Original Research Article……….

International Journal of Agricultural Invention
(online available at www.agriinventionjournal.com)

International Journal of Agricultural Invention **11(1): 29-35: January-June, 2026**

ISSN: 2456 – 1797 (P)

Evaluation of genetic variability for yield and associated traits in Wheat (*Triticum aestivum* L.)

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ARTICLE INFO

Original Research Article
Received on January 12, 2026
Revised on January 15, 2026
Accepted on February 11, 2026
Published on February 14, 2026

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PUBLICATION INFO
International Journal of Agricultural Invention (IJAI)
RNI: UPENG/2016/70091
ISSN: 2456-1797 (P)
Vol.: 11, **Issue:** 1, **Pages:** 29-35
Journal Homepage URL
http://agriinventionjournal.com/
DOI: 10.46492/IJAI/2026.11.1.5

ABSTRACT

A field experiment was conducted during the 2023-24 cropping season at the Research Farm of J.V. College, Baraut (U.P.), affiliated with Chaudhary Charan Singh University, Meerut, to assess genetic variability for yield and its contributing traits in wheat (*Triticum aestivum* L.). The study involved 25 genotypes procured from IIWBR, Karnal, and IARI, New Delhi, evaluated in a randomized block design with three replications under highland agro-ecological conditions. Observations were recorded on eleven agronomic traits, including phenological, morphological, and yield-related parameters. Analysis of variance revealed significant differences among genotypes for most traits, indicating the presence of substantial genetic variability. Traits such as number of tillers per plant, grains per ear, 1000-grain weight, and harvest index showed strong association with grain yield per plant. The results suggest considerable scope for selection and genetic improvement of wheat genotypes for enhanced productivity under similar agro-climatic conditions.

KEYWORDS
Genetic Variability, Wheat, Yield Components, Randomized Block Design

HOW TO CITE THIS ARTICLE
Singh, K., Nagar, A., Kumar, P., Gupta, R. K., Panwar, A., Tripathi, A., Guru, A. (2026) Evaluation of genetic variability for yield and associated traits in Wheat (*Triticum aestivum* L.), *International Journal of Agricultural Invention,* 11(1): 29-35. DOI: 10.46492/IJAI/2026.11.1.5

Wheat (*Triticum aestivum* L.), a self-pollinated cereal crop from the family Gramineae (Poaceae), plays a pivotal role in global food security by providing nearly 20% of the world's caloric intake. It serves as a major source of carbohydrates, proteins, minerals, and vitamins for millions of people (El-Beltagi *et al*., 2021). Common bread wheat (*Triticum aestivum* L.) and durum wheat (*Triticum durum*) together account for nearly 90% of the world's wheat production. The classification of wheat by (Sakamura, 1918) divided it into diploids (2n=14), tetraploids (2n=28), and hexaploids (2n=42), with bread wheat being a hexaploid species (AABBDD genome) having a haploid DNA content of approximately 1.7×10^{10} base pairs (Bennett and Smith, 1976). Due to increasing demand driven by population growth and shifting dietary preferences, wheat cultivation has expanded into non-traditional and environmentally challenging regions, often characterized by high temperatures and moisture stress (Grote *et al*., 2021).

In India, wheat is the second largest cereal crop after rice, with an area of 30.47 million hectares and a production of 106.84 million tonnes during the 2021-22 rabi season, yielding an average productivity of 3507 kg/ha (Directorate of Economics and Statistics, 2022). Meeting future food demands while maintaining productivity under diverse and changing agro-climatic conditions requires the development of high-yielding, stable, and widely adaptable wheat varieties. This can only be achieved through the effective exploitation of existing genetic variability within wheat germplasm. The extent of genetic variability for yield and its component traits plays a critical role in designing successful breeding programs (Begna, 2021; Khan *et al*., 2013). Understanding the degree of heritability and genetic advance is essential for predicting selection response and improving targeted traits (Memon *et al*., 2007; Mangi *et al*., 2008). Additionally, exploring genetic associations among various yield-contributing traits can help breeders implement effective indirect selection strategies to improve grain yield.

Genetic diversity analysis using biometric tools such as Mahalanobis D^2 statistics (Mahalanobis, 1936) further assists in identifying genetically diverse and promising parents, enhancing the probability of obtaining superior recombinants. High heritability estimates coupled with substantial genetic advance provide an ideal basis for selection, ensuring genetic gain for yield improvement (Waqar-ul-Haq *et al*., 2008). Considering these aspects, the present study was undertaken to assess the magnitude of genetic variability, heritability, and genetic advance; to evaluate the genetic association among important yield-contributing traits; and to determine the genetic diversity among wheat genotypes, with the ultimate goal of identifying potential lines for yield improvement and breeding advancement.

Material and Methods

The field experiment was conducted during the 2023–24 cropping season at the Research Farm of J. V. College, Baraut, Baghpat, affiliated with Chaudhary Charan Singh University, Meerut (U.P.), under highland agro-ecological conditions with mixed farming systems.

The soil type was clay-loam, with an annual rainfall ranging from 750 to 1190 mm and temperature extremes between 30°C and 15°C. The study utilized 25 wheat (*Triticum aestivum* L.) genotypes obtained from IIWBR, Karnal, and IARI, New Delhi. The experiment followed a randomized block design (RBD) with three replications, with each genotype sown in a 1.5 m × 1 m plot at 30 cm row spacing and 8 cm plant spacing. Observations were recorded on five randomly selected plants per plot for 11 agronomic traits including days to 50% heading, days to maturity, plant height (cm), ear length (cm), flag leaf area (cm^2), number of tillers per plant, number of grains per ear, grain yield per plant (g), 1000-grain weight (g), biological yield per plant (g), and harvest index (%), following standard procedures. Data were subjected to analysis of variance (ANOVA) using the General Linear Model (GLM) procedure in SAS software (SAS Institute, 2004), considering genotypes as fixed effects and replications as random. Significant treatment means were separated using the Student-Newman-Keuls (SNK) test at a 5% level of significance. Genetic parameters such as genotypic and phenotypic coefficients of variation (Burton, 1952), heritability (Burton and Devane, 1978), and genetic advance (Johnson *et al*., 1955) were estimated. Genetic divergence was assessed through Principal Component Analysis (PCA) and cluster analysis following the methods of (Beale, 1969; Spark, 1973).

Results and Discussion

Analysis of Variance

Genetic variability is crucial for selecting superior wheat genotypes. Analysis of variance (table 1) among 25 genotypes showed significant differences for most of the 11 studied traits, indicating ample variability for selection and yield improvement. Highly significant variation ($P < 0.001$) was observed for days to 50% heading, days to maturity, plant height, productive tillers per plant, grains per ear, and harvest index, while biological yield and grain yield showed significance at $P < 0.05$. However, spike length, flag leaf area, and 1000-grain weight showed non-significant differences, indicating limited variability. These findings are consistent with earlier reports by (Nukasani *et al*., 2019, Meena *et al*., 2014, Bhushan *et al*., 2022, Majumder *et al*., 2008, Sawant *et al*., 2023, Pandey *et al*., 2021, and Singh *et al*., 2019).

Table 1. ANOVA table showing mean squares for genotypes, error mean square and replication mean squares

Characters	Replication	Treatment	Error
Degree of freedom	2	24	48
Days to 50% flowering	0.25	11.36**	0.81
Days to maturity	1.01	16.55**	3.89
Plant height	3.59	18.76	12.69
Ear length	0.92	1.71*	0.47
Flag leaf area	80.64	47.29**	21.78
No. of tiller/plant	0.77	5.01**	1.76
No. of grain/ear	51.62	138.87**	46.5
Grain yield/plant	27.33	8.72	7.03
1000-grains weight	22.5	27.74**	6.49
Biological yield/plant	130.47	33.48	42.67

Note: Where, df = Degrees of freedom, ns=non-significant, * and **indicates significant and highly significant respectively.

Variability Parameters and per se Performance

On average all the genotypes were day to 50% flowering 92.69 days after sowing. Accession number WDA-30 (99.00) was late in day to 50% flowering as compared to the rest accessions (Table 2). High variability was observed among genotypes tested for days to 50% flowering, days to maturity. On average genotypes were taken 91-99 and 8 days to flower, mature respectively. All genotypes were matured on average of 129.39 and half days after sowing, for the genotypes were 38 days after flowering. Genotypes like HD-2985, DBW-369, (91.00), HD-3043, DBW-107 (91.67), WB-2 (92.00) and WH-1021 (92.67) earlier day to 50% flowering the other genotypes.

Genotype WDA-30 (99.00) is the late day to 50% flowering one among the sown genotypes. DBW-369 is the earliest genotype to give day to maturity among the other genotypes and HD-3043 (133.00) is the one that gave day to maturity late. Genotype DBW-370 (91.13) lowest plant height than the other genotypes and WDA-30 (101.07) highest plant height as compared to the rest genotypes tested. Low coefficient of variation was recorded for days to 50% flowering (1.97), days to maturity (4.32), plant height (0.001). Very wide ranges were recorded for days to 50% flowering (91.00-99.00), days to maturity (123.67-133.00) and plant height (91.13-101.07) in this study. Highly significant differences were observed among wheat genotypes for spike length, whereas differences for flag leaf area were non-significant (table 3).

Table 2. **Mean performance of three traits recorded as affected by genotypes**

Genotypes	Day to 50% Flowering	Day to Maturity	Plant Height
HD3043	91.67	133.00	98.40
DBW107	91.67	130.00	99.80
PBW527	93.33	127.67	95.87
PBW596	91.67	132.00	98.60
WB2	92.00	130.33	97.53
HD2985	91.00	127.00	99.53
PBW723	91.67	127.33	98.07
HS542	91.67	131.33	95.93
PBW725	94.00	129.33	93.87
WH1021	92.67	126.00	95.07
WH1402	92.33	130.33	96.80
HI1665	91.67	131.00	95.60
PBW677	91.33	131.00	98.27
DBW371	91.67	132.00	98.13
GW366	91.33	131.00	96.87
DBW370	94.00	127.33	91.13
VL907	92.00	130.00	93.80
HD3386	93.67	127.67	99.87
DBW369	91.00	123.67	100.67
HD3086	92.67	132.67	100.20
HD3226	92.33	131.33	99.93
DBW222	92.67	128.33	99.60
WDA7028	92.33	129.33	96.13
WDA30	99.00	126.00	101.07
HTWYT46	98.00	129.00	100.13
Mean	92.69	129.39	97.63
C.V.	0.97	1.52	3.65
S.E.	0.52	1.14	2.06
C.D. 5%	1.48	3.24	-
C.D. 1%	1.97	4.32	-
Min	91.00	123.67	91.13
MAX	99.00	133.00	101.07

The average spike length was 10.95 cm, ranging from 8.57 to 11.99 cm, with a coefficient of variation (CV) of 6.25%. Relatively longer spikes were recorded in HD-2985 (11.99 cm), HD-3043 (11.69 cm), and DBW-107 (11.43 cm), while the shortest spikes occurred in HD-3386 (8.57 cm), PBW-527 (9.72 cm), and WH-1021 (9.90 cm). The CV for flag leaf area was 18.35%. Highly significant differences were also found among genotypes for most yield-related traits including 1000-grain weight, biological yield, grain yield, and harvest index. CV values recorded were: number of tillers per plant (19.95%), 1000-grain weight (5.50%), biological yield (22.55%), grain yield (22.21%), and harvest index (7.94%).

Table 3. Mean performance of 8 traits recorded as affected by genotypes, mean with the same letter are not significantly different

Genotypes	Elcm	FLAsqcm	NTPP	NGPE	GYPP	1000GWg	BYPPg	HI%
HD3043	11.69	22.76	7.33	55.67	13.37	45.77	30.80	44.30
DBW107	11.43	28.58	7.67	49.60	12.37	45.42	28.27	43.81
PBW527	9.72	21.32	6.93	47.13	10.99	41.58	26.60	41.23
PBW596	10.94	20.37	6.53	59.47	12.78	45.74	29.53	43.33
WB2	11.09	22.53	6.93	56.20	13.13	45.44	30.27	43.22
HD2985	11.99	26.91	7.33	58.07	11.90	44.31	30.20	40.03
PBW723	11.70	28.78	6.60	54.93	12.63	47.23	29.87	42.37
HS542	11.35	22.29	6.87	50.53	12.20	47.96	27.80	43.88
PBW725	10.63	26.38	8.27	52.67	11.88	44.53	27.60	42.92
WH1021	9.90	19.56	6.80	51.67	11.21	44.93	**28.40**	**39.50**
WH1402	10.78	22.37	8.00	52.87	13.57	43.82	32.73	41.48
HI1665	10.81	19.86	7.73	51.67	12.73	48.50	30.20	42.15
PBW677	11.31	25.01	7.93	50.07	14.86	47.04	34.07	42.46
DBW371	11.06	25.09	6.53	52.87	13.64	45.16	31.47	43.26
GW366	11.16	22.12	6.73	50.07	12.93	46.31	30.40	41.72
DBW370	11.05	30.24	7.47	51.27	14.86	46.27	36.33	40.43
VL907	10.09	30.39	6.73	38.27	8.77	43.33	21.53	38.79
HD3386	8.57	34.54	9.00	34.67	9.99	39.67	29.07	34.60
DBW369	10.85	28.96	6.20	40.83	11.81	46.50	29.27	39.97
HD3086	11.63	27.00	4.67	56.53	12.52	52.51	31.87	40.42
HD3226	11.57	29.43	4.60	57.27	11.46	44.37	27.95	41.06
DBW222	11.50	30.55	3.60	53.60	10.47	47.14	26.07	40.66
WDA7028	10.47	24.36	4.93	36.73	9.19	50.69	26.53	37.58
WDA30	11.50	22.33	4.87	52.47	11.01	51.81	26.00	42.62
HTWYT46	10.83	24.23	5.87	41.27	8.17	51.46	21.33	39.02
Mean	10.95	25.44	6.65	50.25	11.94	46.30	28.97	41.23
C.V.	6.25	18.35	19.95	13.57	22.21	5.50	22.55	7.94
S.E.	0.39	2.69	0.77	3.94	1.53	1.47	3.77	1.89
C.D. 5%	1.12	7.66	2.18	11.19	-	4.18	-	-
C.D. 1%	1.50	10.22	2.90	14.93	-	5.58	-	-
Min	8.57	19.56	3.60	34.67	8.17	39.67	21.33	34.60
MAX	11.99	34.54	9.00	59.47	14.86	52.51	36.33	44.30

Note: Where, **DF**= day to flowering, **DM=** day to maturity, **PH**= plant height, **ELcm=**ear length cm, **FLAsqcm**=flag leaf area, **NTPP=**number of tillers per plant**, NGPE=**number of grains per ear**, BYPP=**biological yield per plant**, GYPP=** grain yield per plant, **1000-** grain weight, **HI**= harvest index

Mondal *et al.* (2007) similarly reported significant variation among wheat accessions for several traits except plant height and ear length. The top five high-yielding genotypes identified were DBW-370 (14.86 g), PBW-677 (14.86 g), DBW-371 (13.64 g), HD-3043 (13.37 g), and WB-2 (13.13 g). A wide range was observed for ear length (8.57-11.99 cm), while narrow ranges were recorded for days to maturity (123.67-133.00), flag leaf area (19.56-34.54), number of tillers per plant (3.60-9.00), number of grains per spike (34.67-59.47), 1000-grain weight (39.67-52.51 g), biological yield per plant (21.33-36.33 g), grain yield per plant (8.17-14.86 g), and harvest index (34.60-44.30%).

Genotypic and Phenotypic Coefficient of Variation (GCV)

Phenotypic and genotypic coefficients of variation (PCV and GCV) quantify variability within a population and are crucial for initiating effective crop improvement programs. In the present study (table 4), PCV values were generally higher than GCV for all characters, indicating a strong influence of environmental factors on trait expression. High GCV was noted for number of grains per ear (11.04), flag leaf area (11.46), and biological yield per plant (6.04), suggesting good prospects for selection. Low GCV was recorded for ear length (5.88), days to maturity (1.59), plant height (1.46), grain yield (6.30), and harvest index (2.90).

Table 4. Genotypic and phenotypic coefficient of variability, heritability, genetic advance, and genetic advance percent of the mean of the 11 traits of Whet varieties

Characters	Heritability (Broad Sense)	Genetic Advance 5 %	Genetic Advance Mean 5%	GCV (%)	PCV (%)
Days to 50% flowering	0.93	3.72	4.02	2.02	2.10
Days to maturity	0.77	3.70	2.86	1.59	1.82
Plant height (cm.)	0.32	1.67	1.71	1.46	2.56
Ear length cm	0.73	1.13	10.33	5.88	6.90
Flag leaf area	0.54	4.41	17.34	11.46	15.61
No. of tiller per plant	0.65	1.73	26.00	15.66	19.44
No. of grain per ear	0.67	9.32	18.55	11.04	13.54
Grain yield /plant	0.20	0.68	5.73	6.30	14.29
1000-grain weight g	077	4.80	10.36	5.75	6.57
Biological yield / plant g	-0.27	-1.89	-6.52	6.04	11.53
Harvest index %	0.29	1.32	3.20	2.90	5.43

These findings align with earlier results by (Singh *et al*., 2019, Ullah *et al*., 2021 and Kumawat *et al*., 2023), who reported substantial variability in traits such as plant height, number of tillers, and flag leaf area. High PCV values were recorded for flag leaf area (15.61), number of grains per ear (13.54), biological yield per plant (11.53), number of tillers per plant (19.44), and grain yield per plant (14.29). Low PCV was observed for days to 50% flowering, days to maturity, and 1000-grain weight, similar to findings by (Fufa *et al*., 2024). A wide difference between PCV and GCV for days to maturity, 1000-grain weight, and harvest index indicates considerable environmental influence. Overall, the high GCV and PCV for yield-related traits demonstrate significant genetic variability, allowing effective selection for improvement, consistent with (Devesh *et al*., 2018). Conversely, traits such as days to flowering, maturity, and 1000-grain weight show limited scope for selection, supporting observations by (Ullah *et al*., 2021).

Heritability

The estimated heritability for the 11 studied characters is presented in table 4. The heritability estimates for the 11 studied wheat traits ranged from 4.26% to 94.3%, indicating varied potential for genetic improvement. According to (Wright, 1991), heritability, along with genetic coefficient of variation (GCV), helps predict genetic advance through selection. Low heritability was observed for grain yield per plant (0.20) and plant height (0.32%) despite high GCV and phenotypic coefficient of variation (PCV), suggesting limited but possible selection response.

Singh and Ceccerelli (1996) noted that traits with heritability above 80% are easily selectable, while those below 40% pose selection challenges. In this study, moderate heritability (40-80%) was recorded for traits like 1000-grain weight (0.77), days to 50% flowering (0.93), days to maturity (0.77), and harvest index (0.29), aligning with (Yadav *et al*., 2003). However, contrary reports by (Fratini *et al*., 2007 and Abebe, 2008) suggest harvest index is highly heritable. Low heritability for biological yield, plant height, and flag leaf area further limits genetic improvement through direct selection.

Genetic Advance

The genetic advance as percent of mean (GAM) at 5% selection intensity is presented in table 5, showing values ranging from 1.67% for plant height to 26.00% for number of tillers per plant. The highest genetic advance was observed for number of grains per ear, followed by number of tillers per plant, which also showed high heritability, PCV, and GCV values. In contrast, traits like grain yield per plant, ear length, plant height, and harvest index recorded low genetic advances due to low variability, as indicated by their low GCV and PCV values. Although heritability estimates provide a basis for selection, they should be interpreted alongside genetic advance, as high heritability does not always correlate with high genetic gain (Yadav *et al*., 2003). Characters like plant height with low GCV and GAM were more environmentally influenced, making selection for such traits less effective.

Table 5. Phenotypic correlation coefficients (rp) of yield and yield related traits for the 11 Wheat genotypes grown at J. V. College Research site, CCS University (in 2023/24 growing season)

Characters	D50%H	DM	PHcm	Elcm	FLAsqcm	PTPP	NGPE	1000GWg	BYPPg	HI%	GYPP
D50%H	1	-0.3	0.136	-0.136	-0.035	-0.233	-0.194	0.374	-0.419	-0.188	-0.427
DM		1	-0.036	0.266	-0.251	0.025	0.342	0.099	0.174	0.428	0.302
PHcm			1	0.296	0.154	-0.376	0.09	0.235	-0.154	-0.015	-0.169
Elcm				1	-0.1	-0.385	0.689*	0.518	0.253	0.644*	0.429
FLAsqcm					1	-0.037	-0.339	-0.263	-0.039	-0.484	-0.204
PTPP						1	-0.127	-0.584	0.36	0.047	0.361
NGPE							1	0.102	0.45	0.709*	0.622*
1000GWg								1	-0.1	0.162	-0.074
BYPPg									1	0.274	0.911**
HI%										1	0.622*

Note: Where, **DF**= day to flowering, **DM=** day to maturity, **PH**= plant height, **ELcm=**ear length cm**, FLAsqcm=**flag leaf area, **NTPP=**number of tillers per plant**, NGPE=**number of grain per ear**, BYPP**=biological yield per plant**, GYPP**= grain yield per plant, **1000-** grain weight, **HI**= harvest index, ***and Significant at 5% and ** 1% respectively**

Table 6. Genotypic correlation coefficients (rg) of yield and yield related traits for the 11 Wheat genotypes grown at J. V. College Research site, CCS University (in 2023/24 growing season)

Characters	D50%H	DM	PHcm	Elcm	FLAsqcm	NTPP	NGPE	1000GWg	BYPPg	HI%	GYPP
D50%H	1	-0.394	0.308	-0.147	-0.077	-0.348	-0.236	0.423	0.957**	-0.382	-1.114
DM		1	0.024	0.297	-0.587	-0.016	0.392	0.193	-0.232	1.071	0.712*
PHcm			1	0.944**	0.676*	-0.740**	0.221	0.624*	-1.052	-0.448	0.661*
Elcm				1	-0.302	-0.568	0.899**	0.656*	-0.226	1.58	0.818**
FLAsqcm					1	-0.204	-0.709*	-0.157	0.726**	-1.135	-1.101
PTPP						1	-0.281	-0.912**	-0.12	0.38	0.459
NGPE							1	0.124	-0.709*	1.56	1.367
1000GWg								1	0.419	0.435	-0.401
BYPPg									1	-1.681	0.127
HI%										1	2.183

Note: Where, **DF**= day to flowering, **DM=** day to maturity, **PH**= plant height, **ELcm=**ear length cm**, FLAsqcm=**flag leaf area, **NTPP=**number of tillers per plant**, NGPE=**number of grain per ear**, BYPP**=biological yield per plant**, GYPP**= grain yield per plant, **1000-** grain weight, **HI**= harvest index, ***** and **Significant at 5%** and **** 1% respectively**

Correlation Coefficients

Grain yield in wheat is influenced by multiple interrelated traits, making genetic variation among these traits crucial for breeders in selecting desirable types. Understanding the relationship between these traits and their association with yield helps establish effective selection criteria (Singh and Ceccarelli, 1996). Correlation analysis, as shown in tables 5 and 6, highlights these associations, with similar findings reported by (Sharma, 1999). Indirect selection for yield improvement is possible by targeting traits that are more heritable and easier to select, emphasizing the importance of understanding trait interrelationships. A significant and positive phenotypic correlation was observed between days to 50% flowering and biological yield, number of grains per ear and grain yield per plant, and ear length with 1000-grain weight (table 6), aligning with findings by (Tigist, 2015).

Additionally, 1000-grain weight showed significant positive correlation with both biological and grain yield. Conversely, plant height had a significant negative phenotypic correlation with flag leaf area, as reported by (Kumar *et al*., 2004, Tigist, 2015 and Vir *et al*., 2001). Plant height also exhibited a highly significant negative genotypic and phenotypic correlation with the number of tillers per plant and a low negative correlation with harvest index. Moreover, plant height was positively correlated with days to 50% flowering and maturity, while grains per ear showed a significant positive genotypic correlation with grain yield per plant, consistent with (Kumar *et al*., 2004), who also reported positive correlations of grain yield with flag leaf area, days to maturity, and plant height. No significant correlation was found between grain yield and days to 50% flowering, biological yield, 1000-grain weight, number of tillers, ear length, flag leaf area, and harvest index.

Additionally, grain yield showed a strong negative genotypic correlation with flag leaf area and harvest index, while number of tillers and biological yield were negatively correlated with yield, and 1000-grain weight had a highly significant negative relationship with biological yield.

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