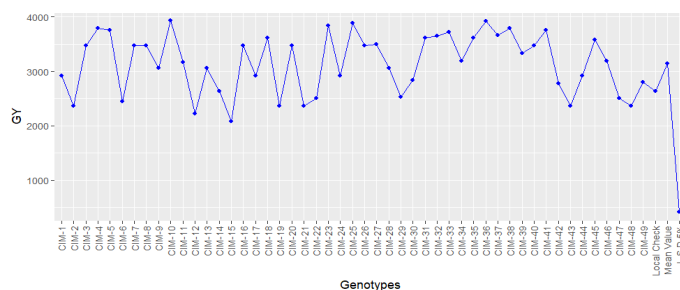


Figure 5: Mean values for grain yield (GY) at ARS Swabi, during 2021-22.

Genotypic and phenotypic correlations

Days to heading (DH): DH exhibited positive phenotypic relationship with DM and GY, while negatively correlated with PH. Genotypically, DH exhibited a substantial positive correlation with DM and negatively correlated with PH (Table 4). This correlation study shows that breeding for early maturity can be ensured by selecting genotypes with early heading. Moreover, earliness result in short stature plants due to time factor and photosynthetic units diversion. In the previous study, Sawant *et al.* (2023) also reported significant positive phenotypic and genotypic association between DH and DM.

Days to maturity (DM): DM exhibited a strong substantial positive relationship with DH and GFD at both phenotypic and genotypic levels. This confirms the association of early heading with early maturity. Furthermore, genotypes took more days to maturity helps in proper filling of grains due to available time. DM showed a substantial negative relationship with PH at the phenotypic level (Table 4). Previously, Sawant *et al.* (2023); Sheera *et al.* (2022) also reported negative association of DM with PH at the phenotypic level.

Grain filling duration (GFD): GFD exhibited a strong positive significant relationship with DM at both phenotypic and genotypic levels (Table 4). Delay in maturity provides ample time for grain filling. Due consideration is given to wheat lines with properly filled grains in optimum time and mature timely. Study by Sharma *et al.* (2023) noticed that GFD revealed a substantial negative genotypic correlation with DH. Early heading will provide enough time for genotypes to fill grains appropriately.

Plant height (PH): PH exhibited a strong positive association with SL and negative relationship with DH and DM at the phenotypic level. Spike length contributes to plant height in a positive way. At the genotypic level, plant height displayed significant positive relationships with SL and TSW, while negative connection with DH (Table 4). Notably, Sawant *et al.* (2023) also described similar findings, observing substantial positive phenotypic and genotypic correlations between PH and SL as well as with TSW.

Productive tiller plant⁻¹ (PTP): PTP exhibited a positive phenotypic and genotypic relationship with GY, indicating a strong relationship between these traits (Table 4). PTP is a major yield component and contributes to grain yield directly. More the productive tillers, more will be the spikes and thus grain yield. Previously, Sugandh *et al.* (2022) reported a significant positive phenotypic correlation between PTP and GY, which supported our results.

Spike length (SL): Highly significant positive association of SL was detected with PH at both phenotypic and genotypic levels (Table 4). Plant height includes spike excluding awns and contributes to plant height directly. Longer spike is desirable as longer spike often bears more spikelets and thus grains. Previous study by Sugandh *et al.* (2022); Sawant *et al.* (2023) both re-

ported a substantial positive relationship between SL and PH at phenotypic and genotypic levels, which is in accordance with our research findings.

Thousand seed weight (TSW): A significant positive relationship of TSW was displayed with PH at the genotypic level (Table 4). Similarly, Sheera *et al.* (2022) in their previous study also reported similar results for 1000-grain weight. They founded significant positive genotypic correlation of TSW with plant height. Thousand grain weight is also an important yield-related trait. Heavier grains result in more thousand kernel weight and thus more grain yield.

Grain yield (GY): GY exhibited highly significant positive phenotypic and genotypic associations with PTP, while significant positive phenotypic association with DH (Table 4). More tillers per unit area contribute to seed yield via more spikes and more seeds. Our results are also supported by Pawan *et al.* (2024), who had reported significant positive genotypic correlation of GY with PTP.

Conclusions and Recommendations

Considerable genetic variability was observed among 50 wheat lines for yield components as evidenced by ANOVA. This provides chances of genetic improvement of wheat lines for yield and yield components through direct and indirect selection. GFD and GY displayed high broad sense heritability and genetic advance as a percentage of the mean, predicting a role of non-additive gene action. Therefore, for yield improvement, indirect selection through association study would be rewarding. GY displayed a strong positive relationship with PTP at both phenotypic and genotypic levels. Lines with more tillers per plant must be selected to increase grain yield and meet the challenges of food security. Notably, CIMMYT lines CIM-10 and CIM-36 demonstrated excellent results in terms of yield and could be commercialized to enhance wheat productivity.

Acknowledgments

The authors would like to express their gratitude to the Director of Agriculture Research Station Swabi, Pakistan, for generously providing the agricultural land necessary for conducting this experiment, along with all the associated agricultural inputs and resources.

Novelty Statement

This study uncovers the unprecedented potential of CIM-10 and CIM-36 wheat lines, which exhibit exceptional yield-related traits, offering a revolutionary solution to address the escalating national demand for food.

Author's Contribution

Aizaz Akbar and Imtiaz Ali: Conceptualization, conducted field trial, Methodology, data collection, data analysis and writing.

Ijaz Ahmad: Supervision, validation and editing.

Aftab Jehan: Review this study and incorporated the minutes

Muhammad Haris: Visualization and draft preparation.

Conflict of interest

The authors have declared no conflict of interest.

References

- Allard, R.W. and Bradshaw, A.D. 1964. Implications of genotype by environment interactions in applied plant breeding. *Crop Sci.*, 4(5): 503-508. <https://doi.org/10.2135/cropsci1964.0011183X000400050021x>
- Amitava, R., Kumar, A., Singh, A., Mandi, A. and Barman, M. 2021. Analysis of genetic diversity and correlation studies on grain yield and its component characters in bread wheat genotypes. *J. Pharma. Innov.*, 10(5): 341-345.
- Barma, N.C.D., Hossain, A., Hakim, M.A., Mottaleb, K.A., Alam, M.A., Reza, M.M.A. and Rohman, M.M. 2019. Progress and challenges of wheat production in the era of climate change: A Bangladesh perspective. In M. Hasanuzzaman, K. Nahar, M. Hossain (Eds.) *Wheat Production in Changing Environments* (pp. 615-679). Singapore: Springer. https://doi.org/10.1007/978-981-13-6883-7_24
- Baye, A., Baye, B., Muluken, B. and Bitwoded, D. 2020. Genotypic and phenotypic correlation and path coefficient analysis for yield and yield-related traits in advanced bread wheat lines. *Cogent Food and Agric.*, 6(1): 2-17. <https://doi.org/10.1080/23311932.2020.1752603>
- Belay A., Recha, J.W., Woldeamanue, T. and Morton, J.F. 2017. Smallholder farmers' adaptation to climate change and determinants of their adaptation decisions in the Central Rift Valley of Ethiopia. *Agric Food Secur.*, 6:1-14. <https://doi.org/10.1186/s40066-017-0100-1>
- Charan, S., Yadav, S., Khare, V., Gupta, V., Kamble, U.R., Gupta, O.P., Kumar, R., Saini, P., Bairwa, R.K., Khobra, R., Sheoran, S., Kumar, S., Kurhade, A.K., Mishra, C.N., Gupta, A., Tyagi, B.S., Ahlawat, O.P., Singh, G. and Tiwari, R. 2024. Unraveling the Secrets of Early-Maturity and Short-Duration Bread Wheat in Unpredictable Environments. *Plants*. 13(20): 2-25. <https://doi.org/10.3390/plants13202855>
- Chethan, S.E. and Gurjar, D. 2023. Studies of genetic variability, heritability and genetic advance for yield component traits in bread wheat (*Triticum aestivum* L.). *Electron. J. Plant Breed.*, 13(4): 1214-1219. <https://doi.org/10.37992/2022.1304.155>
- Choudhary, L., Goyal, V.K., Pandey, S., Moitra, P.K. and Shukl, R.S. 2020. Assessment of genetic variability in advance breeding lines of wheat. *J. Pharm. Innov.*, 9(5): 239-244.
- Demeke, Z., Mekonnen, F., Geleta, N. and Abebe, K. 2024. Genetic variability, heritability and genetic advance for yield and yield related traits of bread wheat genotypes. *Int. J. Econ. Plants.*, 11(1): 38-47. <https://doi.org/10.23910/2/2024.5039b>
- Gomez, K.A. and Gomez, A.A. 1984. *Statistical Procedures for Agricultural Research*. 2nd ed. John Wiley and Sons Inc. New York, USA.
- Gop. 2023. *Pakistan Economic Survey*. Pakistan Bureau of Statistics, p 22, Islamabad, Pakistan. (<https://www.pbs.gov.pk>).
- Gurvinder, K., Singh, I., Behl, R.K. and Dhankar, A. 2024. Effect of different integrated nutrient management approaches on growth, yield attributes and yield of wheat *Triticum aestivum* (L.) crop. *Asian J. Soil Sci. Plant Nutri.*, 10(1): 457-468. <https://doi.org/10.9734/ajsspn/2024/v10i1252>
- Hassani, I., Nimbale, S., Singh, V. and Noori, A. 2022. Genetic variability analysis and correlation studies of bread wheat (*Triticum aestivum* L.) genotypes. *Ekin J. Crop Breed. Genet.* 8(2): 139-145.
- Hong, L., Shi, Z., Ma, F., Xu, Y., Han, G., Zhang, J., Liu, D. and An, D. 2022. Identification and validation of plant height, spike length and spike

- compactness loci in common wheat (*Triticum aestivum* L.). BMC Plant Biol., 22(1): 2-17. <https://doi.org/10.1186/s12870-022-03968-0>
- Johnson, H.W., Robinson, H.F. and Comstock, R.E. 1955. Estimates of genetic and environmental variability in soybeans. Agron. J., 47(7): 314-318. <https://doi.org/10.2134/agronj1955.00021962004700070009x>
- Khan, M.A., Bashir, E.L. and Bantel, R. 2001. Plant Breeding. National Book Foundation, Islamabad.
- Kwon, S.H. and Torrie, J.H. 1964. Heritability and interrelationships among traits of two soybean populations. Crop Sci., 4(2): 196-198. <https://doi.org/10.2135/cropsci1964.0011183X000400020023x>
- Meyari, S., Nouri, F., Sasani, S., Najafian, G. and Aghayari, F. 2013. Correlation and path analysis of grain yield and its components of some bread wheat under normal and source restriction conditions. Int. J. Farm. Allied Sci., 2(23): 1065-1069.
- Mingxiu, W., Lu, J., Liu, R., Li, Y., Ao, D., Wu, Y. and Zhang, L. 2023. Identification and validation of a major quantitative trait locus for spike length and compactness in the wheat (*Triticum aestivum* L.) line Chuanyu12D7. Front. Plant Sci., 14(3):1-15. <https://doi.org/10.3389/fpls.2023.1186183>
- Patil, P., Prakash, S., Shrivastav, S.P., Kulbhushan, P. and Gurjar, D. 2023. Genetic variability, heritability, genetic advance and divergence analysis in wheat (*Triticum aestivum* L.). Indian J. Agricul. Res., 10(2): 1-6. <https://doi.org/10.18805/IJARE.A-6036>
- Pawan, K.S., Singh, S.V., Yadav, R.K., Singh, L., Shweta, S.K., Singh, H., Tripathia, S., Dwivedi, and Tiwari, U. 2024. Correlation and Path Coefficient Analyses for Grain Yield and Its Contributing Traits in Bread Wheat (*Triticum aestivum* L.). J. Adv. Biol. Biotechnol., 27(3):208-218. <https://doi.org/10.9734/jabb/2024/v27i3735>
- Philomin, J., Singh, R.P., Braun, H.J., Espino, J.H., Herrera, L.C., Govindan, V., Mondal, S., Poland, J. and Shrestha, S. 2020. Genomic Selection for Grain Yield in the CIMMYT Wheat Breeding Program—Status and Perspectives. Front. Plant Sci., 11(03):1-18. <https://doi.org/10.3389/fpls.2020.564183>
- Salma, B., Dadshani, S., Koua, P., Léon, J. and Ballvora, A. 2022. Identification of QTLs for wheat heading time across multiple-environments. Theor. Appl. Genet., 135(6):2833-2848. <https://doi.org/10.1007/s00122-022-04152-6>
- Sawant, S.P., Kamble, M.S. and Pawar, R.M. 2023. Genetic variability, correlation and path analysis for yield and yield related contributing characters in wheat (*Triticum aestivum* L.). Advances in life Sci., 5(21): 9700-9703.
- Senbeta A.F., Worku, W. 2023. Ethiopia's wheat production pathways to self-sufficiency through land area expansion, irrigation advance, and yield gap closure. Heliyon. 9(10):1-13. <https://doi.org/10.1016/j.heliyon.2023.e20720>
- Sharma, S., Tripathi, M.K., Tiwari, S., Solanki, R.S., Chauhan, S., Tripathi, N., Dwivedi, N. and Kandalkar, V.S. 2023. The Exploitation of genetic variability and trait association analysis for diverse quantitative traits in bread wheat. Curr. J. Appl. Sci. Technol., 42(8): 19-33. <https://doi.org/10.9734/cjast/2023/v42i84087>
- Sheera, A., Dey, T., Pandey, M.K., Raina, V. and Mukhtar, B. 2022. Studies on genetic variability for yield attributes and nutritional composition in micronutrient efficient genotypes of wheat. J. Pharma. Innov., 11(5): 613-617.
- Shoab, Z., Yonas, M. W., Akbar, M.M. and Ahmad, A. 2024. Enhancing wheat yield through optimal sowing techniques in arid region of Pakistan. Sarhad J. of Agri., 40(2): 672-679. <https://doi.org/10.17582/journal.sja/2024/40.2.672.679>
- Singh, R.K. and Chaudhary, B.D. 1985. Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Dehli, India.
- Singh, S.P., Chand, P., Singh, V., Singh, A., Tiwari, A., Singh, A. and Kumar, M. (2024). Morphological Characterization and Assessment of Genetic Variability, Heritability and Genetic Advance in Bread Wheat (*Triticum aestivum* L.). Plant Cell Biotech. Mol. Biol., 25(1-2): 120-128. <https://doi.org/10.56557/pcbmb/2024/v25i1-28626>
- Statistix 8.1. 2006. Statistix 8 user guide, version 1.0. Analytical Software, PO Box 12185, Tallahassee FL 32317 USA. Copyright © 2006 by Analytical Software.
- Sugandh, C., Tyagi, S.D., Gupta, A. and Singh, S. 2022. Genetic variability, correlation, path coefficient and cluster analysis in bread wheat

- under rainfed conditions. *J. Pharm. Innov.*, 11(11): 818-823.
- Sumit, K.M., Surin, S.S., Verma, N., Bhargaw, P.K., Kumari, M. and Mishra, D.K. 2024. Studies on genetic variability, correlation and path coefficient analysis for yield and yield contributing traits in bread wheat. *J. Exp. Agric. Int.*, 46(6): 389-397. <https://doi.org/10.9734/jeai/2024/v46i62490>
- Tanveer, H., Singh, R.K., Singh, H. and Singh, S. 2022. Genetic variability and character association in bread wheat. *Skuast J. Res.*, 24(1): 46-52. <https://doi.org/10.5958/2349-297X.2022.00004.6>
- Tao, L., Q., Wang, J., Yang, Z., Tang, Y., Su, Y., Zhang, J., Qiu, X., Pu, X., Pan, Z. and Zhang, H. 2021. High-resolution detection of quantitative trait loci for seven important yield-related traits in wheat (*Triticum aestivum* L.) using a high-density SLAF-seq genetic map. *BMC Genomic Data.* 23(37):2-16.
- USDA. 2023. World Agriculture Production, United States Department of Agriculture, Foreign Agricultural Services.
- Yundong, Y., Lyu, B., Qi, J., Liu, X., Wang, Y., Delaplace, P. and Du, Y. 2024. A novel regulator of wheat tillering LT1 identified by using an upgraded BSA method, uni-BSA. *Mol. Breeding.*, 44(7):47-81. <https://doi.org/10.1007/s11032-024-01484-7>
- Zhenning, T., Chen, Y., Meng, S., Duan, M., Zhang, J. and Ye, N. 2023. Environmental Stimuli: A Major Challenge during Grain Filling in Cereals. *Int. J. Mol. Sci.*, 24(3): 2-18. <https://doi.org/10.3390/ijms24032255>