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ASSESSMENT OF GENETIC VARIABILITY AND YIELD-CONTRIBUTING TRAITS IN BREAD WHEAT (*TRITICUM AESTIVUM* L.)

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ABSTRACT

Bread wheat is a major staple crop, but its productivity is increasingly limited by climate variability and scarce genetic resources. This study assessed genetic variability, heritability, correlation, and path relationships among yield and related traits in 51 genotypes during the *Rabi* season of 2023–2024. Variance analysis showed significant differences among genotypes for all traits, indicating considerable genetic diversity. Phenotypic coefficients of variation were slightly higher than genotypic values, suggesting limited environmental influence. High heritability combined with high genetic advance was observed for plot yield, harvest index, total biomass, tillers per meter, and grains per spike, indicating the dominance of additive gene action and good potential for selection. Correlation and path analyses identified harvest index and total biomass as key contributors to grain yield due to their strong positive direct effects. Genotypes 5009, 5029, 5011, and 5007 were identified as high yielding and promising for future wheat improvement programs.

Keywords: Bread wheat, morphological traits, genetic variability, correlation analysis, path coefficient analysis

Introduction

Bread wheat (*Triticum aestivum* L.) is one of the most important cereal crops globally and serves as a primary source of food and nutrition for a large portion of the world's population. It significantly contributes to daily caloric and protein intake and plays a crucial role in ensuring food and nutritional security, particularly in developing countries like India, where wheat is a staple food for millions of people (Gaddam *et al.*, 2025a). Owing to its wide adaptability, high productivity, and diverse end uses, wheat occupies a prominent position in global agriculture and food systems. However, sustaining and enhancing wheat productivity has become increasingly challenging due to shrinking arable land, declining soil fertility, and rising production costs.

The continuous growth of the global population, coupled with the adverse effects of climate change, has intensified the demand for high-yielding, stable, and climate-resilient wheat varieties (Ezzat *et al.* 2024).

Abiotic stresses such as drought, heat, and salinity, along with biotic stresses including diseases and pests, pose serious threats to wheat production and yield stability across different agro-climatic regions. These challenges necessitate the development of improved wheat genotypes capable of maintaining productivity under diverse and changing environmental conditions.

The success of wheat improvement programs largely depends on the availability and effective utilization of genetic variability within the species (Akbar *et al.*, 2025). Genetic variability serves as the foundation for selection, providing breeders with opportunities to enhance complex traits such as grain yield, quality attributes, and stress tolerance. A broad genetic base enables the identification of superior genotypes and facilitates the development of varieties with improved performance and adaptability (Gaddam *et al.*, 2025b). Therefore, understanding the magnitude, nature, and distribution of variability among wheat genotypes is essential for formulating efficient and sustainable breeding strategies (Singh *et al.*, 2025).

Morphological characterization remains a fundamental and practical approach for assessing genetic diversity in wheat, especially during the preliminary evaluation of germplasm. This approach involves assessing easily observable and measurable traits, such as plant height, the number of tillers per plant, spike length, the number of grains per spike, and grain weight. These traits not only have a direct influence on grain yield but also serve as reliable descriptors for differentiating genotypes and identifying promising parental lines for hybridization (Ezzat *et al.*, 2024). Despite advancements in molecular techniques, morphological traits continue to be widely used due to their simplicity, cost-effectiveness, and direct relevance to agronomic performance.

The estimation of genetic parameters such as genotypic and phenotypic coefficients of variation, heritability, and genetic advance provides valuable insights into the extent of genetic control over various traits and their potential for improvement through selection (Gaddam *et al.*, 2025a). High heritability in conjunction with high genetic advance generally indicates the predominance of additive gene action, suggesting that selection for such traits can be effective and lead to significant genetic gains. Additionally, the study of correlations among grain yield and its component traits helps in identifying traits that contribute most to yield improvement and can be exploited for indirect selection, thereby enhancing the efficiency of breeding programs (Rani *et al.*, 2024).

This study was conducted to assess the genetic variability and morphological diversity among various bread wheat genotypes. The results of this research aim to help identify superior genotypes and important yield-related traits. This information will be valuable for future wheat improvement programs focused on enhancing productivity, stability, and adaptability in different environmental conditions.

Material and Methods

Experimental site and plant material

The present investigation was conducted during the *Rabi* season of 2023–24 at the AB Block Farm of Bidhan Chandra Krishi Viswavidyalaya, Kalyani Simanta, Nadia, West Bengal, India. The experimental site is located at Lat 22° 59' 22.34" N, Long 88° 25' 32.64" E with an elevation of 11.7 m above mean sea level, and falls under the Medium Gangetic New Alluvial Plains agro-climatic zone. The region experiences a sub-tropical climate with cool and dry winter conditions favourable for wheat cultivation. During the cropping season, temperatures ranged from

10.8 °C in January to 42.2 °C in April. The soil of the experimental field was sandy loam in texture, well-drained, uniform in fertility, and moderately fertile with a neutral pH. The experimental material consisted of 51 advanced breeding lines of bread wheat procured from the International Maize and Wheat Improvement Centre (CIMMYT), Mexico. The experiment was laid out in a Randomized Block Design (RBD) with three replications. Each plot measured 6.0 m × 1.2 m, with a spacing of 0.5 m between plots and 20 cm row-to-row spacing. The field was prepared by two ploughing operations using a cultivator and spade, followed by proper levelling to achieve a fine tilth. The recommended dose of fertilizers were applied at 150:60:50 kg ha⁻¹ of N:P₂O₅:K₂O during land preparation. Standard agronomic practices were followed uniformly throughout the crop growth period.

Data collection

The observations were recorded for different phenological, morphological, and yield-related traits. Phenological parameters included days to 50% heading (DH), days to 50% flowering (DF), and days to maturity (DM), were calculated from the date of sowing. Morphological traits such as plant height (PH) in cm and spike length (SL) in cm were recorded at maturity. Plant height was measured from the soil surface to the tip of the spike, excluding awns, while spike length was measured from the base of the spike to the tip. Yield contributing traits included number of tillers per meter (T/m), number of grains per spike (G/S), and thousand-grain weight (TGW) in g. Tillers per meter were counted from a one-meter row length during the maximum tillering stage. Grains per spike were counted from randomly selected spikes after harvest, and thousand-grain weight was recorded by weighing 1000 well-filled grains from each replication. Biological and yield traits included total biomass (TB) in kg and plot yield (PY) in kg, which were recorded at harvest by weighing the total above-ground biomass and cleaned grain yield, respectively. Harvest index (HI) was calculated as the ratio of grain yield to total biomass. Observations for all traits were recorded from the selected five plants in each replication, and mean values were used for statistical analysis.

Statistical Analysis

The data recorded were subjected to statistical analysis using mean values obtained from three replications. Analysis of variance (ANOVA) was performed to test the significance of differences among genotypes, and the significance of treatment effects was tested at the 5% level of probability. Genetic parameters, including genotypic variance and

phenotypic variance, were estimated as per Burton (1952). The genotypic coefficient of variation and phenotypic coefficient of variation were computed following Burton and DeVane (1953). Heritability in the broad sense was estimated using the formula given by Lush (1940), while genetic advance was calculated according to Johnson *et al.* (1955). Genetic advance as a percentage of the mean was obtained by dividing the genetic advance by the corresponding trait mean.

Correlation coefficients were computed to determine the nature and strength of associations among grain yield and its component traits. To further partition these correlations into direct and indirect effects, path coefficient analysis was performed with grain yield as the dependent variable (Dewey and Lu, 1959). This analysis helped identify traits with significant direct contributions to yield and those influencing yield indirectly through other traits. All statistical analyses were carried out using R statistical software version 4.2.0, using variability package for ANOVA, correlation, and path analysis.

Results and Discussion

Analysis of variance (ANOVA)

The ANOVA revealed significant differences (Table 1) among wheat genotypes for all eleven characters evaluated, demonstrating the presence of ample genetic variability. Genotype effects were highly significant ($p \leq 0.01$) for traits *viz.* plant height, days to heading, days to 50% flowering, days to maturity, tillers per meter, grains per spike, thousand-grain weight, total biomass, harvest index, and plot yield, while spike length showed significance at the 5% level. The higher mean square values for genotypes compared with error indicated that the variation was mainly genetic in nature. Replication effects were mostly non-significant, suggesting uniform experimental conditions. These findings highlight good potential for selection and improvement of yield and related traits in wheat.

Mean performance

The evaluation of fifty-one wheat genotypes revealed wide variability for the traits studied (Table 2), indicating the presence of sufficient genetic diversity suitable for selection and crop improvement. Plant height ranged from 78.50 to 96.25 cm, reflecting variation in plant architecture that may influence lodging resistance and biomass production. Similar results were reported in diverse wheat germplasm (Dutamo *et al.*, 2015, Anand *et al.*, 2024). Days to maturity varied from 92.33 to 107.00 days, suggesting the availability of early to medium-duration genotypes that can be exploited for adaptation to different agro-

climatic conditions and cropping systems. Tillers per meter ranged from 67.33 to 125.67, indicating its major role in determining yield differences among genotypes. Grains per spike varied between 26.00 and 53.33, while thousand-grain weight ranged from 30.92 to 49.03 g, reflecting differences in sink size and grain filling efficiency. Previous studies have reported similar levels of variation for these traits, confirming their significance as key yield determinants in wheat (Slafer *et al.*, 2014, Arya, 2017, Yadav *et al.*, 2021). Genotypes having maximum grain number and grain weight generally recorded superior yield performance, indicating the combined contribution of these traits to enhanced productivity.

Plot yield exhibited a wide range from 1.71 to 3.62 kg, showing significant variations in yield potential between the genotypes evaluated. Genotypes 5009, 5029, 5011 and 5007 are high-yielding, supported by favourable combinations of tiller number, grain weight, total biomass, and harvest index. Harvest index varied from 0.31 to 0.62, highlighting differences in assimilate partitioning efficiency among genotypes. Higher yielding genotypes generally combine greater biomass production with efficient translocation of assimilates to grains, a key factor for yield improvement as emphasised by Donald and Hamblin (1976).

The relatively low coefficients of variation observed for most traits indicated reliable expression under the experimental conditions, suggesting minimal environmental interference. Overall, the observed variability in yield and its component traits provides ample opportunity for identifying superior genotypes and their effective utilization in wheat breeding programmes aimed at enhancing yield and adaptability.

Genetic parameters

Table 3 presents the estimates of variability, heritability, and genetic advance for all the traits studied. Phenotypic variance (PV) was slightly higher than genotypic variance (GV) for all traits. In contrast, environmental variance (EV) was relatively low, indicating that the majority of the observed variation was genetic in origin. The highest PV and GV were recorded for tillers per meter (211.62 and 204.72), followed by grains per spike (46.05 and 43.58, respectively), whereas the lowest values were observed for harvest index (0.00440 and 0.00419). A similar trend of PV exceeding GV with minimal environmental contribution has been reported by Sharma *et al.* (2021).

Phenotypic coefficient of variation (PCV) was slightly higher than genotypic coefficient of variation

(GCV) for all traits, suggesting less environmental effect on trait expression. The highest PCV and GCV values were observed for plot yield (20.46% and 20.33%), followed by grains per spike (16.86% and 16.40%), harvest index (15.98% and 15.62%), tillers per meter (15.51% and 15.26%), and total biomass (13.17% and 12.91%) but days to maturity exhibited the lowest PCV and GCV values (3.58% and 2.52%), suggesting a narrow range of variability for this trait. High GCV and PCV values reflect the presence of exploitable genetic variability and have been associated with effective selection response in yield-related traits. Moderate variability was observed for plant height, days to 50% heading, days to 50% flowering, spike length, and 1000-grain weight, suggesting reasonable scope for genetic improvement (Johnson *et al.*, 1955; Ubale *et al.*, 2025).

Broad-sense heritability estimates ranged from moderate to very high across all traits. High heritability was recorded for plot yield (98.7%), tillers per meter (96.7%), total biomass (96.1%), harvest index (95.5%), grains per spike (94.6%), and 1000-grain weight (94.3%), indicating that these traits are largely governed by genetic factors and that phenotypic selection would be reliable. Similar high heritability estimates for yield and its components have been reported by Singh *et al.* (2020).

The effectiveness of selection is better predicted by the combined assessment of heritability and genetic advance as percent of mean (GAM). High heritability coupled with high GAM was observed for plot yield (41.6%), grains per spike (32.87%), harvest index (31.42%), tillers per meter (30.91%), and total biomass (26.06%). This combination suggests the presence of additive gene action and suggests that direct selection for these traits would be effective in achieving genetic improvement (Johnson *et al.* 1955; Burton and DeVane 1953). In contrast, days to maturity exhibited moderate heritability (49.5%) along with low genetic advance (3.65%), implying the influence of non-additive gene action and environmental factors. Such traits generally respond poorly to simple phenotypic selection and may require alternative breeding strategies.

Correlation analysis

The correlation matrix (Table 4) revealed significant associations among yield and yield-related traits, indicating the degree of relationship between characters. Genotypic correlations were higher in magnitude than phenotypic correlations, suggesting that these associations were largely governed by genetic factors with limited environmental interference.

Plot yield showed strong and highly significant positive correlations showing strong positive associations with harvest index ($r = 0.74$), total biomass ($r = 0.64$), days to 50% flowering ($r = 0.43$), days to 50% heading ($r = 0.42$), and days to maturity ($r = 0.37$) at the genotypic level. Corresponding phenotypic correlations were also positive and significant, particularly with harvest index ($r = 0.74$) and total biomass ($r = 0.62$), showing that the genotypes with greater assimilate production and efficient partitioning tend to achieve higher grain yield. Among phenological traits, days to 50% heading, days to 50% flowering, and days to maturity exhibited strong and highly significant positive correlations with each other ($r = 0.91$ – 1.05), reflecting their close developmental relationships. Positive and significant correlations of flowering and maturity traits with yield suggest that longer growth duration contributed to enhanced biomass accumulation and grain yield. Comparable relationships among the traits have been reported by Saini *et al.* (2024).

Grains per spike showed a significant positive association with plot yield ($r = 0.29$) and harvest index ($r = 0.34$) at the genotypic level, indicating its direct contribution to yield formation. However, grains per spike exhibited a strong negative genotypic correlation with 1000-grain weight ($r = -0.44$), suggesting a compensatory relationship between grain number and grain weight. This trade-off between yield components has been widely documented in wheat and highlights the need for balanced selection strategies (Puri *et al.*, 2025). Total biomass was positively and significantly correlated with plot yield, days to maturity, days to flowering, and spike length, indicating that increased vegetative growth and longer spikes contributed to greater yield potential. Tillers per meter showed a positive association with total biomass but exhibited a weak and non-significant relationship with plot yield, suggesting that tiller number alone may not directly enhance yield unless supported by improved spike fertility and grain filling. These relationships are valuable for indirect selection, as improvement in one trait may result in simultaneous gains in correlated traits.

Path analysis

Path coefficient analysis (Table 5) partitioned the correlation coefficients into direct and indirect effects to better understand the contribution of individual traits to plot yield at both genotypic and phenotypic levels. The magnitude of residual effects was low at both the genotypic (0.0542) and phenotypic (0.0374) levels, indicating that the traits included in the analysis explained most of the variation in plot yield.

At the genotypic level, harvest index exerted the highest positive direct effect on plot yield (0.7527), followed by total biomass (0.6791), days to 50% heading (0.1061), plant height (0.0305), and tillers per meter (0.0176). At the phenotypic level, harvest index (0.8149) and total biomass (0.6813) again showed the strongest positive direct effects on plot yield, confirming their major role in yield determination. These results indicate that genotypes with higher biomass production and more efficient partitioning of assimilates towards grains tend to produce higher yields. Similar findings highlighting harvest index and biomass as primary determinants of grain yield have been reported in wheat by Dvivedi *et al.* (2023).

Days to maturity exhibited a negative direct effect on plot yield at the genotypic level (−0.1490), although its indirect effects via total biomass (0.3202) and harvest index (0.0680) were positive, resulting in an overall positive correlation with yield. This suggests that while prolonged maturity duration alone may not directly enhance yield, its contribution through increased biomass accumulation can be beneficial under favourable environments. Grains per spike showed a small negative direct effect on plot yield at both genotypic (−0.0026) and phenotypic (−0.0363) levels; however, its substantial positive indirect effect via harvest index (0.2590 at G and 0.3047 at P) contributed to its positive association with yield. This indicates that grain number influences yield mainly through its effect on assimilate partitioning rather than through a direct contribution. Similar relationships among yield components have been reported by Singh *et al.* (2021).

Plant height and spike length exhibited low direct effects on plot yield at both levels, but their indirect effects through total biomass and harvest index were positive, suggesting that these traits influence yield indirectly by contributing to overall plant vigour and biomass production. Tillers per meter showed a positive direct effect on yield, though its indirect negative effect via harvest index reduced its overall

contribution, indicating that excessive tillering may not always translate into higher yield unless supported by improved assimilate allocation. The path analysis revealed that harvest index and total biomass are the most important contributors to plot yield due to their strong direct effects at both genotypic and phenotypic levels.

Conclusion

The present investigation revealed substantial genetic variability among the genotypes, indicating a wide scope for genetic improvement. Genotypic effects accounted for most of the observed variation, with relatively low environmental influence indicating stable expression of traits under the experimental conditions. The presence of significant differences for all characters confirms the effectiveness of the germplasm and supports its utility in wheat breeding programmes. High heritability estimates coupled with high genetic advance as a percentage of mean for key traits such as plot yield, tillers per meter, grains per spike, harvest index, and total biomass indicate the effect of additive gene action. These traits are highly responsive to direct phenotypic selection and can be effectively utilized to achieve yield improvement. Correlation analysis revealed strong positive associations of plot yield with harvest index and total biomass, showing the importance of assimilate production and efficient partitioning in yield determination. Positive relationships between phenological traits show their close developmental linkage and contribution to biomass accumulation. Path coefficient analysis reinforced these findings by identifying harvest index and total biomass as the most influential traits due to their strong positive direct effects on grain yield, while other traits contributed mainly through indirect effects. The high-yielding genotypes identified, namely 5009, 5029, 5011, and 5007, represent promising genetic resources for future breeding efforts. Strategic utilization of these genotypes, along with emphasis on the identified key traits, can facilitate the development of high-yielding.

Table 1: Analysis of variances (ANOVA) for eleven characters in wheat.

S.V.	d. f.	PH	DH	DF	DM	SL	T/m	G/S	TGW	TB	HI	PY
Replication	2	3.69	0.28	16.16	7.31	0.02	8.83	0.60	2.35	0.02	0.00023	0.00129
Genotype	50	60.29**	26.76**	34.89**	26.58**	1.41**	621.05**	133.21**	59.84**	1.91**	0.01288**	0.80515**
Error	100	4.72	2.79	3.25	6.75	0.08	6.9	2.47	1.19	0.03	0.00021	0.00354

*and ** represent 5% and 1% level of significance, respectively.

PH = Plant height (cm); DH = Days to 50% heading; DF = Days to 50% flowering; DM = Days to maturity; SL = Spike length (cm); T/m = Tillers per meter; G/S = Grains per spike; TGW = 1000-grain weight (g); TB = Total biomass (kg); HI = Harvest index; PY = Plot yield (kg)

Table 2 : Performance evaluation of wheat genotypes across eleven morphological traits.

Genotype	PH	DH	DF	DM	SL	T/m	G/S	TGW	TB	HI	PY
5001	78.75	59.33	63.00	95.67	9.60	71.67	53.33	41.09	4.99	0.43	2.13
5002	94.25	70.00	76.33	103.33	10.85	79.00	50.67	38.55	5.50	0.56	3.08
5003	84.75	60.00	65.33	101.33	10.35	95.67	40.33	39.10	5.23	0.34	1.80
5004	88.50	63.67	70.67	104.00	11.35	77.67	47.33	35.15	6.31	0.52	3.28
5005	84.00	68.33	75.00	105.67	10.05	106.33	42.00	39.18	6.09	0.31	1.91
5006	86.50	61.00	65.33	100.33	10.65	103.33	45.00	42.15	6.75	0.36	2.46
5007	88.50	63.00	67.67	102.67	11.45	101.00	47.00	34.52	7.27	0.47	3.40
5008	79.25	60.67	65.00	102.33	10.45	94.33	33.33	38.14	6.24	0.33	2.04
5009	90.75	63.00	69.67	104.67	11.15	90.00	50.00	42.88	7.26	0.50	3.62
5010	88.75	65.33	71.33	102.67	10.55	84.00	41.00	45.82	6.76	0.46	3.08
5011	94.25	67.33	72.33	102.00	12.45	95.00	47.00	35.74	7.22	0.48	3.44
5012	91.25	68.67	74.67	104.67	10.90	92.67	44.67	37.88	6.92	0.49	3.39
5013	94.00	63.00	69.33	103.00	11.50	90.67	42.00	44.01	6.46	0.46	2.96
5014	85.00	61.67	68.00	101.00	10.10	92.00	39.67	39.67	5.81	0.40	2.35
5015	95.50	63.67	70.33	101.67	10.90	84.33	37.33	42.05	5.87	0.43	2.55
5016	90.75	63.00	70.33	105.33	11.95	105.33	47.33	36.92	7.21	0.44	3.15
5017	95.25	64.00	71.00	103.00	11.90	76.67	47.33	42.28	6.29	0.38	2.40
5018	96.25	63.00	70.67	104.67	12.20	125.67	52.33	34.72	6.68	0.40	2.67
5019	90.50	64.00	70.33	105.67	12.00	84.33	50.33	33.51	4.02	0.50	2.01
5020	89.00	62.33	68.33	103.67	10.85	86.67	51.33	32.81	6.44	0.40	2.59
5021	86.25	60.00	66.33	99.67	12.05	90.67	45.00	41.55	6.97	0.36	2.54
5022	89.25	61.33	68.00	102.67	12.05	89.00	41.00	39.81	6.64	0.41	2.70
5023	87.25	64.00	69.67	104.33	10.25	112.33	43.33	34.49	6.18	0.37	2.28
5024	87.75	62.67	69.33	102.00	10.55	106.00	46.67	30.92	6.72	0.50	3.38
5025	92.75	62.00	67.00	99.33	11.40	72.00	37.33	35.16	6.21	0.33	2.02
5026	92.75	64.00	70.33	102.67	12.25	105.33	37.33	47.50	6.67	0.37	2.47
5027	88.75	61.33	67.33	103.67	9.90	117.67	39.67	33.81	6.33	0.36	2.26
5028	81.25	60.33	67.00	101.33	10.20	91.00	35.00	39.93	6.98	0.36	2.48
5029	85.25	63.67	70.67	104.33	10.40	99.33	38.00	40.25	5.83	0.62	3.60
5030	78.50	58.00	63.33	96.67	10.00	76.67	43.67	38.00	3.93	0.44	1.73
5031	84.00	61.67	69.67	102.33	10.55	83.00	33.00	43.14	6.85	0.41	2.78
5032	88.00	60.67	66.00	97.67	10.55	89.67	26.00	34.67	6.91	0.39	2.72
5033	88.25	64.33	72.00	103.67	10.80	107.33	35.00	46.42	6.66	0.39	2.60
5034	88.00	65.00	70.67	106.67	10.35	82.67	28.67	41.48	6.82	0.36	2.43
5035	90.25	63.00	69.67	102.33	11.40	84.33	43.00	35.35	6.55	0.34	2.21
5036	83.50	61.33	68.00	103.33	10.60	109.00	39.00	37.62	6.20	0.33	2.06
5037	91.75	61.00	65.67	98.00	11.30	95.33	32.33	39.78	4.78	0.36	1.71
5038	91.00	66.00	72.33	104.67	10.65	87.00	31.00	43.35	5.77	0.42	2.40
5039	91.50	64.33	72.00	104.67	10.90	69.00	35.00	45.09	6.15	0.45	2.78
5040	90.00	63.00	70.67	104.67	11.45	71.33	37.00	47.05	5.78	0.41	2.35
5041	83.75	59.67	65.00	99.67	11.35	107.00	35.67	47.78	6.25	0.34	2.11
5042	86.75	62.33	68.00	101.00	11.00	97.00	34.67	47.07	6.13	0.50	3.08
5043	88.50	62.33	67.67	103.67	11.15	100.33	31.67	42.79	5.63	0.37	2.10
5044	80.25	60.00	64.67	98.00	10.70	111.33	31.00	42.09	5.46	0.46	2.51
5045	84.25	51.33	58.33	92.33	10.70	67.33	39.33	43.29	4.29	0.42	1.82
5046	80.50	58.67	62.67	97.33	10.50	99.00	41.67	34.94	6.11	0.51	3.08
5047	92.00	62.67	68.00	100.33	11.25	111.00	38.33	39.88	5.96	0.38	2.24
5048	85.25	60.67	66.67	99.00	10.20	125.67	41.67	38.41	6.16	0.42	2.56
5049	93.50	67.00	74.67	107.00	11.70	117.33	31.67	49.03	6.39	0.40	2.58
5050	87.00	63.67	70.00	103.67	10.70	91.33	31.00	40.22	5.47	0.37	2.00
5051	88.00	60.67	66.33	99.00	10.20	80.33	39.67	45.72	4.84	0.37	1.81
Mean	88.07	62.58	68.67	102.02	10.95	93.78	40.25	40.05	6.14	0.42	2.54
Range	Min.	78.50	51.33	58.33	92.33	9.60	67.33	26.00	30.92	0.31	1.71
	Max.	96.25	70.00	76.33	107.00	12.45	125.67	53.33	49.03	0.62	3.62
CD (5%)	3.52	2.70	2.92	4.21	0.47	4.26	2.54	1.77	0.26	0.02	0.10
CV (%)	2.47	2.67	2.63	2.55	2.64	2.80	3.90	2.72	2.60	3.51	2.34

PH = Plant height (cm); DH = Days to 50% heading; DF = Days to 50% flowering; DM = Days to maturity; SL = Spike length (cm); T/m = Tillers per meter; G/S = Grains per spike; TGW = 1000-grain weight (g); TB = Total biomass (kg); HI = Harvest index; PY = Plot yield (kg); CD = Critical Difference

Table 3 : Estimates of variance components for eleven quantitative characters.

Trait	PV	GV	EV	PCV (%)	GCV (%)	H ² _b (%)	GA	GAM
Plant height	23.24	18.53	4.72	5.47	4.89	79.7	7.92	8.99
Days to 50% heading	10.78	7.99	2.79	5.25	4.52	74.1	5.01	8.01
Days to 50% flowering	13.80	10.55	3.25	5.41	4.73	76.4	5.85	8.52
Days to maturity	13.36	6.61	6.75	3.58	2.52	49.5	3.72	3.65
Spike length	0.53	0.44	0.08	6.63	6.08	84.1	1.26	11.48
Tillers/m	211.62	204.72	6.90	15.51	15.26	96.7	28.99	30.91
Grains/spike	46.05	43.58	2.47	16.86	16.4	94.6	13.23	32.87
1000 grain weight	20.74	19.55	1.19	11.37	11.04	94.3	8.84	22.08
Total biomass	0.65	0.63	0.03	13.17	12.91	96.1	1.6	26.06
Harvest index	0.00440	0.00419	0.00021	15.98	15.62	95.5	0.13	31.42
Plot yield	0.2707	0.2672	0.00354	20.46	20.33	98.7	1.06	41.6

PV: Phenotypic variance; GV: Genotypic variance; EV: Environmental variance; PCV: Phenotypic coefficient of variance; GCV: Genotypic coefficient of variance; H²_b(%): Heritability; GA: Genetic advance; GAM: Genetic advance as % of mean

Table 4 : Genotypic and phenotypic association among yield and yield-related characters in wheat.

Trait	PH	DH	DF	DM	SL	T/m	G/S	TGW	TB	HI	PY
PH	1	0.6209**	0.6633**	0.6017**	0.695**	-0.0029	0.1681	0.0368	0.2857*	0.12	0.2872*
DH	0.4915**	1	1.0504**	0.9589**	0.2748	0.1236	0.1137	0.0116	0.3822**	0.2267	0.4209**
DF	0.5437**	0.8155**	1	0.9148**	0.2933*	0.0943	0.0945	0.0779	0.3915**	0.2387	0.4336**
DM	0.3146*	0.5640**	0.6263**	1	0.3404*	0.2356	0.0657	-0.0042	0.4715**	0.0903	0.3685**
SL	0.5947**	0.1787	0.2787*	0.1954	1	0.0468	0.2137	0.0628	0.306*	0.0795	0.2561
T/m	-0.0093	0.0980	0.0778	0.1735	0.0465	1	-0.0467	-0.1346	0.3133*	-0.1492	0.0957
G/S	0.1525	0.0868	0.0866	0.0334	0.2008	-0.0543	1	-0.4425**	0.0502	0.3439*	0.2929*
TGW	0.0399	0.0058	0.0720	0.0077	0.0634	-0.1214	-0.424 **	1	-0.0671	-0.1012	-0.1158
TB	0.2408	0.3232*	0.3391*	0.3480*	0.2727*	0.3027*	0.0344	-0.0669	1	-0.0281	0.6414**
HI	0.1043	0.2054	0.1989	0.0477	0.0693	-0.1421	0.3391*	-0.0929	-0.0589	1	0.7447**
PY	0.2495	0.3733**	0.3748**	0.2615*	0.2310	0.0946	0.2857*	-0.1109	0.6241**	0.7387**	1

*and ** represent significant at 5 (%) and 1 (%) level of significant, respectively.

Note: Values above the diagonal represent genotypic correlations, while those below the diagonal represent phenotypic correlations. PH = Plant height (cm); DH = Days to 50% heading; DF = Days to 50% flowering; DM = Days to maturity; SL = Spike length (cm); T/m = Tillers per meter; G/S = Grains per spike; TGW = 1000-grain weight (g); TB = Total biomass (kg); HI = Harvest index; PY = Plot yield (kg)

Table 5 : Direct and indirect effects of ten characters on plot yield in wheat at genotypic (G) and phenotypic (P) levels.

Traits	Level	Direct effect	PH	DH	DF	DM	SL	T/m	G/S	TGW	TB	HI
PH	G	0.0305	0.0305	0.0659	0.0067	-0.0897	-0.0102	-0.00005	-0.00044	0.00016	0.1941	0.0904
	P	0.0269	0.0269	-0.0074	-0.0186	0.00044	-0.00558	-0.00019	-0.00553	0.00027	0.164	0.0953
DH	G	0.1061	0.0189	0.1061	0.0106	-0.1429	-0.0041	0.00218	-0.00030	0.00005	0.2596	0.1707
	P	-0.0150	0.0132	-0.0150	-0.0279	0.00079	-0.00168	0.00198	-0.00315	0.00004	0.22	0.1852
DF	G	0.0101	0.0202	0.1115	0.0101	-0.1512	-0.0043	0.00166	-0.00025	0.00034	0.2659	0.1797
	P	-0.0343	0.0146	-0.0122	-0.0343	0.00088	-0.00262	0.00157	-0.00314	0.00049	0.231	0.1783
DM	G	0.1490	0.0183	0.1018	0.0102	-0.1490	-0.0050	0.00415	-0.00017	-0.00002	0.3202	0.068
	P	0.0141	0.0085	-0.0084	-0.0215	0.00141	-0.00183	0.0035	-0.00121	0.00005	0.237	0.0444
SL	G	-0.0147	0.0212	0.0292	0.003	-0.0507	-0.0147	0.00082	-0.00056	0.00027	0.2078	0.0599
	P	-0.00938	0.016	-0.0027	-0.0096	0.00027	-0.00938	0.00094	-0.00728	0.00043	0.1859	0.0559
T/m	G	0.0176	-0.0001	0.0131	0.001	-0.0351	-0.00069	0.0176	0.00012	-0.00058	0.2127	-0.1124
	P	0.02016	-0.00025	-0.00147	-0.00267	0.0035	-0.00044	0.02016	0.00197	-0.00082	0.2061	-0.1282
G/S	G	-0.0026	0.0051	0.0121	0.001	-0.0098	-0.0032	-0.00082	-0.0026	-0.00191	0.0341	0.259
	P	-0.0363	0.0041	-0.0013	-0.00297	-0.00121	-0.00728	-0.00109	-0.0363	-0.00287	0.0234	0.3047
TGW	G	0.00431	0.0011	0.0012	0.0008	0.0006	-0.00093	-0.00237	0.00117	0.00431	-0.0456	-0.0762
	P	0.00677	0.0011	-0.0001	-0.00247	0.00005	-0.00060	-0.00245	0.01538	0.00677	-0.0455	-0.0831
TB	G	0.6791	0.0087	0.0406	0.004	-0.0703	-0.0045	0.00552	-0.00013	-0.00029	0.6791	-0.0212
	P	0.6813	0.00648	-0.00484	-0.01162	-0.00124	-0.00256	0.0061	-0.00124	-0.00045	0.6813	-0.0502
HI	G	0.7527	0.0037	0.0241	0.0024	-0.0135	-0.0012	-0.00263	-0.00091	-0.00044	-0.0191	0.7527
	P	0.8149	0.00286	-0.00309	-0.00681	-0.00121	-0.00058	-0.00288	-0.01233	-0.00063	-0.0381	0.8149
Residual (G) = 0.0542, Residual (P) = 0.0374												

PH = Plant height (cm); DH = Days to 50% heading; DF = Days to 50% flowering; DM = Days to maturity; SL = Spike length (cm); T/m = Tillers per meter; G/S = Grains per spike; TGW = 1000-grain weight (g); TB = Total biomass (kg); HI = Harvest index; PY = Plot yield (kg)

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