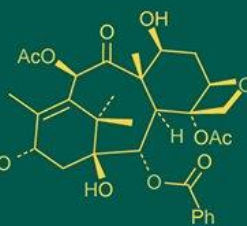
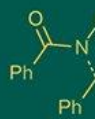


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Variability studies of yield and yield associated traits in wheat genotypes

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Abstract

During the rabi 2020-21 season, a study at Sardarkrushinagar Dantiwada Agricultural University's Agronomy Instructional Farm assessed variability analysis in thirty wheat genotypes using a randomized block design with four replications. Eleven traits were evaluated grain yield per plant, days to heading, days to maturity, plant height, effective tillers per meter, grains per spike, spike length, 1000-grain weight, ear weight, biological yield, and harvest index. ANOVA revealed significant genetic variability across all traits. Phenotypic coefficient of variation (PCV) slightly exceeded genotypic coefficient of variation (GCV), indicating minimal environmental impact. High GCV and PCV were noted for grains per spike and ear weight, with moderate values for grain yield, plant height, and biological yield. Traits like days to heading and grains per spike showed high heritability (>98%) and genetic advance, ideal for selection. Grain yield correlated positively with key traits, and path analysis highlighted effective tillers and 1000-grain weight as major yield contributors.

Keywords: Wheat, GCV, PCV, variability

Introduction

Wheat (*Triticum aestivum* L.), a vital cereal grass from the *Poaceae* family and *Triticum* genus, stands as the world's leading cereal crop. Often hailed as the 'Cereal Monarch' due to its vast cultivation area, exceptional yield potential and significant role in global grain trade, wheat holds a unique place in agriculture. It serves as a primary source of nutrition and energy, forming the basis for diverse products such as bread, chapati, pasta, biscuits, and animal fodder. Globally, wheat is cultivated across 220.4 million hectares, yielding approximately 798.97 million tonnes annually. It supplies roughly 20% of the caloric intake for the global population FAO (2023) ^[13]. In India, wheat spans 30.28 million hectares, producing 102.46 million tonnes DA&FW (2022) ^[39]. As the global population continues to grow, the demand for wheat is steadily rising, underscoring its critical role in food security, it is the second most important food crop in the developing world after rice (Giraldo *et al.*, 2019) ^[14]. Its global significance stems from its adaptability to diverse agroclimatic conditions, underpinning food security in both developed and developing nations. Wheat's genetic variability is a cornerstone of its resilience, enabling breeders to develop varieties tailored to specific environments, yield goals, and disease resistance. This variability manifests in traits like grain yield, plant height, days to maturity, and spike characteristics, offering a rich reservoir for crop improvement. Phenotypic and genotypic diversity among wheat genotypes ensures a broad genetic base, critical for addressing challenges like climate change and evolving pathogens. Genetic diversity in wheat is assessed through morphological traits and molecular tools, revealing differences that guide breeding programs. High heritability and genetic advance in traits such as grain number per spike and tillering capacity indicate strong genetic control, making them prime targets for selection.

The success of crop improvement initiatives hinges on the genetic diversity present within available germplasm (Harlan, 1976; Moose and Mumm, 2008) ^[16, 27], as it provides the raw material for breeding advancements. A thorough evaluation of this diversity enables breeders to select optimal parental lines for developing superior varieties. Greater genetic divergence between parents often leads to enhanced heterosis in their offspring (Joshi and Dhawan, 1966) ^[22], boosting traits like yield and resilience. With this in mind, the current study assesses 30 wheat genotypes to investigate genetic variability, heritability and genetic advance for yield and related traits.

Materials and Methods

The study involved thirty wheat genotypes (Table 1) cultivated during the rabi season of 2020-21 at the Agronomy Instructional Farm, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar. The genotypes were arranged in a randomized block design with four replications. Each genotype was planted in a single-row plot measuring 3.0 m in length, with 22.5 cm between rows and 10 cm between plants within a row. Border rows were included to minimize edge effects. Standard agronomic practices were applied to ensure a healthy and competitive wheat crop. Data were collected from five randomly chosen competitive plants per genotype in each replication, focusing on 11 agro-morphological traits: days to heading, days to maturity, plant height (cm), effective tillers per meter, grains per spike, spike length (cm), 1000-grain weight (g), ear weight (g), biological yield per plant (g), harvest index (%), and grain yield per plant (g). Calculation of harvest index as per the formula given by Donald and Humblin (1976) [9]. Analysis of variance for treatment means was performed using the model outlined by Panse and Sukhatme (1961) [29]. Genotypic and phenotypic coefficients of variation (GCV and PCV) were calculated following Searle's (1961) [33] methodology. Broad-sense heritability (h^2) and genetic advance as a percentage of the mean were determined using Allard's (1960) [4] formulas. Correlation coefficient and path coefficient was calculated as per method suggested by Al-Jibouri *et al.* (1958) [3] and Dewey and Lu (1959) [8], respectively. Statistical software TNAUSTAT was used for analysis the data of the present study.

Results

The analysis of variance (Table 2) revealed highly significant ($p < 0.01\%$) differences among the tested genotypes for all the traits and highest value was estimated for number of effective tillers per meter followed by plant height and days to heading, ear weight was the lowest. This indicated that the selected genotypes were genetically variable and significant amount of variability existed among them.

The Genotypic (GCV) and Phenotypic (PCV) coefficients of variation (Fig. 1) were observed in the experimental material for all the characters studied (Table 3). The higher magnitudes of GCV and PCV were recorded for Ear weight, Number of grains per spike, Grain yield per plant and Number of effective tillers per meter. However, Days to maturity, 1000 grain weight, Harvest index, Plant height, Days to heading and Spike length exhibited least genotypic and phenotypic coefficient of variation. On an average, the higher magnitude of GCV and PCV were recorded for Ear weight (18.41 and 22.18), Number of grains per spike (18.34 and 21.90), Grain yield per plant (11.91 and 17.80) and Number of effective tillers per meter (11.89 and 12.39), respectively, suggesting sufficient variability are available and thus exhibited scope for genetic improvement through selection for all these traits.

The analysis showed a significant gap between Genotypic (GCV) and Phenotypic (PCV) coefficients of variation for harvest index and biological yield per plant compared to other traits, indicating a strong environmental influence on these characteristics. In contrast, minimal differences between PCV and GCV were observed for days to heading, days to maturity, and number of effective tillers per meter,

suggesting that these traits are less affected by environmental factors and their expression is primarily driven by genetic factors.

Heritability reflects the extent to which traits are passed from parents to offspring (Lush, 1949) [24]. In this study, high heritability was observed for Days to heading, Number of effective tillers per meter, grains per spike, Number of grains per spike, and Ear weight with moderate heritability for days to maturity, plant height, spike length, 1000 grain weight, biological yield per plant and grain yield per plant (Table 3).

High heritability alone does not guarantee substantial genetic advance (Fig. 2), as noted by Johnson *et al.* (1955) [21]. Combining heritability with genetic advance provides clearer insights into gene action, as emphasized by Dudley and Moll (1969) [10]. Traits exhibiting high heritability and high genetic advance as a percentage of the mean such as Number of effective tillers per meter, Number of grains per spike and Ear weight indicate strong additive gene action, making them ideal candidates for direct selection.

The correlation analysis revealed strong positive and significant associations between grain yield per plant and traits such as number of effective tillers per meter, number of grains per spike, spike length, ear weight, biological yield per plant, harvest index and 1000-grain weight, while significant negative correlations were observed with days to maturity and plant height (Table 4). Among the component traits, number of grains per spike showed a significant positive correlation with both 1000-grain weight and grain yield per plant. Additionally, grain weight and ear weight exhibited significant positive correlations with yield, highlighting their potential for use in yield enhancement. Conversely, grain yield per plant showed significant negative correlations with plant height (-0.051) and days to maturity (-0.257) and peduncle length (-0.82).

Shrivastava and Sharma (1976) [36] recommended using only direct yield components in path analysis. The analysis revealed that number of effective tillers per meter (1.05) exerted the strongest positive direct effect on grain yield, followed by days to heading (0.742), 1000 grain weight (0.73), ear weight (0.68), plant height (0.44), days to maturity (0.34) and spike length (0.27) identifying them as key contributors to grain yield (Table 5).

Such relationships arise from complex gene interactions, making it challenging to isolate specific trait effects through selection. Correlation studies alone provide limited insight into each trait's contribution to grain yield. Understanding the genetic basis of these correlations is crucial before launching breeding programs targeting yield enhancement via component traits. Path-coefficient analysis proves more effective by separating direct and indirect effects of correlations, allowing breeders to evaluate the relative importance of each trait and prioritize those with the greatest impact on yield improvement.

Discussion

The analysis of variance revealed highly significant differences among genotypes for all the studied traits, indicating the presence of substantial genetic variability in the experimental material. Such variability provides ample scope for effective selection and genetic improvement. Similar observations have been reported by Asif *et al.* (2004) and Tripathi *et al.* (2011) [5, 40].

The estimates of Genotypic (GCV) and Phenotypic (PCV) coefficients of variation showed considerable variation among traits. Higher GCV and PCV values were recorded for ear weight, number of grains per spike, grain yield per plant, and number of effective tillers per meter, indicating greater genetic variability and better prospects for improvement through selection. In contrast, days to maturity, 1000-grain weight, harvest index, plant height, days to heading, and spike length exhibited comparatively lower variability. Similar findings were reported by Ali et al. (2008) [2], Baranwal et al. (2012) [6], Hakimi et al. (2017) [15], Jamil et al. (2017) [20], Rathwa et al. (2018) [31], Thapa et al. (2019) [38], and Malbhage et al. (2020) [25].

The wider differences between PCV and GCV for harvest index and biological yield per plant suggested a greater influence of environmental factors on these traits. Conversely, the narrow differences observed for days to heading, days to maturity, and number of effective tillers per meter indicated that these traits were predominantly governed by genetic factors with relatively less environmental influence, in agreement with Shankarrao et al. (2010) [35].

High heritability was observed for days to heading, number of effective tillers per meter, grains per spike, number of grains per spike, and ear weight, whereas moderate heritability was recorded for days to maturity, plant height, spike length, 1000-grain weight, biological yield per plant, and grain yield per plant. High heritability coupled with high genetic advance was observed for number of effective tillers per meter, number of grains per spike, and ear weight, indicating the predominance of additive gene action and the effectiveness of direct selection for these traits. In contrast, days to heading exhibited high heritability but moderate genetic advance, suggesting the involvement of non-additive gene effects. These findings are consistent with Baranwal et al. (2012) [6], Yadav et al. (2014) [41], Islam et al. (2017) [18],

Jaiswal et al. (2020) [19], Abinasa et al. (2011) [1], Sabit et al. (2017) [32].

Correlation analysis showed that grain yield per plant was positively and significantly associated with number of effective tillers per meter, number of grains per spike, spike length, ear weight, biological yield per plant, harvest index, and 1000-grain weight, whereas significant negative correlations were observed with days to maturity and plant height. The strongest positive associations with grain yield were recorded for biological yield, grains per spike, and 1000-grain weight, suggesting that these traits are important contributors to yield improvement. Similar results have been reported by Baranwal et al. (2012) [6], Mecha et al. (2017) [26], Sabit et al. (2017) [32], Islam et al. (2017) [18], and Nagar et al. (2018) [28].

Path coefficient analysis identified number of effective tillers per meter as the trait with the highest positive direct effect on grain yield, followed by days to heading, 1000-grain weight, ear weight, plant height, days to maturity, and spike length. In contrast, harvest index and number of grains per spike exhibited negative direct effects. These results suggest that direct selection for traits with high positive direct effects would be more effective for improving grain yield. Similar findings have been reported by Fellahi et al. (2013) [12], Dutamo et al. (2015) [11], Hakimi et al. (2017) [15], Sabit et al. (2017) [32], Shamuyarira et al. (2019) [34], Tabassum et al. (2018) [37], Baye et al. (2020) [7], Kumar et al. (2018) [23], and Rajput (2018) [30].

Overall, the combined results of variability, heritability, correlation, and path coefficient analyses indicate that number of effective tillers per meter, ear weight, number of grains per spike, and 1000-grain weight are the most reliable selection criteria for improving grain yield. These traits possess substantial genetic variability, favorable heritability, and strong direct or indirect contributions to yield, making them valuable targets in wheat breeding programmes.

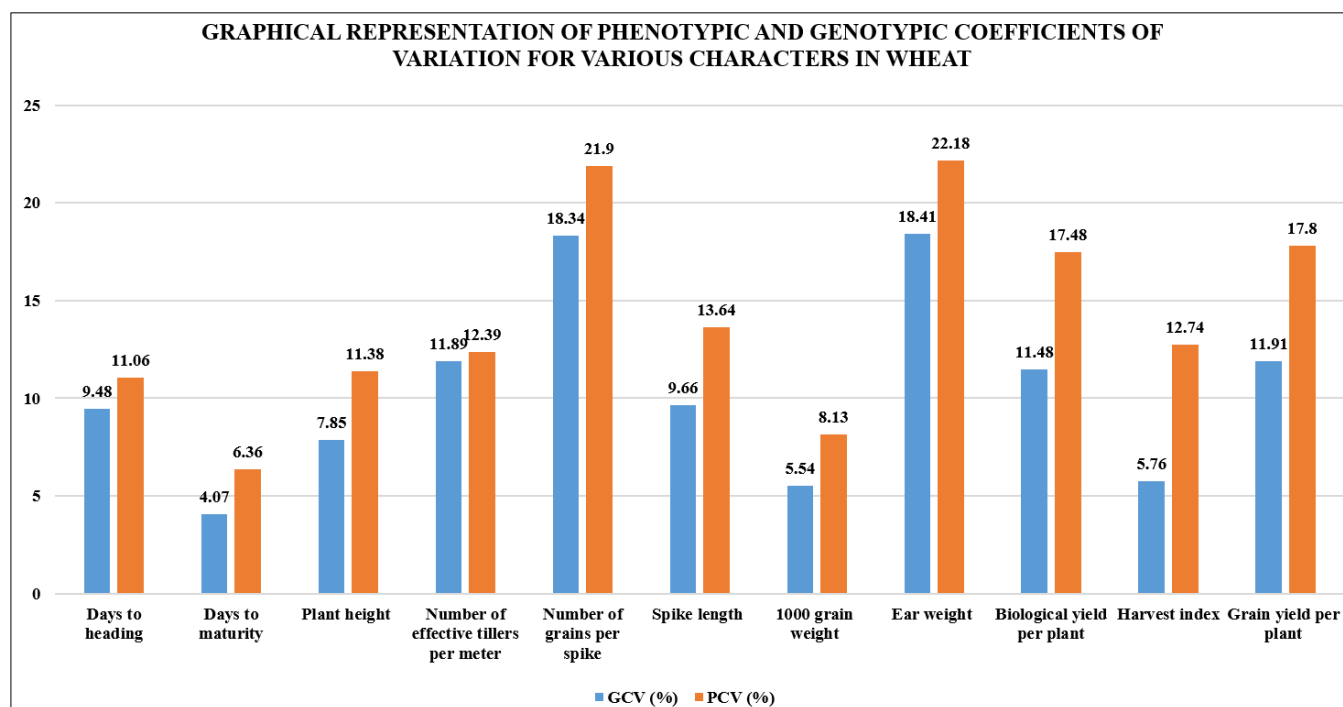


Fig 1: Graphical representation of genotypic and phenotypic coefficient of variation for 11 characters in wheat

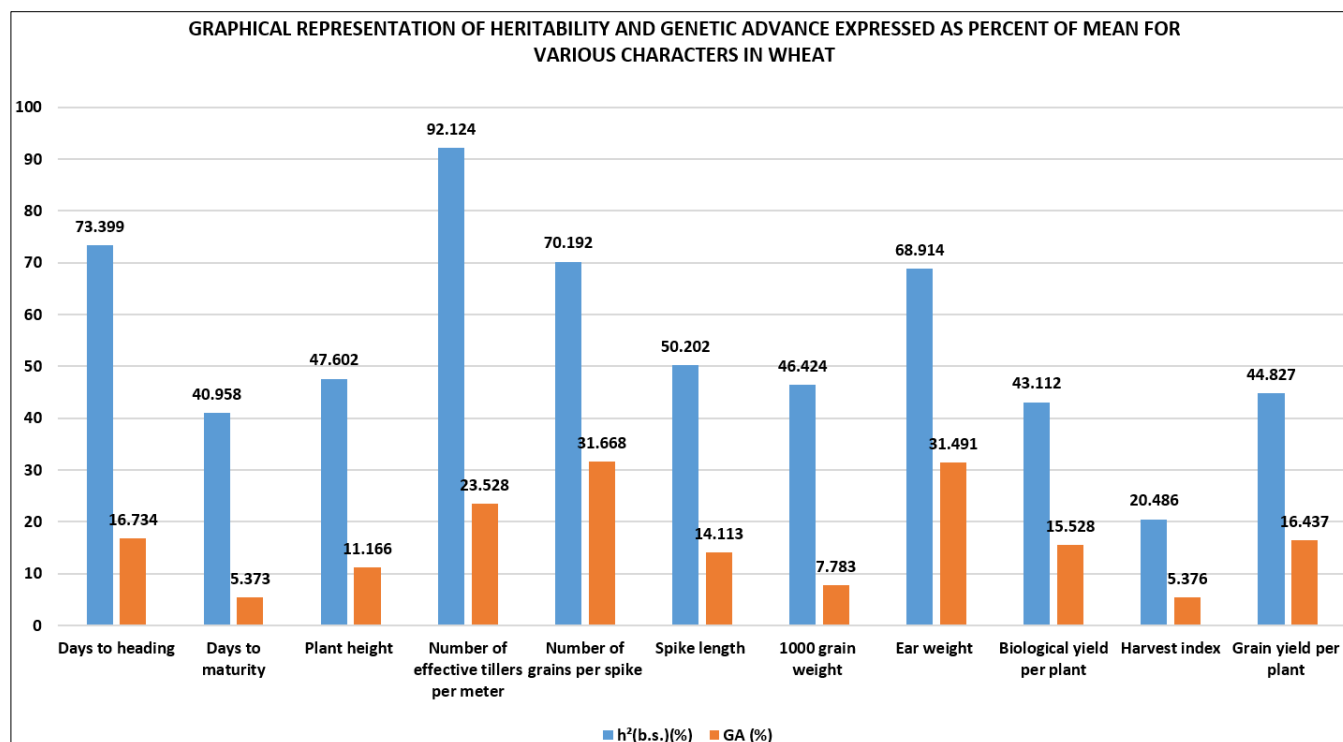


Fig 2: Graphical representation of heritability (b.s) and genetic advance expressed as percent of mean for 11 characters in wheat

Table 1: List of genotypes

Sr. No.	Genotypes	Source	Sr. No.	Genotypes	Source
1	VA2019-02	SDAU, Vijapur, Gujarat	16	GW 366	SDAU, Vijapur, Gujarat
2	VA2019-03		17	GW 451	
3	VA2019-04		18	GW 496	
4	VA2019-17		19	GW 1339	
5	VA2019-18		20	HI 1544	
6	VA2019-19		21	HD 2932	
7	VA2019-34		22	HD 2864	
8	VA2019-35		23	LOK 1	
9	VA2019-36		24	MP 3288	
10	VA2019-37		25	DBW 110	
11	VA2016-22		26	GDW 1255	
12	VD2019-3		27	A-9-30-01	
13	VD2019-4		28	Agra Local	
14	VD2019-5		29	Lal Bahadur	
15	GW 322		30	A-206	

Table 2: Analysis of variance (ANOVA) for different characters of wheat genotypes

Sr. No.	Characters	Mean sum of squares		
		Replications	Treatments	Error
	Degree of freedom	3	29	87
1.	Days to heading	1.540	152.717**	23.697
2.	Days to maturity	7.861	95.085**	40.094
3.	Plant height (cm)	1.912	227.983**	68.019
4.	Number of effective tillers per meter	10.724	381.036**	7.974
5.	Number of grains per spike	0.327	81.587**	7.831
6.	Spike length (cm)	0.016	4.368**	1.342
7.	1000 grain weight (g)	0.696	24.568**	1.393
8.	Ear weight (g)	0.013	1.222**	0.123
9.	Biological yield per plant (g)	0.656	12.404**	3.078
10.	Harvest index (%)	3.571	74.584**	36.730
11.	Grain yield per plant (g)	0.065	3.724**	0.874

*, ** significant at 5% and 1% level of significance, respectively

Table 3: Genetic parameter of variation for grain yield and its contributing characters in wheat

S. No.	Characters	GCV	PCV	ECV	$h^2_{(b.s.)}$ (%)	GA	GA (%)
1.	Days to heading	9.48	11.06	7.80	73.39	10.44	16.73
2.	Days to maturity	4.07	6.36	6.17	40.95	5.51	5.37
3.	Plant height (cm)	7.85	11.38	9.69	47.60	9.50	11.16
4.	Number of effective tillers per meter	11.89	12.39	4.99	92.12	19.09	23.52
5.	Number of grains per spike	18.34	21.90	12.29	70.19	7.41	31.66
6.	Spike length (cm)	9.66	13.64	11.98	50.20	1.36	14.11
7.	1000 grain weight (g)	5.54	8.13	3.00	46.42	3.06	7.78
8.	Ear weight (g)	18.41	22.18	12.36	68.91	0.89	31.49
9.	Biological yield per plant (g)	11.48	17.48	13.19	43.11	2.06	15.52
10.	Harvest index (%)	5.76	12.74	11.36	20.48	2.86	5.37
11.	Grain yield per plant (g)	11.91	17.80	13.21	44.82	1.16	16.43

Where,

GCV (%) and PCV (%) are genotypic and phenotypic coefficient of variance, respectively. h^2 (b.s) (%), GA and GAM are broad sense heritability, genetic advance and genetic advance expressed as percent of mean, respectively.

Table 4: Genotypic (σ^2_g) and phenotypic correlation (σ^2_p) coefficient for different characters of wheat

	Correlation	DH	DM	PH	TIL/MTR	NGS	SL	GW	EW	BY	HI	GY
DH	σ^2_g	1.000	0.541**	0.451**	-0.749**	-0.084 ^{NS}	0.228*	-0.442**	-0.151 ^{NS}	0.096 ^{NS}	-0.206*	0.010
	σ^2_p	1.000	0.633**	0.561**	-0.573**	0.190*	0.463**	0.060 ^{NS}	0.146 ^{NS}	0.266**	0.110 ^{NS}	0.326**
DM	σ^2_g		1.000	0.418**	-0.658**	-0.305**	-0.061 ^{NS}	-0.488**	-0.244**	-0.165 ^{NS}	-0.350**	-0.257**
	σ^2_p		1.000	0.632**	-0.349**	0.213*	0.452**	0.287**	0.247**	0.299**	0.243**	0.379**
PH	σ^2_g			1.000	-0.622**	-0.107 ^{NS}	0.244**	-0.322**	-0.363**	0.268**	-0.650**	-0.051**
	σ^2_p			1.000	-0.293**	0.267**	0.538**	0.286**	0.121 ^{NS}	0.417**	0.045 ^{NS}	0.406**
TIL/MTR	σ^2_g				1.000	0.176 ^{NS}	-0.139 ^{NS}	0.409**	0.082 ^{NS}	0.101 ^{NS}	0.350**	0.267**
	σ^2_p				1.000	0.183*	-0.042 ^{NS}	0.334**	0.112 ^{NS}	0.080 ^{NS}	0.150 ^{NS}	0.229*
NGS	σ^2_g					1.000	0.038 ^{NS}	0.570**	0.556**	0.563**	0.283**	0.739**
	σ^2_p					1.000	0.395**	0.701**	0.677**	0.596**	0.382**	0.797**
SL	σ^2_g						1.000	0.024 ^{NS}	-0.038 ^{NS}	0.589**	-0.363**	0.447**
	σ^2_p						1.000	0.495**	0.355**	0.645**	0.237**	0.701**
GW	σ^2_g							1.000	0.150 ^{NS}	0.303**	0.418**	0.576**
	σ^2_p							1.000	0.465**	0.505**	0.484**	0.756**
EW	σ^2_g								1.000	0.082 ^{NS}	0.582**	0.428**
	σ^2_p								1.000	0.348**	0.499**	0.616**
BY	σ^2_g									1.000	-0.989**	0.831**
	σ^2_p									1.000	0.333**	0.768**
HI	σ^2_g										1.000	0.228*
	σ^2_p										1.000	0.448**
GY	σ^2_g											1.000
	σ^2_p											1.000

*, ** significant at 0.05% and 0.01% level of significance, respectively

Table 5: Direct and indirect effects of yield component on grain yield in wheat

Sr. No.	Character	DH	DM	PH	TIL/MTR	NGS	SL	GW	EW	BY	HI	Genotypic correlation with GY
1.	DH	0.742	0.185	0.202	-0.788	0.003	0.061	-0.322	-0.103	0.005	0.024	0.010
2.	DM	0.401	0.342	0.187	-0.693	0.011	-0.016	-0.356	-0.167	-0.009	0.041	-0.257**
3.	PH	0.335	0.143	0.448	-0.655	0.004	0.066	-0.235	-0.249	0.014	0.077	-0.051
4.	TIL/MTR	-0.555	-0.225	-0.279	1.053	-0.006	-0.037	0.298	0.056	0.005	-0.041	0.267**
5.	NGS	-0.062	-0.104	-0.048	0.185	-0.037	0.010	0.416	0.382	0.030	-0.033	0.739**
6.	SL	0.169	-0.020	0.109	-0.146	-0.001	0.270	0.017	-0.026	0.032	0.043	0.447**
7.	GW	-0.328	-0.166	-0.144	0.430	-0.021	0.006	0.730	0.103	0.016	-0.050	0.576**

8.	EW	-0.112	-0.083	-0.162	0.086	-0.020	-0.010	0.109	0.687	0.004	-0.069	0.428**
9.	BY	0.071	-0.056	0.120	0.106	-0.021	0.159	0.221	0.056	0.054	0.118	0.831**
10.	HI	-0.153	-0.119	-0.291	0.368	-0.010	-0.098	0.305	0.400	-0.054	-0.119	0.228*

*, ** significant at 0.05% and 0.01% level of significance respectively (Residual value: 0.0663)

Conclusion

Analysis of variance showed significant differences among thirty wheat genotypes for eleven traits. PCV exceeded GCV, indicating environmental influence, but traits like days to heading and grains per spike showed minimal environmental impact. High heritability and genetic advance for Number of effective tillers per meter, grains per spike and ear weight suggest additive gene effects. Grain yield correlated positively with Number of effective tillers per meter, days to heading and 1000-grain weight showing strong direct effects in path analysis, despite a negative effect from harvest index. Low residual effect indicates significant trait contributions to yield.

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