

Genetic Variability and Trait Association Studies for Yield Related Traits in Bread Wheat (*Triticum aestivum* L.)

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DOI: [https://doi.org/10.63001/tbs.2026.v21.i02.S.I\(2\).pp21404-21417](https://doi.org/10.63001/tbs.2026.v21.i02.S.I(2).pp21404-21417)

KEYWORDS

Bread wheat,
genetic variability,
heritability,
genetic advance,
correlation, path coefficient,
grain yield.

Received on:

25-04-2026

Accepted on:

11-05-2026

Published on:

22-05-2026

Abstract

The present investigation was carried out to assess genetic variability and trait association for yield and yield-contributing traits in bread wheat (*Triticum aestivum* L.). A total of 296 wheat genotypes, including 292 lines from the Wheat Association Mapping Initiative (WAMI) spring wheat panel and four check varieties, were evaluated during Rabi 2024–2025 at the Main Experiment Station, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya, Uttar Pradesh. The experiment was laid out in an Augmented Randomized Complete Block Design with six blocks. Observations were recorded for days to anthesis, days to maturity, plant height, spike length, spikelets per spike, grains per spike, test weight and grain yield per plant. Analysis of variance revealed significant differences among genotypes for most of the studied traits, indicating the presence of substantial genetic variability. Descriptive statistics showed a wide range for plant height, grains per spike, test weight and grain yield per plant, suggesting considerable phenotypic diversity in the experimental material. The highest GCV and PCV were recorded for grain yield per plant, followed by grains per spike, spikelets per spike, test weight and spike length. High heritability coupled with high genetic advance was observed for grain yield per plant, grains per spike, spikelets per spike, test weight and spike length, indicating the predominance of additive gene action and good response to selection. Correlation analysis showed that grain yield per plant had significant positive association with spike length, spikelets per spike, grains per spike and test weight. Path coefficient analysis further confirmed that spike length had the highest positive direct effect on grain yield per plant, followed by spikelets per spike, test weight and grains per spike. Therefore, these traits may be considered as important selection criteria for improving grain yield in bread wheat breeding programmes.

Introduction

Bread wheat (*Triticum aestivum* L.) is one of the most important cereal crops grown worldwide and plays a central role in global food and nutritional security. It is an allohexaploid species with chromosome number $2n = 6x = 42$ and belongs to the family Poaceae. Wheat is widely cultivated across diverse agro-climatic regions due to its

adaptability, nutritional value and importance as a staple food crop. In India, wheat is the second most important cereal crop after rice and contributes substantially to national food security. However, increasing population pressure, climate variability, disease incidence and environmental stresses continue to limit wheat productivity, creating

a continuous need for the development of high-yielding and stable wheat genotypes (Yadav et al., 2025; Nikhil et al., 2025).

Grain yield in wheat is a complex quantitative trait governed by several component characters and influenced by both genetic and environmental factors. Traits such as days to flowering, days to maturity, plant height, spike length, spikelets per spike, grains per spike, thousand grain weight, biological yield, harvest index and grain yield per plant contribute directly or indirectly to yield expression. Since direct selection for grain yield alone is often less effective due to its polygenic inheritance and environmental sensitivity, identification of associated yield-contributing traits is essential for improving selection efficiency (Das et al., 2024; Kour et al., 2025; Yadav et al., 2025).

Genetic variability is the basic requirement for any crop improvement programme, as it provides the raw material for selection and development of superior genotypes. The success of a breeding programme largely depends on the magnitude of variability present in the breeding material and the extent to which desirable traits are heritable. Analysis of variance (ANOVA) is commonly used to determine the significance of differences

among genotypes for different quantitative traits. Significant variation among genotypes indicates the presence of useful genetic diversity, which can be further exploited through selection and hybridization (Kour et al., 2025; Balda et al., 2025; Singh et al., 2025).

Descriptive statistics such as mean, range, standard deviation and standard error provide useful information on the extent of phenotypic variation present among genotypes. A wide range for yield and yield-contributing traits indicates the presence of diverse genetic material that may be useful in breeding programmes. Such estimates help in identifying promising genotypes and traits with greater variability for further improvement. Previous studies have reported wide phenotypic variability among wheat genotypes for traits such as plant height, spike length, grains per spike, thousand grain weight, biological yield and grain yield (Balda et al., 2025; Vijeth et al., 2025; Nikhil et al., 2025).

The estimation of genetic parameters, including genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance, is important for understanding the nature and magnitude of genetic control over different

traits. PCV values are generally higher than GCV values because phenotypic expression is influenced by both genetic and environmental factors. A narrow difference between GCV and PCV suggests lower environmental influence, whereas a wider difference indicates higher environmental effect on trait expression. High heritability coupled with high genetic advance indicates the predominance of additive gene action and suggests that selection based on phenotypic performance may be effective (Nikhil et al., 2025; Kour et al., 2025; Vijeth et al., 2025).

Correlation analysis is an important biometrical tool used to determine the strength and direction of association among different traits. It helps breeders identify traits that are positively or negatively associated with grain yield and can therefore be used as indirect selection criteria. Positive correlation of grain yield with traits such as grains per spike, spike length, thousand grain weight, biological yield and harvest index indicates that improvement in these traits may contribute to higher yield. On the other hand, negative correlations among traits indicate possible trade-offs that should be considered during selection (Das et al., 2024; Kour et al., 2025; Yadav et al., 2025).

Morphological and yield-related traits such as days to anthesis, days to maturity, plant height, spike length, number of spikelets per spike, number of grains per spike, thousand grain weight, and grain yield play an important role in determining the overall performance and yield potential of wheat genotypes. Evaluation of these traits helps in identifying the extent of phenotypic variability and selecting superior genotypes for breeding programmes. Since grain yield is a complex quantitative character and is influenced by several component traits, the study of morphological variability and trait association provides useful information for effective selection. Earlier studies also reported that yield-contributing traits such as spike length, grains per spike, productive tillers, thousand grain weight, biological yield and harvest index showed significant association with grain yield and can be used as important selection criteria for wheat improvement (Das et al., 2024; Kour et al., 2025; Yadav et al., 2025; Nikhil et al., 2025).

In wheat breeding, the combined use of ANOVA, descriptive statistics, genetic variability parameters and correlation analysis provides a strong basis for identifying important traits and superior genotypes. These biometrical approaches

help in understanding the extent of variability, inheritance pattern and association among yield-contributing traits. Therefore, the present investigation was undertaken to assess analysis of variance, descriptive statistics, genetic parameters and correlation among yield and yield-contributing traits in bread wheat genotypes. The information generated from this study will help in identifying useful selection criteria for improving grain yield and related traits in wheat breeding programmes.

Material and Method:

Experimental Material and Site

The present investigation was conducted using 296 bread wheat (*Triticum aestivum* L.) genotypes, comprising 292 diverse lines from the Wheat Association Mapping Initiative (WAMI) spring wheat panel along with four check varieties, namely HD-2967, HD-3086, DBW-252 and DBW-187. The field experiment was carried out during the Rabi season of 2024–2025 at the Main Experiment Station, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya, Uttar Pradesh, India. The experimental site is located at 26.261276° N latitude and 81.824622° E longitude, with an altitude of approximately 101 m above mean sea level.

The soil of the experimental field was nearly neutral, with a pH of about 7.4.

The experiment was laid out in an Augmented Randomized Complete Block Design (Augmented RCBD). The material was divided into six blocks. Blocks 1 to 5 consisted of 48 test genotypes along with four check varieties in each block, while Block 6 consisted of 52 test genotypes along with the same four checks. Each genotype was sown in a single row of 3.0 m length, maintaining a spacing of 20 cm between rows and 5 cm between plants. The crop was raised by following the recommended agronomic practices of the region to ensure proper crop growth and development.

Observations Recorded

Observations were recorded from five randomly selected plants from each plot for all traits, except days to 50% anthesis and days to maturity, which were recorded on a plot basis. Days to 50% anthesis were recorded when approximately 50% of the plants in a genotype showed flowering, while days to maturity were recorded when the plants of a genotype reached full physiological maturity.

Plant height was measured in centimetres from the base of the plant to the tip of the tallest spike, excluding awns. Spike

length was measured in centimetres from the base of the spike to its tip. The number of spikelets per spike was counted manually from the selected spikes. Similarly, the number of grains per spike was recorded after threshing each selected spike separately. For thousand grain weight, 100 grains were weighed and the obtained value was multiplied by ten to express it as 1000-grain weight in grams. Grain yield per plant was recorded in grams by weighing the grains obtained from each selected plant after drying the grains to approximately 13% moisture content.

The recorded observations were used to evaluate the extent of variation among wheat genotypes and to determine the contribution of different agronomic traits toward grain yield.

Statistical Analysis

The recorded data were analysed using R statistical software (version 4.3.2) in the RStudio environment. Analysis of variance (ANOVA) was performed to test the significance of variation among the wheat genotypes following the standard procedure of experimental design and analysis (Box, 1980). Since the experiment was conducted in an Augmented Randomized Complete Block Design, adjusted means were

estimated according to the method described by Federer (1965), and genotypic differences were tested using appropriate F-tests.

The extent of variability among the genotypes was estimated through phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) as suggested by Burton and Devane (1953). Broad-sense heritability (H^2) was estimated following Hanson et al. (1956), while genetic advance as percent of mean was calculated according to Johnson et al. (1955). These parameters were used to assess the magnitude of genetic variability and the expected response to selection.

To understand the association among yield and yield-contributing traits, phenotypic correlation coefficients were estimated using the method proposed by Al-Jibouri et al. (1958), based on the adjusted mean values. Further, path coefficient analysis was performed following Dewey and Lu (1959) to partition correlation coefficients into direct and indirect effects, which helped to identify the relative contribution of individual traits toward grain yield in bread wheat.

Result:

Analysis of variance

Analysis of variance revealed significant differences among wheat genotypes for most of the studied traits, indicating the presence of sufficient variability in the experimental material (Table 1). The mean sum of squares due to treatments eliminating blocks was significant for days to anthesis (DTA: 7.84*) and highly significant for plant height (PH: 82.37**), spike length (SL: 1.47**), number of spikelets per spike (SPLT: 6.28**), number of grains per spike (GN: 55.87**), test weight (TW: 29.05**) and grain yield per plant (GYPP: 8.41**). However, days to maturity (DTM: 12.20 ns) showed non-significant variation.

The block effect ignoring treatments was significant for DTM (33.99*) and highly significant for PH (354.34**), SL (2.82**),

SPLT (12.42**), GN (153.30**), TW (115.31**) and GYPP (38.15**), while DTA (7.27 ns) was non-significant. Among the check varieties, highly significant differences were observed for DTA (106.49**), DTM (114.79**), SPLT (9.77**), GN (50.27**) and GYPP (7.43**), whereas PH (9.83 ns), SL (0.39 ns) and TW (3.84 ns) were non-significant.

The source test and test vs. check showed significant variation for DTA (6.83*) and highly significant variation for PH (83.12**), SL (1.48**), SPLT (6.25**), GN (55.93**), TW (29.31**) and GYPP (8.42**), while DTM (11.14 ns) was non-significant. Overall, the results confirmed considerable genetic variability for most yield and yield-contributing traits, suggesting that these traits can be effectively used for selection in wheat improvement programmes.

Table 1. ANOVA for yield and yield-contributing traits in bread wheat

Source	Mean Sum of Squares (MSS)							
	DTA	DTM	PH	SL	SPLT	GN	TW	
Block (ignoring Treatments)	7.27	33.99 *	354.34 **	2.82 **	12.42 **	153.3 **	115.31 **	38.15 **
Treatment (eliminating Blocks)	7.84 *	12.20 ns	82.37 **	1.47 **	6.28 **	55.87 **	29.05 **	8.41 **
Treatment: Check	106.49 **	114.79 **	9.83 ns	0.39 ns	9.77 **	50.27 **	3.84 ns	7.43 **

Treatment: Test and Test vs. Check	6.83 *	11.14 ns	83.12 **	1.48 **	6.25 **	55.93 **	29.31 **	8.42 **
Residuals	3.22	8.95	3.05	0.14	0.27	1.57	1.64	0.12

ns = non-significant; * = significant at 5%; ** = significant at 1%.

DTA = Days to anthesis; DTM = Days to maturity; PH = Plant height; SL = Spike length; SPLT = Spikelets per spike; GN = Grains per spike; TW = Test weight; GYPP = Grain yield per plant

Descriptive statistics

Descriptive statistics showed considerable variation among the wheat genotypes for all the studied yield and yield-contributing traits (Table 2). Days to anthesis (DTA) ranged from 82.10 to 98.43 days, with a mean of 89.60 days, while days to maturity (DTM) varied from 117.94 to 135.19 days, with a mean of 126.07 days. Plant height (PH) showed a wide range from 74.97 to 122.32 cm, with an average value of 97.65 cm, indicating substantial variation for plant stature among the genotypes.

Spike length (SL) ranged from 6.08 to 13.88 cm, with a mean of 10.14 cm. The number of spikelets per spike (SPLT) varied from 12.82 to 27.63, with an average of

18.62, while the number of grains per spike (GN) ranged from 22.83 to 71.51, with a mean value of 45.99. Test weight (TW) also exhibited considerable variability, ranging from 28.00 to 57.20 g, with a mean of 41.75 g. Grain yield per plant (GYPP) ranged widely from 0.62 to 17.32 g, with a mean of 8.52 g.

The wide range observed for plant height, grains per spike, test weight and grain yield per plant indicated the presence of appreciable phenotypic variability among the evaluated wheat genotypes. This variability may be useful for selecting superior genotypes for yield improvement in bread wheat.

Table 2. Descriptive statistics for yield and yield-contributing traits in bread wheat

Trait	Mean	Std. Error	Std. Deviation	Min	Max
DTA	89.6	0.16	2.74	82.1	98.43
DTM	126.07	0.2	3.5	117.94	135.19
PH	97.65	0.55	9.42	74.97	122.32
SL	10.14	0.07	1.22	6.08	13.88
SPLT	18.62	0.15	2.5	12.82	27.63
GN	45.99	0.42	7.3	22.83	71.51

TW	41.75	0.32	5.5	28	57.2
GYPP	8.52	0.17	2.96	0.62	17.32

Genetic parameters

The estimates of genetic parameters revealed substantial variability among the wheat genotypes for most of the studied traits (Table 3). The highest genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were recorded for grain yield per plant (GYPP: 34.14% and 34.38%), followed by grains per spike (GN: 15.64% and 15.87%), spikelets per spike (SPLT: 13.37% and 13.66%), test weight (TW: 13.04% and 13.39%) and spike length (SL: 11.39% and 11.95%). Lower GCV and PCV were observed for days to maturity (DTM: 1.28% and 2.70%) and days to anthesis (DTA: 2.09% and 2.90%), indicating limited variability for these phenological traits.

The difference between GCV and PCV was narrow for most traits, particularly GYPP, GN, SPLT, TW, PH and SL,

suggesting less environmental influence and greater genetic control over these traits. Broad-sense heritability was highest for GYPP (98.62%), followed by GN (97.05%), PH (96.36%), SPLT (95.83%), TW (94.76%) and SL (90.78%). Moderate heritability was observed for DTA (52.20%), whereas DTM showed low heritability (22.67%).

Genetic advance as percent of mean (GAM) was highest for GYPP (69.95%), followed by GN (31.78%), SPLT (27.01%), TW (26.18%), SL (22.38%) and PH (18.64%). Low GAM was recorded for DTA (3.12%) and DTM (1.26%). The combination of high heritability with high genetic advance for GYPP, GN, SPLT, TW and SL indicates the predominance of additive gene action and suggests that these traits may respond effectively to phenotypic selection in wheat breeding programmes.

Table 3. Genetic parameters for yield and yield-contributing traits in bread wheat

Trait	GCV	PCV	ECV	hBS	GA	GAM
DTA	2.09	2.9	2	52.2	2.8	3.12
DTM	1.28	2.7	2.37	22.67	1.59	1.26
PH	9.2	9.38	1.79	96.36	18.2	18.64
SL	11.39	11.95	3.63	90.78	2.27	22.38
SPLT	13.37	13.66	2.79	95.83	5.03	27.01
GN	15.64	15.87	2.73	97.05	14.61	31.78
TW	13.04	13.39	3.06	94.76	10.93	26.18

GYPP	34.14		34.38	4.04	98.62	5.96	69.95
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Pearson correlation analysis

Pearson correlation analysis revealed significant associations among several yield and yield-contributing traits in bread wheat genotypes (Figure.1). Grain yield per plant (GYPP) showed a highly significant positive correlation with spike length (SL: $r = 0.4155^*$), number of spikelets per spike (SPLT: $r = 0.3648^*$), number of grains per spike (GN: $r = 0.3052^*$) and test weight (TW: $r = 0.2038^*$). This indicates that improvement in these traits may contribute to higher grain yield per plant.

Days to anthesis (DTA) showed a significant negative correlation with GYPP ($r = -0.1176^*$), while plant height (PH) also exhibited a significant negative association with GYPP ($r = -0.1252^*$). Days to maturity (DTM) showed a very weak and non-significant correlation with GYPP ($r = -0.0029$), indicating little association of maturity duration with grain yield in the present material.

Among the yield-contributing traits, spike length showed a highly significant positive correlation with spikelets per spike ($r = 0.3284^*$), and significant positive correlations with grains per spike ($r = 0.1240^*$) and test weight ($r = 0.1378^*$). Spikelets per spike also showed a highly significant positive correlation with grains per spike ($r = 0.3313^*$). Plant height showed a highly significant positive correlation with test weight ($r = 0.2416^*$), suggesting that taller genotypes tended to have higher test weight.

The correlation results indicated that spike length, spikelets per spike, grains per spike and test weight were the most important traits positively associated with grain yield per plant. Therefore, these traits may be considered useful selection criteria for improving grain yield in bread wheat breeding programmes.

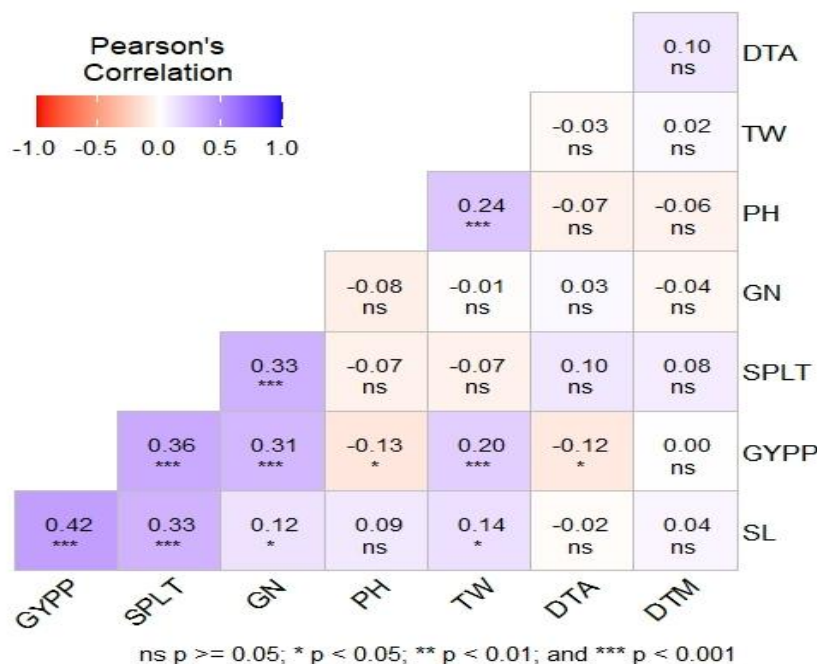


Figure 1. Pearson correlation heatmap of yield traits in bread wheat

Path coefficient analysis

Path coefficient analysis was carried out to partition the correlation coefficients into direct and indirect effects of different yield-contributing traits on grain yield per plant (GYPP) (Table 5). The results revealed that spike length (SL) exerted the highest positive direct effect on GYPP (0.3048), followed by spikelets per spike (SPLT: 0.2232), test weight (TW: 0.2213) and grains per spike (GN: 0.1833). These traits also showed positive correlation with GYPP, indicating that their association with grain yield was mainly due to their direct contribution.

Among the studied traits, days to anthesis (DTA), days to maturity (DTM) and plant height (PH) showed negative direct effects on GYPP, with values of -0.1460, -0.0275 and -0.1877, respectively. Plant height also showed a negative correlation with GYPP (-0.1252), indicating that taller plants may not directly contribute to higher grain yield in the present material.

Spike length showed a strong positive correlation with GYPP (0.4155) and also had the highest positive direct effect (0.3048), suggesting that spike length is an important trait for direct selection. Spikelets per spike also showed a positive correlation with

GYPP (0.3648) along with a positive direct effect (0.2232), indicating its important role in yield improvement. Similarly, grains per spike had a positive direct effect (0.1833) and positive correlation with GYPP (0.3052), suggesting that improvement in grain number may enhance grain yield per plant.

The indirect effects also indicated that spike length contributed positively to GYPP through spikelets per spike (0.0733), grains per spike (0.0227) and test weight (0.0305). Spikelets per spike contributed positively through spike length (0.1001) and grains per spike (0.0607), while grains per spike contributed positively through spikelets per spike (0.0740) and spike length (0.0378).

The coefficient of determination (R^2) was 0.3499, indicating that the traits included in the path analysis explained 34.99% of the total variation in grain yield per plant. The residual effect was 0.8063, suggesting that other traits or environmental factors not included in the present analysis may also influence grain yield.

The path analysis indicated that spike length, spikelets per spike, grains per spike and test weight were the most important traits contributing directly to grain yield per plant. Therefore, these traits may be used as effective selection criteria for improving grain yield in bread wheat breeding programmes.

Table 5. Path coefficient analysis for grain yield per plant in bread wheat

Trait	DTA	DTM	PH	SL	SPLT	GN	TW	GYPP
DTA	-0.1460	-0.0028	0.0141	-0.0052	0.0230	0.0056	-0.0063	-0.1176
DTM	-0.0148	-0.0275	0.0118	0.0124	0.0168	-0.0069	0.0053	-0.0029
PH	0.0109	0.0017	-0.1877	0.0280	-0.0161	-0.0155	0.0535	-0.1252
SL	0.0025	-0.0011	-0.0172	0.3048	0.0733	0.0227	0.0305	0.4155
SPLT	-0.0151	-0.0021	0.0136	0.1001	0.2232	0.0607	-0.0157	0.3648
GN	-0.0045	0.0010	0.0159	0.0378	0.0740	0.1833	-0.0022	0.3052
TW	0.0042	-0.0007	-0.0453	0.0420	-0.0158	-0.0019	0.2213	0.2038

R Square=0.34999, Residual effect=0.8063

Discussion:

The present study showed significant variability among bread wheat genotypes for most yield and yield-contributing traits, indicating that the experimental material had sufficient genetic diversity for selection.

Significant differences for DTA, PH, SL, SPLT, GN, TW and GYPP suggested that these traits can be effectively used in wheat improvement. Similar findings were reported by Nikhil et al. (2025) and Yadav et al.

(2025), who also observed significant genetic variability for yield-related traits in wheat.

Descriptive statistics further confirmed wide phenotypic variation, particularly for plant height, grains per spike, test weight and grain yield per plant. The wide range for GYPP, GN and TW indicated the presence of promising genotypes with better yield potential. Similar variability for yield and its contributing traits was also reported by Das et al. (2024) and Nikhil et al. (2025).

The genetic parameters showed that PCV was slightly higher than GCV for all traits, indicating some environmental influence. However, the narrow difference between GCV and PCV for GYPP, GN, SPLT, TW, PH and SL suggested that these traits were largely controlled by genetic factors. High heritability coupled with high genetic advance for GYPP, GN, SPLT, TW and SL indicated the predominance of additive gene action and good response to selection. These results are in agreement with Das et al. (2024) and Kour et al. (2025).

Correlation analysis revealed that GYPP had positive and significant association with SL, SPLT, GN and TW, indicating that improvement in these traits may increase grain yield per plant. Negative

association of GYPP with DTA and PH suggested that delayed anthesis and taller plant height may not be favourable for yield in the present material. Similar positive associations of grain yield with yield-related traits were reported by Das et al. (2024), Kour et al. (2025) and Yadav et al. (2025).

Path coefficient analysis showed that SL had the highest positive direct effect on GYPP, followed by SPLT, TW and GN. These traits also showed positive correlation with grain yield, confirming their direct contribution to yield improvement. Similar findings were reported by Yadav et al. (2025), who observed positive direct effects of spike-related and grain-related traits on grain yield. The R^2 value of 0.3499 indicated that the studied traits explained 34.99% variation in GYPP, while the residual effect suggested the influence of other traits or environmental factors.

Overall, spike length, spikelets per spike, grains per spike and test weight were identified as important traits for improving grain yield per plant. Therefore, these traits may be used as effective selection criteria in bread wheat breeding programmes.

Conclusion

The present study revealed the presence of considerable genetic variability

among bread wheat genotypes for most yield and yield-contributing traits. Significant differences for DTA, PH, SL, SPLT, GN, TW and GYPP indicated that the experimental material has useful variability for selection. High GCV, PCV, heritability and genetic advance were recorded for grain yield per plant, grains per spike, spikelets per spike, test weight and spike length, suggesting that these traits are mainly governed by genetic factors and may respond effectively to selection. Correlation and path coefficient analyses showed that spike length, spikelets per spike, grains per spike and test weight had positive association and direct contribution toward grain yield per plant. Therefore, these traits can be considered as important selection criteria for improving grain yield in bread wheat breeding programmes.

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