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EXPLORING GENETIC VARIABILITY AND DIVERGENCE FOR YIELD IMPROVEMENT IN BREAD WHEAT (*TRITICUM AESTIVUM* L.)

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ABSTRACT

Genetic variability and divergence analysis play a crucial role in the improvement of bread wheat (*Triticum aestivum L.*) under diverse environmental conditions. The present study evaluated 30 genetically diverse wheat genotypes across three sowing environments (timely, late and very late) over two consecutive growing seasons (2023 to 2025). The experiment was conducted using a randomized block design with three replications, and eleven agro-morphological and yield-related traits were assessed. Significant variation among genotypes and environments was observed for most traits, indicating substantial genetic diversity. Delayed sowing negatively affected growth and yield traits causing significant reductions in plant height, spike length, grain weight and overall productivity. Estimates of phenotypic and genotypic coefficients of variation revealed moderate to high variability for key traits such as grain yield and biological yield, while heritability estimates varied across environments, with high values recorded for phonological traits. Correlation analysis indicated that grain yield was positively associated with effective tillers, grains per spike, spike length, and thousand-grain weight across environments. Principal component analysis explained over 85% of total variation, highlighting the major contribution of yield-related traits. Mahalanobis D^2 analysis grouped genotypes into distinct clusters, with clusters III and IV showing greater genetic divergence and superior performance. Traits such as days to maturity and flowering contributed significantly to genetic divergence under different sowing conditions. The findings suggest that selection of genotypes from highly divergent clusters with desirable traits can enhance breeding efficiency. Overall, the study provides valuable insights into genetic variability, trait associations, and selection strategies for developing high-yielding and climate-resilient wheat varieties.

KEYWORDS: Bread wheat; genetic variability; genetic divergence; grain yield; PCA; genotype × environment interaction

INTRODUCTION

Bread wheat (*Triticum aestivum* L.) is one of the most important cereal crops globally and belongs to the family Poaceae and the genus Triticum, which includes species exhibiting wide variation in genome composition and ploidy levels. Cultivated bread wheat is an allohexaploid (2n = 6x = AABBDD) formed through two sequential allopolyploidization events, conferring substantial genomic plasticity and enabling adaptation to diverse agro-climatic conditions (Zhang *et al.*, 2024). Archaeological evidence suggests that wheat was first domesticated in South-western Asia and subsequently spread to ancient Egyptian and Greek civilizations. At present, major centre of genetic diversity are located in Central Asia, the Near East, the Mediterranean Basin, Ethiopia, with the Hindukush region representing a prominent hotspot for variability in hexaploid wheat. Given this extensive genetic diversity and broad ecological distribution, understanding variation among wheat genotypes is fundamental for crop improvement. Morphological and phenotypic characterization therefore provides a practical basis for assessing wheat adaptation under changing climatic conditions (Bita & Gerats, 2013; Hyles*et al.*, 2020). Grain yield is a complex polygenic trait influenced by interactions among genetic, physiological, morphological, and environmental factors. Yield-contributing traits such as number of productive tillers, grain size, and test weight are highly interrelated and jointly determine overall productivity (Kumar *et al.*, 2023). Consequently, the identification of genetically divergent genotypes based on these traits is crucial for effective parental selection and the exploitation of heterosis in breeding programs. In addition to inherent genetic differences, wheat performance is strongly influenced by genotype × environment (G×E) interaction, as environmental factors such as sowing time, soil properties, temperature, and humidity substantially affect phenotypic expression. While yield stability analysis helps identify broadly adapted genotypes, genetic divergence analysis complements stability studies by revealing the extent and pattern of variability among genotypes across environments. Assessing divergence enables breeders to group genotypes into distinct clusters, thereby facilitating the selection of genetically diverse parents for hybridization and population improvement. Accordingly, the present study emphasizes divergence group analysis using multivariate statistical approaches. Mahalanobis' D^2 statistics was employed to quantify genetic divergence among wheat genotypes based on multiple morpho-physiological and yield-related traits. Genotypes were subsequently grouped into clusters using appropriate clustering techniques, and inter- and intra-cluster distances were estimated to assess the magnitude of genetic diversity. In addition, principal component analysis (PCA) was utilized to identify key traits contributing most to total variability and to visualize relationships among genotypes. Together, these statistical tools provide a robust framework for understanding genetic diversity, identifying superior and diverse parental combinations, and supporting strategic decision-making in wheat breeding programs aimed at enhancing yield potential and climate resilience.

MATERIAL AND METHODS

Plant Materials

A customary of thirty genetically diverse genotypes of wheat procured from Indian institute of Wheat and Barley, Karnal, along with two checks comprising high-yielding, disease-resistant, water lodging-tolerant, heat heat-tolerant were constituted the investigational material for this study. A list of all genotypes is mentioned in **Supplementary Table 1**.

Experimental conditions

The present experimentation was conducted at the Research farm of IFTM University, Moradabad, 28°49′52″N and 78°45′58″E, and the elevation is 271.230M (889.86Ft) during the two Rabi seasons 2023-2024 and 2024 -2025. The environments were created by three dates of sowing. All the 30 genetically diverse wheat genotypes were sown in RBD Design with three repetitions in three different atmospheres during Rabi 2023-2024 and 2024-2025. Each genotype was accommodated in two rows of two meters in length, along with a 25cm row-to-row distance. The experiment was conducted under irrigated conditions. Recommended crop production and protection practices were followed to raise a successful crop.

Phenotypic estimation of quantitative traits

Yield and related traits were recorded using a randomized approach. In separately plan, five competitive plants were haphazardly tagged for observations across the three environments. The mean values for each treatment were premeditated, and the traits studied, along with the methods used for their measurement. The traits recorded included: (a) days to 50% flowering, (b) days to maturity, (c) plant height, (d) spike length, (e) spikelets per spike, (f) effective tillers, (g) grains per spike, (h) 1000-seed weight, (i) grain yield (kg/ha), (j) biological yield (kg/ha), and (k) harvest index. The collected data were averaged and subjected to analysis

Statistical analysis

The analysis of variance (ANOVA) was conducted using the "agricole" package, while other statistical analyses were performed in RStudio, running R version 4.5.2 by various packages, for graphical representation, Origin Pro 2026 (version10.3.0.180).

Results

Analysis of variance

The combined analysis of variance (ANOVA) across environments and years was conducted to assess genotypic adaptability and differential environmental responses. Data were pooled over two years and multiple environments, revealing sufficient variability between years; however, the genotype × year interaction was non-significant (Supplementary Table 2). In contrast, the pooled ANOVA showed a significant genotype × environment (G×E) interaction for all traits except spikelets per spike (SPS), indicating differential genotypic performance across environments. These results highlight the importance of stability analysis for identifying genotypes with both broad and specific adaptability under varying sowing conditions (Table 1).

Table 1. Pooled analysis of variance for the 11 Agro-morphological traits for the various environments in two growing periods (2023-2024, 2024-2025)

	GEN	ENV	GEN: ENV	ENV: REP	Residuals
Df	29	2	58	6	174
DFF	186***	7605.3***	9.2**	44*	2.6
DTM	456.7**	9456.4**	23.5***	30	2.2
PH	189.6***	15510.7***	22.3***	45	3.4
SL	1.62**	332.92**	0.39**	22.91*	0.17
SPS	9.26***	1003.97**	1.01	27.64	0.77
ET	2.79***	437.91***	0.37**	30.47**	0.42
GS	108.9***	18979***	14***	40.5	3
TW	44.32***	653.47***	1.86**	29.89*	1.25

GY	10898442***	6303348727***	6506645***	8540794	2173978
BY	13261812***	765854374***	1341845***	8570577**	1088655
HI	19.56***	1690.9***	8.48***	21.11**	0.62

Where,"***"= Significant at p<0.001, "**"= Significant at p<0.01, and "*"= Significant at p<0.05, GEN Genotypes, ENV environments, REP Replication, D.f degree of freedom, DFF Days to 50% flowering, DTM days to maturity, PH plant height, SL spike length, SPS spikelets per spike, ET effective tillers, GS grain per spike, TW 1000 seed weight, GY grain yield per hectare, BY biological yield per hectare, HI harvest index.

Mean performance of yield and yield contributory characters:

Variation in mean performance of 11 agro-morphological traits across environments was illustrated using violin plots, where red, sky blue, and green represent timely, late, and very late sowing, respectively (Supplementary Figure 1). Delayed sowing accelerated phonological development and significantly reduced growth and yield. Days to 50% flowering decreased from 76.45 to 66.45 and 58.08 days, while days to maturity declined from 138.51 to 127.82 and 118.02 days under timely, late, and very late sowing, respectively (Table 2). Similarly, plant height, spike length, spikelets per spike, and effective tillers per plant showed substantial reductions. Grains per spike and test weight also declined markedly. Grain and biological yields were highest under timely sowing and decreased sharply with delay, along with a reduction in harvest index, indicating the adverse effect of late planting on overall productivity.

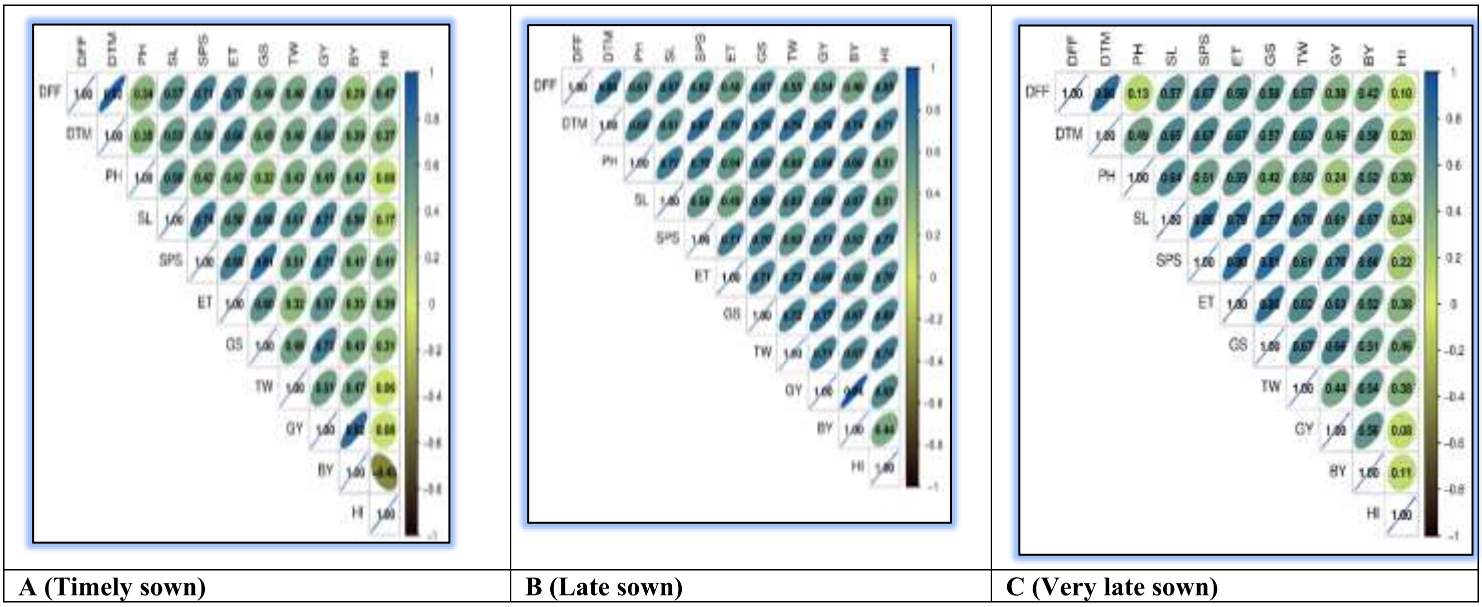
Estimation of genetic variability of Agro-morphological traits across cropping seasons

Genetic variability is essential for effective crop improvement. In this study, PCV, GCV, heritability (H^2), and genetic advance (GA, GAM) were estimated for 11 traits across timely (E1), late (E2), and very late (E3) sowing (Table 2). Moderate to high variability was observed for key traits, particularly biological and grain yield, while days to maturity showed low variability. High heritability was recorded for phonological traits (DTM and DFF), whereas effective tillers per plant exhibited consistently low heritability. Genetic advance was highest for biological yield and grain yield across environments. Overall, traits with higher variability, heritability, and GA such as biological yield, grain yield, and maturity are promising targets for selection, while traits like spike length and effective tillers have limited improvement potential.

Pearson Correlation Coefficient of Agro-Morphological Traits

Grain yield exhibited strong and significant positive correlations with most yield-contributing traits across environments. Under timely sowing (E1), it was positively associated with ET, DFF, DTM, TW, SL, SPS, GS, and PH, but negatively correlated with HI (Figure 1a). In late sowing (E2), grain yield maintained significant positive associations with DFF, DTM, TW, SL, ET, SPS, GS, and BY, while its relationship with HI was non-significant (Figure 1b). Under very late sowing (E3), grain yield showed strong positive correlations with GS, ET, SPS, DTM, HI, TW, DFF, SL, PH, and BY, indicating greater dependence on multiple traits under stress (Figure 1c). Overall, spike length, grains per spike, and effective tillers per plant consistently exhibited strong positive associations with grain yield, whereas the role of harvest index varied across environments.

Figure 1 Pearson correlation coefficient of 11 Agro-morphological traits of 30 wheat genotypes over the three environmental conditions.



A (Timely sown) **B (Late sown)** **C (Very late sown)**

Principal component analysis:

Trait relationships were inferred from vector angles, where acute, right, and obtuse angles indicated positive, null, and negative correlations, respectively. Across all environments, four principal components (PCs) with eigenvalues >0.5 explained most of the variation: 85.13% (E1), 85.64% (E2), and 87.89% (E3). Under timely sowing, PC1 (54.87%)

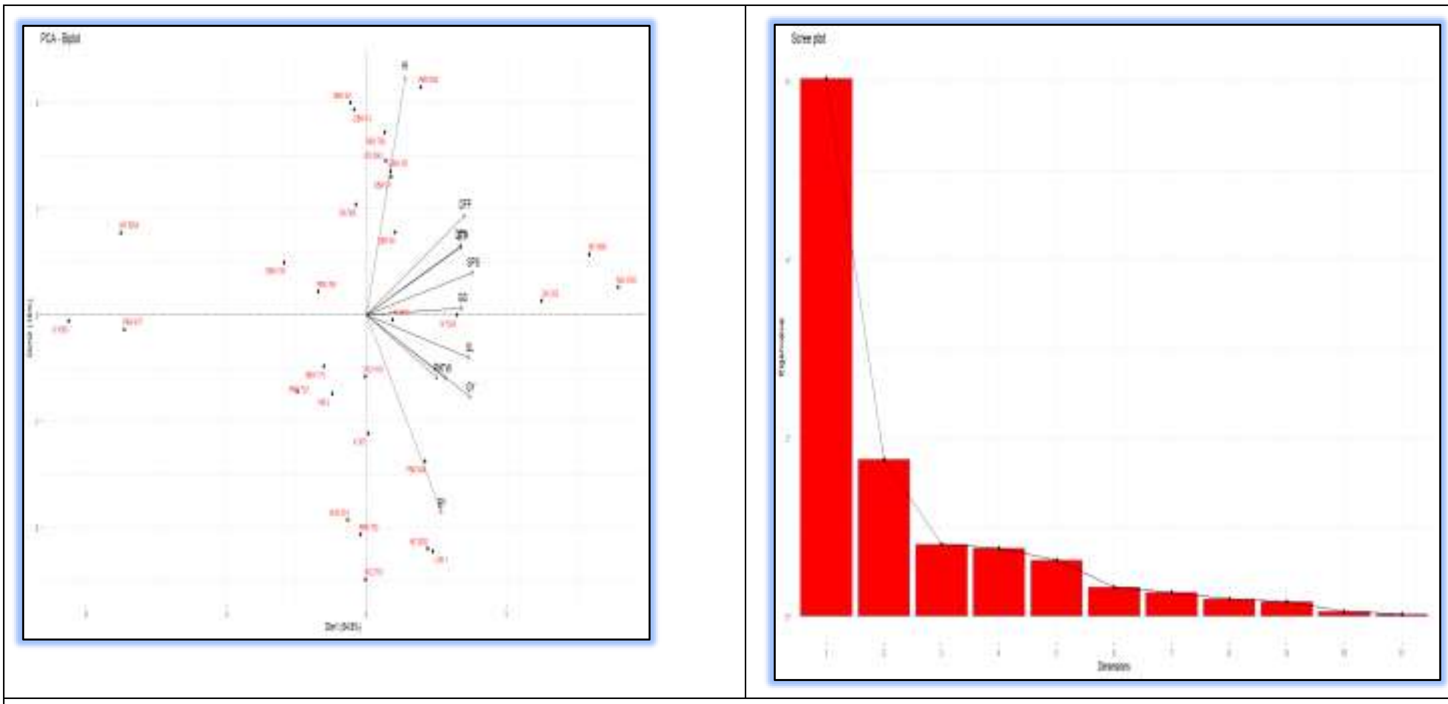
was dominated by yield and related traits (SPS, GY, SL, GS, DFF, DTM, ET), while PC2 (16%) was influenced by biological yield and harvest index. PC3 and PC4 contributed minor variation. In late sowing, PC1 (59.55%) captured major yield variation, with PC2 (10.98%) driven by HI and PH. Under very late sowing, PC1 alone explained 69.72% of total variation, with subsequent PCs reflecting contributions from HI, BY phonological traits and yield components (Figures 2, 3; Table 3).

Table 3. Eigen value and eigenvectors for the PCA dimensions of 11 Agro-morphological traits of 30 wheat genotypes under timely, late and very late sown conditions.

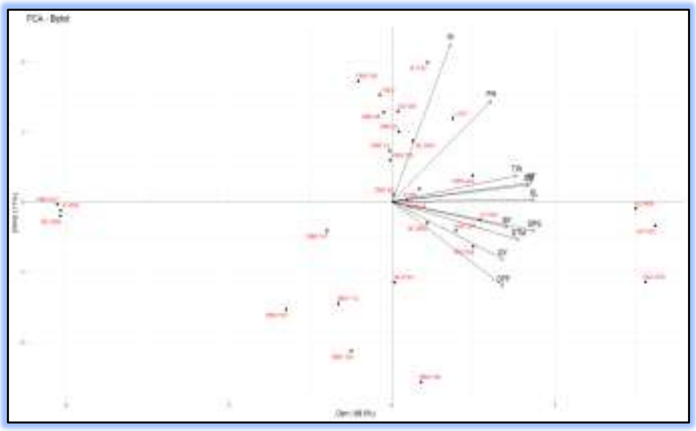
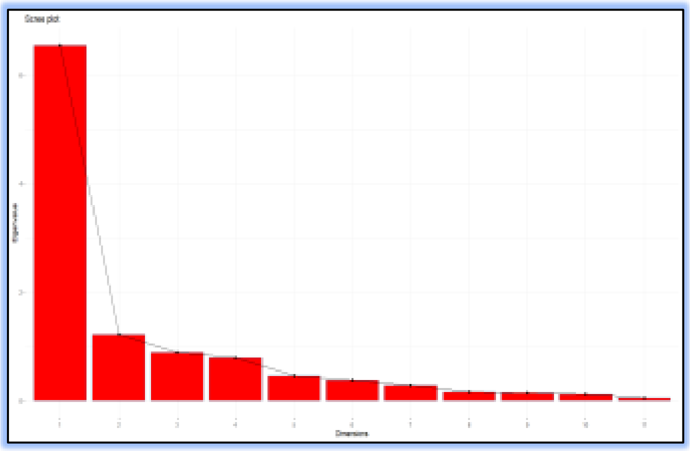
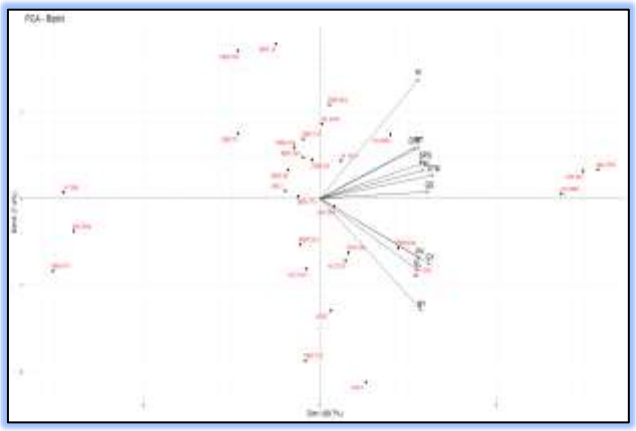
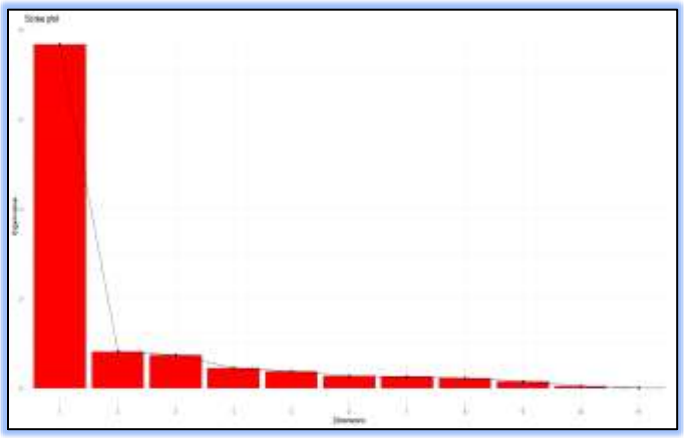
	TIMELY SOWN				**LATE SOWN**				**VERY LATE SOWN**			
	PC 1	PC 2	PC 3	PC 4	PC 1	PC 2	PC 3	PC 4	PC 1	PC 2	PC 3	PC 4
DFF	10.97	7.43	18.04	0.22	7.69	14.31	28.00	5.03	7.64	5.37	36.06	0.02
DTM	10.25	3.63	32.39	0.42	9.94	2.93	5.17	17.65	11.02	1.11	0.26	3.52
PH	5.77	2.97	0.02	58.32	6.11	20.43	17.72	16.17	8.51	7.53	8.38	6.44
SL	11.97	1.37	4.69	3.23	12.48	0.01	2.99	0.14	8.11	10.78	14.79	16.48
SPS	12.86	1.33	9.18	1.45	12.52	1.69	0.43	1.87	9.46	2.73	0.01	37.71
ET	10.23	3.49	0.74	0.89	12.06	0.72	0.05	1.92	8.43	5.50	19.73	0.12
GS	10.41	0.04	27.45	8.12	11.53	0.55	2.28	15.34	10.16	0.09	0.11	1.59
TW	7.25	3.03	0.04	12.19	9.66	1.35	2.79	2.84	9.18	1.65	5.34	31.93
GY	12.22	5.03	0.03	8.33	7.62	6.68	6.95	31.26	10.37	9.05	6.69	0.23
BY	6.37	29.26	3.09	4.84	8.26	1.29	18.79	3.57	8.83	26.47	8.31	0.33
HI	1.70	42.42	4.32	1.98	2.14	50.04	14.84	4.21	8.29	29.72	0.30	1.63
EV	6.04	1.76	0.81	0.76	6.55	1.21	0.88	0.78	7.67	0.81	0.74	0.45
PV	54.87	16.00	7.32	6.94	59.55	10.98	8.01	7.11	69.72	7.39	6.69	4.09
CPV	54.87	70.87	78.19	85.13	59.55	70.53	78.54	85.64	69.72	77.11	83.80	87.89

Where, DFF Days to 50% flowering, DTM days to maturity , PH plant height, SL spike length, SPS spikelets per spike, ET effective tillers, GS grain per spike, TW 1000 seed weight, GY grain yield per hectare, BY biological yield per hectare, HI harvest index.

Figure 2, 3.Biplots, screed plots of the first two principal components, PC1 and PC2, of 30 wheat genotypes over various environmental conditions:



A (Timely sown)

	
B (Late sown)	
	
C (Very late sown)	

Genetic divergence analysis:
Mahalanobis D^2 analysis grouped the 30 genotypes into three distinct, non-overlapping clusters across environments (Table 5). Clusters III and IV contained the majority of genotypes under timely, late, and very late sowing, indicating greater genetic similarity within these groups. Hierarchical clustering further confirmed genetic relationships through dendrograms for each environment (Figure 5a–c). Trait contributions to genetic divergence varied across environments (Table 4; Figure 4a–c). Days to maturity (DTM) contributed the most under timely (27.2%) and late sowing (52.0%), whereas days to 50% flowering (DFF) was the major contributor under very late sowing (27.3%). In contrast, spikes per square meter, grain yield, and biological yield showed minimal contributions in respective environments, highlighting environment-specific trait influence on genetic divergence.

Table 4 Percentage of contribution of 11 Agro-morphological traits of 30 genotypes of timely sown , late sown and, very late sown.

Traits	TIMELY SOWN (%)	LATE SOWN (%)	VERY LATE SOWN (%)
DFF	4.9	9.8	27.3
DTM	27.2	52	18.9
PH	10.8	6.1	10.9
SL	4.7	2.2	3.9
SPS	0.9	4.6	2.4
ET	1.8	2.6	4.2
GS	10.5	2.9	3.6
TW	4.2	9.3	14.6
GY	10.2	1.6	9.9
BY	3.8	1.9	1.6
HI	22.4	7	2.7

Where, **DFF** Days to 50% flowering, **DTM** days to maturity , **PH** plant height, **SL** spike length, **SPS**spikelets per spike, **ET** effective tillers, **GS** grain per spike, **TW** 1000 seed weight**, GY** grain yield per hectare, **BY** biological yield per hectare, **HI** harvest index.

Table 6 Inter – intra cluster distance of 30 genotypes of timely, late and, very late sown conditions

	TIMELY SOWN				LATE SOWN				VERY LATE SOWN			
	C1	**C2**	**C3**	**C4**	**C1**	**C2**	**C3**	**C4**	**C1**	**C2**	**C3**	**C4**
C1	**3.22**	5.21	4.00	6.10	**3.44**	3.80	5.94	6.04	**2.73**	3.31	6.61	5.79
C2		**1.61**	5.16	10.19		**3.04**	4.95	6.91		**2.80**	5.57	6.97
C3			**3.03**	6.77			**1.28**	10.68			**1.23**	11.60
C4				**2.20**				**0.83**				**0.94**

Inter and intra Cluster distance analysis:

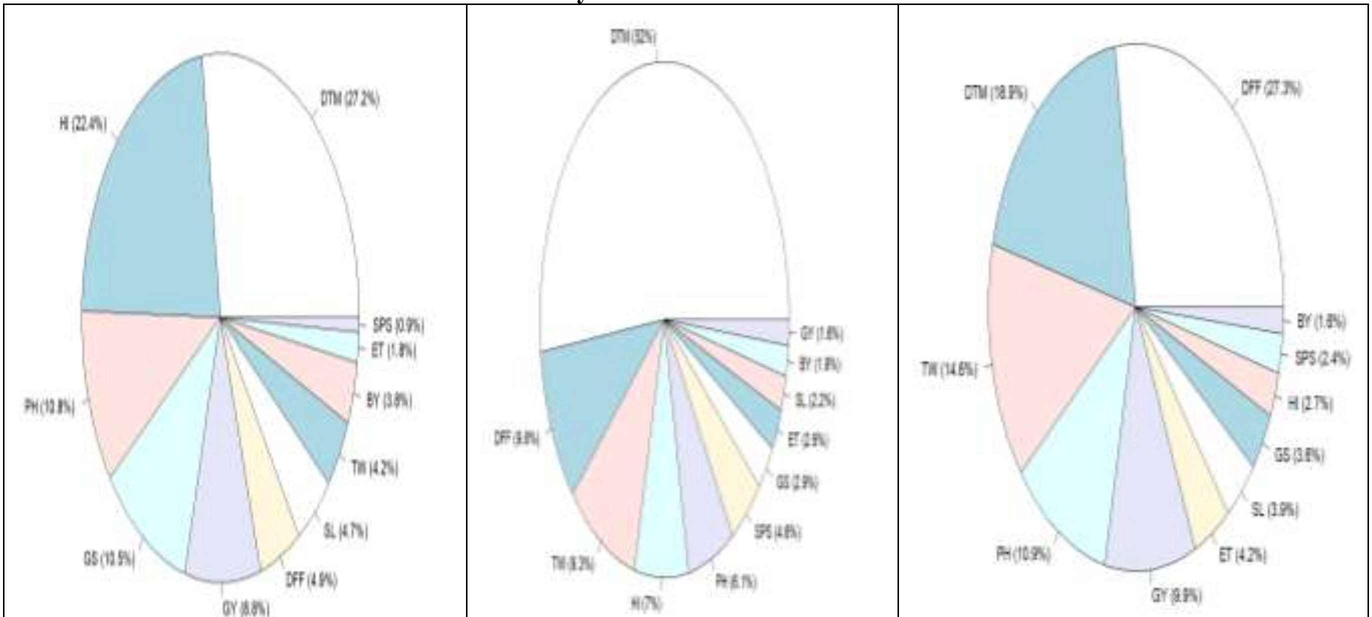
Across all sowing environments, the thirty wheat genotypes were grouped into four distinct clusters based on genetic divergence (Figures 5a–c). Under timely sowing, Clusters II and III contained the highest number of genotypes (10 and 14), whereas Clusters I and IV included only three each. Inter-cluster distances were greatest in Cluster IV (10.19), indicating substantial genetic divergence, and lowest in Cluster I (4.00). Intra-cluster distances were highest in Clusters III and I (3.03 and 3.22) and lower in Clusters IV and II (2.20 and 1.61) (Table 6; Figures 6a–c). A similar pattern was observed under late sowing, with Clusters III and IV harbouring the most genotypes (4 and 20). Cluster IV exhibited the maximum inter-cluster distance (10.68), while Cluster I had the minimum (3.80). Intra-cluster distances were highest for Clusters I and II (3.44 and 3.04) and lowest for Clusters III and IV (1.28 and 0.83). Under very late sowing, Clusters III (4 genotypes) and IV (19 genotypes) remained the largest. Cluster IV showed the highest inter-cluster distance (11.60), while Cluster II had the lowest (3.31), and intra-cluster distances were greatest for Clusters II and I (2.80 and 2.73) (Table 6).

Overall, the substantial inter-cluster distances indicate high genetic diversity among clusters. Hybridization between genotypes from widely separated clusters, particularly those with superior cluster means for key traits, is recommended to develop promising recombinants in subsequent segregating generations for wheat improvement.

Cluster mean performance

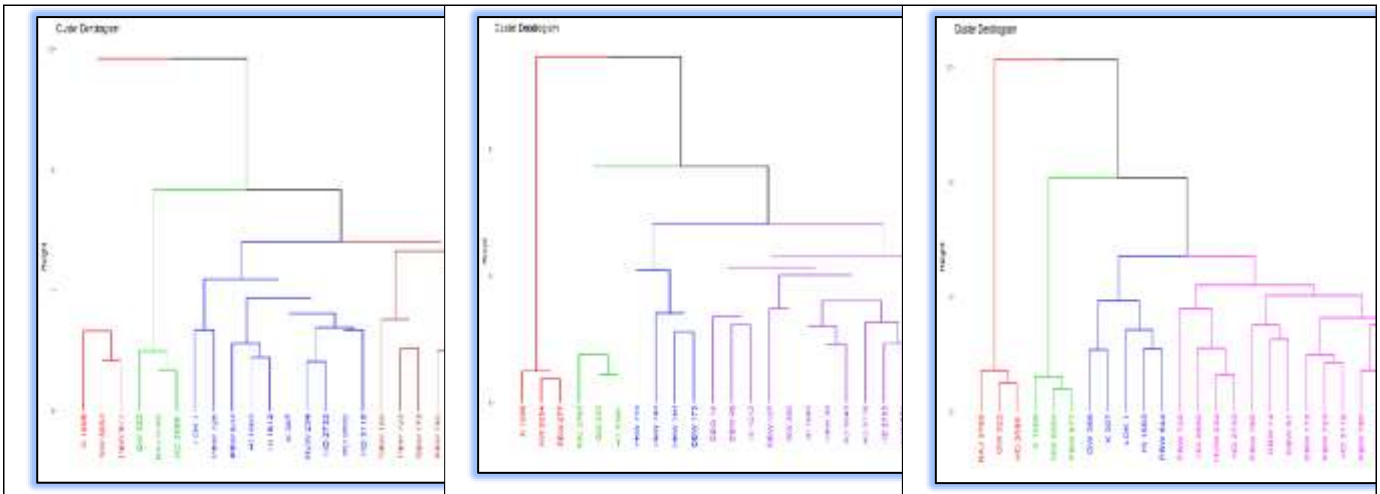
Cluster mean performance for agro-morphological traits is summarized in Table 7. For days to 50% flowering, Cluster IV consistently exhibited the highest values across all environments (85.33, 76.22, and 66.33 days under timely, late, and very late sowing, respectively), while the lowest means were recorded in Cluster II under timely (65.67) and late sowing (58.44), and in Cluster I under very late sowing (52.89). Clear cluster-wise variation was also observed for days to maturity and plant height. Under timely sowing, Cluster I showed late maturity (138.13 days) and tall plants (96.90 cm), whereas Cluster II had early maturity (122.11 days) and shorter stature (84.00 cm). With delayed sowing, Cluster IV emerged as the latest-maturing and tallest cluster, while minimum values shifted with environment, reflecting strong environmental effects on cluster performance.

Figure 4 Percentage of contribution of 11 Agro-morphological traits of 30 wheat genotypes for timely, late, and very late sown conditions.



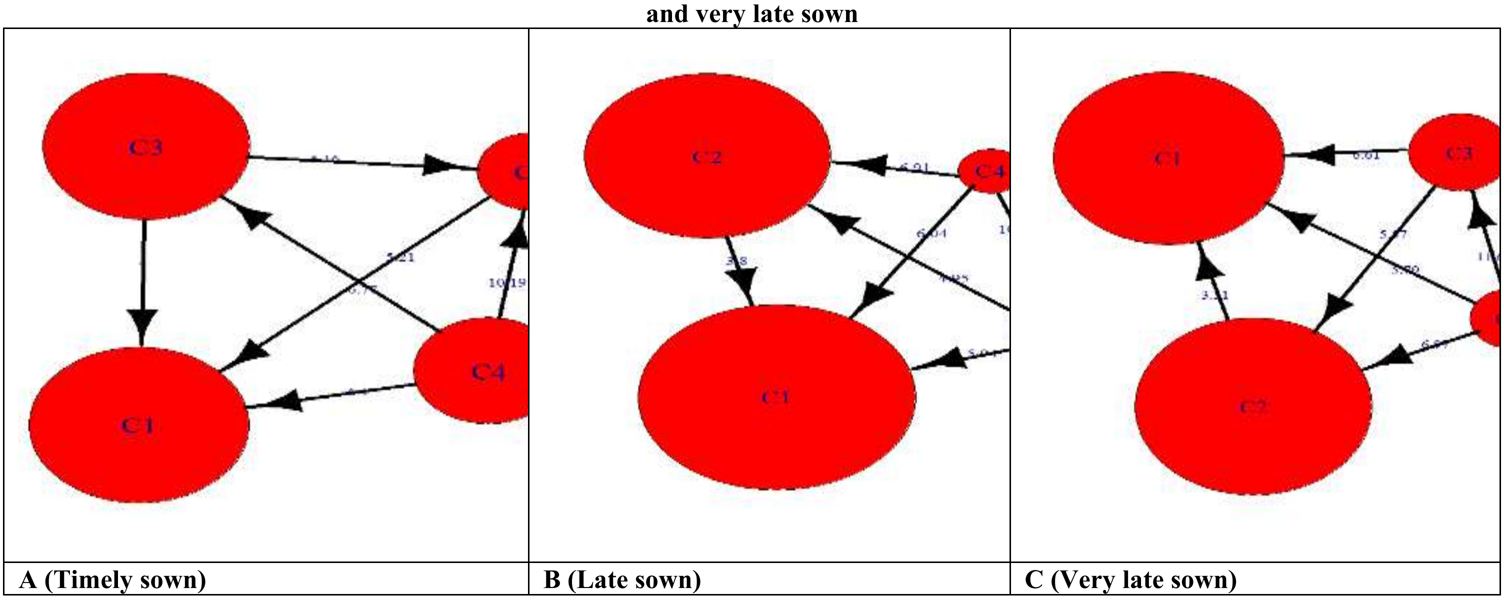
A (Timely sown)	B (Late sown)	C (Very late sown)

Figure 5 Classification of 30 wheat genotypes based on hierarchical clustering pattern over the three environmental conditions



A (Timely sown)	B (Late sown)	C (Very late sown)

Figure 6 Inter-intra cluster distances of 30 wheat genotypes for various environments viz. Timely sown, Late sown and very late sown



A (Timely sown)	B (Late sown)	C (Very late sown)

Table 5 Classification of 30 wheat genotypes based on hierarchical clustering pattern for various environmental conditions.

ENV	Bunches	No of genotype	Genotypes name
TIMEY	1	3	K1006, NW 5054, PBW677
	2	3	GW322, RAJ3765, HD3086
	3	10	LOK1, PBW725, PBW644, HI 1563, HI1612, K307, HUW234, HD2733, HD2932, HD3118
	4	14	DBW150, PBW723, DBW173, PBW780, PBW804, DBW51, DBW14, DBW46, PBW 765, WB2, DBW 39, GW 366, DBW 107, HD3043.

LATE	1	3	K1006, NW5054, PBW677
	2	3	RAJ3765, GW322, HD3086
	3	4	PBW723, PBW780, DBW150, DBW173
	4	20	DBW14. DBW46, HI1612, DBW107, GW366, HI1563, DBW39, HD3023, HD3118, HD2733, HUW234, HD2932, PBW725, PBW765, DBW51, WB2, PBW804, K307, PBW644, LOK1
VERY LATE	1	3	RAJ3765, GW 322, HD3086
	2	3	K1006, NW5054, PBW677
	3	5	GW366, K307, LOK1, HI1563, PBW 644
	4	19	PBW 725, HD2932, HUW234, HD2733, PBW765, DBW14, DBW51, DBW173, PBW723, HD3118, PBW780, PBW804, WB2, DBW39, DBW, 107, DBW46, DBW150, HI1612, HD3043

Table 7 Cluster mean of 4 prime clusters of 30 wheat genotypes of timely late and very late sown conditions.

	TIMELY				LATE SOWN				VERY LATE SOWN			
Bunches	1	2	3	4	1	2	3	4	1	2	3	4
DFF	75.67	65.67	78.18	85.33	65.60	58.44	69.22	76.22	52.89	57.88	65.83	66.33
DTM	138.13	122.11	140.11	150.17	128.43	110.06	129.17	138.83	105.44	118.65	126.17	128.33
PH	96.90	84.00	93.48	97.00	82.38	72.15	76.73	81.29	61.44	68.24	77.42	77.83
SL	10.52	8.98	10.37	11.61	8.07	6.85	7.84	8.61	6.10	6.56	7.54	7.42
SPS	20.81	18.28	21.29	23.78	16.08	13.58	15.87	18.01	11.67	14.83	16.17	17.50
ET	9.56	8.44	9.71	10.56	6.77	5.44	6.36	7.89	4.17	5.69	7.33	7.67
GS	69.12	61.06	70.76	79.33	57.47	49.56	55.50	62.89	35.39	40.81	47.25	48.33
TW	29.80	24.10	28.58	32.22	26.55	20.88	25.87	29.74	18.60	23.84	28.41	27.77
GY	6053.44	5153.83	5704.82	6788.17	18124.03	13940.46	18618.93	23287.94	2191.21	2813.61	3387.04	3422.79
BY	16047.66	12992.56	13924.22	16285.61	11414.05	8808.64	10709.15	12745.03	6838.44	9450.58	11479.18	11725.64
HI	36.77	37.90	41.09	40.66	35.33	33.54	32.35	35.98	27.44	30.12	33.40	33.06

Where, **DFF** Days to 50% flowering, **DTM** days to maturity , **PH** plant height, **SL** spike length, **SPS** spikelets per spike, **ET** effective tillers, **GS** grain per spike, **TW** 1000 seed weight**, GY** grain yield per hectare, **BY** biological yield per hectare, **HI** harvest index.

Table2 Estimation of genetic parameters of 11 Agro-morphological traits for the 30 wheat genotypes over the three environments:

TIMELY SOWN															
	Range	**Mean±SEm**	**SD**	**CV**	**CD 5%**	**CD 1%**	**EV**	**GV**	**PV**	**ECV**	**GCV**	**PCV**	**H2**	**GA**	**GA % of mean**
DFF	63-85	76.45±1.2373	5.44	7.11	3.50	4.66	4.59	28.48	33.08	2.80	6.98	7.52	0.86	10.20	13.35
DTM	112-151	138.51±0.93	8.42	6.08	2.65	3.52	2.62	66.07	68.70	1.17	5.87	5.98	0.96	16.42	11.86

PH	81-104.16	94.62±1.20	6.65	7.05	3.41	4.54	4.36	37.84	42.20	2.21	6.50	6.87	0.90	12.00	12.68
SL	8.7-12	10.41±0.31	0.77	7.44	0.89	1.19	0.30	0.37	0.67	5.25	5.86	7.87	0.55	0.94	8.99
SPS	17.83-24.5	21.02±0.57	1.47	6.97	1.62	2.15	0.98	1.27	2.25	4.71	5.36	7.13	0.56	1.74	8.29
ET	8.3-10.83	9.57±0.39	0.64	6.64	1.11	1.47	0.46	0.20	0.66	7.07	4.68	8.48	0.30	0.51	5.32
GS	60-80.34	69.83±0.92	5.64	8.06	2.61	3.48	2.55	26.39	28.95	2.29	7.36	7.70	0.91	10.11	14.47
TW	22.73-32.52	29.33±0.79	2.63	9.07	2.25	2.99	1.89	5.68	7.57	4.69	8.13	9.38	0.75	4.26	14.51
GY	14360.51-23411.71	5910.91±86.25	2641.03	13.56	244.19	324.89	22322.26	191906.10	214228.37	2.53	7.41	7.83	0.90	854.12	14.45
BY	12781.64-17351.93	15122.72±359.79	1385.20	9.16	1018.53	1355.16	388359.20	1768320.28	2156679.48	4.12	8.79	9.71	0.82	2480.48	16.40
HI	34.25-42.41	38.85±0.33	2.64	6.78	0.94	1.26	0.33	6.83	7.17	1.49	6.73	6.89	0.95	5.26	13.53
LATE SOWN														
DFF	57.5-76.83	66.45±0.942	5.30	7.95	2.67	3.55	2.66	22.84	25.50	2.46	7.19	7.60	0.90	9.32	14.02
DTM	107.83-139.6	127.82±0.701	8.56	6.70	1.98	2.64	1.47	69.57	71.04	0.95	6.53	6.59	0.98	17.00	13.30
PH	71.66-85.84	80.2738±0.83	4.24	5.29	2.35	3.13	2.07	15.19	17.26	1.79	4.85	5.18	0.88	7.53	9.38
SL	6.78-8.733	7.93±0.16	0.48	5.98	0.47	0.63	0.08	0.16	0.25	3.65	5.11	6.28	0.66	0.68	8.56
SPS	13.34-18.31	15.97±0.37	1.20	7.53	1.06	1.41	0.42	0.91	1.33	4.06	5.96	7.21	0.68	1.62	10.15
ET	5.33-8.166	6.61±0.32	0.64	9.65	0.93	1.24	0.32	0.19	0.51	8.61	6.54	10.81	0.37	0.54	8.15
GS	49-63.5	56.88±0.93	3.68	6.48	2.66	3.54	2.65	9.10	11.75	2.86	5.30	6.03	0.77	5.47	9.61
TW	20.28-29.79	26.42±0.54	2.41	9.21	1.55	2.07	0.90	4.37	5.28	3.60	7.91	8.69	0.83	3.92	14.84
GY	5067.97-6885.27	18612.35±1.470	499.68	8.46	4161.73	5537.19	6483868.00	5442524.00	11926390.00	13.68	12.53	18.55	0.46	3246.48	17.44
BY	8270.18-13209.23	11197.60±865.34	1450.63	13.02	2449.67	3259.29	2246473.52	1042272.39	3288745.91	13.39	9.12	16.20	0.32	1183.95	10.57
HI	31.13-39.08	34.67±0.47	1.80	5.21	1.36	1.80	0.69	3.01	3.69	2.39	5.00	5.54	0.81	3.22	9.29

VERY LATE SOWN														
DFF	52.33-66.33	58.08±0.47	4.05	6.96	1.36	1.80	0.69	13.97	14.66	1.43	6.44	6.59	0.95	7.52	12.94
DTM	113.16-128.33	118.02±0.91	2.80	2.32	2.58	3.43	2.49	30.02	32.51	1.34	4.64	4.83	0.92	10.85	9.19
PH	60.66-78	68.40±1.11	5.40	7.88	3.16	4.21	3.75	21.84	25.59	2.83	6.83	7.39	0.85	8.89	13.00
SL	5.95-7.63	6.63±0.20	0.44	6.62	0.58	0.77	0.13	0.10	0.23	5.35	4.79	7.18	0.45	0.44	6.59
SPS	11.5-17.5	14.71±0.55	1.36	9.28	1.57	2.09	0.92	0.87	1.79	6.52	6.33	9.09	0.49	1.34	9.09
ET	4-7.6	5.26±0.40	0.86	15.13	1.14	1.52	0.49	0.38	0.87	13.30	11.67	17.69	0.44	0.84	15.86
GS	35-48.33	40.85±1.10	3.39	8.28	3.14	4.18	3.69	7.35	11.03	4.70	6.63	8.13	0.67	4.56	11.15
TW	18.43-28.69	23.94±0.56	2.52	10.60	1.59	2.11	0.94	4.70	5.64	4.06	9.05	9.92	0.83	4.08	17.02
GY	2170.83-3422.78	2821.46±72.44	353.07	12.57	205.07	272.85	15743.64	95473.15	111216.79	4.45	10.95	11.82	0.86	589.74	20.90
BY	6526.19-11725.63	9422.04±458.66	1478.33	15.73	1298.43	1727.56	631133.47	1411873.49	2043006.96	8.43	12.61	15.17	0.69	2034.83	21.60
HI	26.73-33.95	30.19±0.52	1.67	5.54	1.49	1.99	0.83	1.87	2.71	3.02	4.53	5.45	0.69	2.35	7.77

DISCUSSION

In present study a total of 30 bread wheat genotypes were studied across different environment for yield and yield contributing characters. A highly noteworthy difference was found among the genetic constitution for all the traits over the various environments over the two years that was more considerable amount of genetic variability among themselves and same conditions has been observed by Kumar *et al.* 2025, Reddy et al 2021.The G*E interaction for timely late and very late sown conditions was showed a significant difference by DFF, SL, ET, TW, BY, GY, and HI and SPS did not show any significant difference for the G*E interaction. The same conditions have been testified through Wani*et al.* (2018), Mishra*et al.* (2024). Rathod *et al.* (2019), Saxena *et al.* (2016), Irfan *et al.*(2018), Khan *et al.* (2018), and Mamrutha*et al.* (2020).To evaluate the performance of wheat genotypes under various conditions, a detailed assessment of Agro-morphological traits was conducted as these characteristics are crucial for mean performance to various environments. To investigate the response of 11 Agro-morphological traits for various environments the significant difference had been observed in DFF, DTM, PH, SL, SPS, GS, ET, TW, BY, SY and HI. The GV observed within the evaluated genotypes serves as the groundwork for CBP, enabling selection of superior genotypes. Consequently, the greater the variability within the breeding material for a given trait, the higher the potential for enhancement through selection. As evident from the results, PCV estimates were greater than GCV for all morphological traits, proving a substantial influence of the environment on trait expression. These findings are consistent with studies conducted by Gowda*et al.* (2011), Kumar *et al.* (2021), Kamwar*et al.* (2020), Singh*et al.* (2022). The heritability in the broad sense was classified as less than 40% considered as poor, 40-80% considered as moderate, and greater than 80% considered as high, as indicated by Pratap*et al* (2024). Higher estimates of variability (80%) were observed for 0.96 in DTM, the low estimates of heritability in timely showing conditions, 0.30 (ET), observed in timely showing conditions. The late showing conditions observed heritability 0.98 in DTM, The low estimates of heritability 40% was observed for ET, GY, whereas in Very late conditions, observed heritability 0.95 DFF and low heritability observed in ET 0.44 these findings were aligned by Saini*et al.*(2025) Prasad *et al.* (2021),Fellahi *et al.* (2013), Waqas *et al.* (2014), Saleem *et al.*(2016) and Jan *et al.* (2020). Association analysis was performed to examine the relationships between key agro-morphological traits and GY under E1, E2, and E3. The results, along with their significance levels, reveal which traits positively or negatively influence yield across different environments. In E1, GY (kg/ha) exhibited a strong positive correlation with ET, DTF, DTM, TW, SL, SPS, GS, and PH, while showing a significant negative correlation with HI. Under late sown conditions, GY correlated significantly with DTF, DTM, TW, SL, ET, SPS, GS, and BY whereas HI and PH showed non-significant correlations with GY. For very late sown conditions, GY demonstrated significant positive correlations with GS, ET, SPS, DTM, HI, TW , DTF, SL, PH, and BY . These findings are in agreement with previous studies that reported similar associations of grain yield with various agro-morphological traits (Baye*et al.*, 2020; Cifci*et al.*, 2012; Wani*et al.*, 2018; Rajput, 2019).PCA was hired to analyse 11 agro structural traits in wheat, for various environmental conditions viz. Timely, Late and Very late sown The information of eleven traits was reduced into four principal components (PCs), for all three environments and all of them had EV greater than 0.5, and these altogether accounted for 85.13% under timely sown, 85.64% under late sown, while under very late sown condition these PCs accounted 87.89% `variation of the overall variation among genotypes under study. This suggests that the traits contributing most significantly to these primary components are vital in distinguishing genotypic response between the two environmental scenarios. Interrelationships among variables were inferred based on the angular distances between vectors in the PCA biplots: angles of 90° denoted absence of correlation, angles less than 90° indicated positive correlations, and those exceeding 90° signified negative correlations. Specifically, PC1 (6.04), PC2 (1.76), PC3 (0.81), PC4 (0.76) were the prominent components for timely sown and for late sown PC1(6.55), PC2(1.21), PC3(0.88), PC4(0.78) were the prominent component while for very late sown condition these four PC1(7.67), PC2(0.81), PC3(0.74), PC4(0.45) identified as prominent PCs components. These findings are consistent with prior research conducted by Wani*et al.* (2018), Bhandari *et al* (2023). The genetic diversity analysis of 30 genotypes across E1, E2, and E3 conditions revealed substantial variability, clear genotype differentiation. The D^2 clustering method consistently grouped the genotypes into four distinct clusters across all environments, with C. III and IV containing the largest number of entries. This recurring pattern indicates broad genetic divergence and stable clustering behaviour under varying environmental conditions, reflecting the robustness of these genotype groups. Trait contribution analysis demonstrated that phonological traits, especially days to maturity under timely (27.2%) and late sowing (52%), and days to 50% flowering under very late sowing (27.3%), were the major contributors to genetic divergence. These results highlight the strong environmental influence on wheat phonology, which aligns with recent reports showing that heat and delayed sowing conditions significantly alter flowering and maturity patterns, thereby contributing heavily to genetic variation. In contrast, traits like SPS and BY showed minimal contribution, suggesting comparatively lesser variability for these traits under stress environments. Inter- and intra-Bunches distance analysis further confirmed wide genetic divergence. Bunches consistently exhibited the highest inter-Bunches distances across environments, indicating its suitability for selecting genetically distant parents. Crosses involving parents from clusters with maximum inter-Bunches distances are more likely to produce transgressive segregants and improve yield and adaptability, as supported by recent wheat breeding studies. Overall, the study demonstrates a strong genetic base among the evaluated wheat genotypes. The observed divergence provides an opportunity to design effective breeding programs by selecting genetically distant and high-performing genotypes, particularly from Clusters III and IV, to develop improved, climate-resilient wheat varieties this study aligns with a previous study of Kaur et al. 2023, Dagade*et al.* 2020, Kushwaha*et al.* 2019, Shyam*et al.* 2018.

CONCLUSIONS

Multi-environment evaluation of thirty genotypes of wheat under timely, late and very late sowing revealed that substantial genetic variability across all agro-morphological traits, underscoring the richness of the germplasm for climate-resilient breeding. Early flowering and maturity in genotypes such as K 1006 and DBW 51 indicated the presence of photoperiod-insensitive and heat-tolerant genetic backgrounds, essential for mitigating terminal heat stress. Yield and biological yield exhibited high genetic variability under favourable conditions, whereas phonological traits, such as days to maturity, showed high heritability but low genetic advance, reflecting strong genetic control with limited scope for selection. Correlation and PCA analyses demonstrated that grain yield is predominantly determined by a coordinated set of traits, with effective tillers, grains per spike, spike length, and thousand-grain weight being consistent contributors even under stress. Stability analyses (Eberhart and Russell, AMMI) identified G18, G19, G21, G24, G25, G3, G6, and G7 as stable, high-yielding genotypes, with G24, G25, G19, G10, and G6 showing broad adaptation across environments. Genetic diversity and clustering highlighted the breeding value of Clusters III and IV and emphasized the role of phonological traits in adaptation. Collectively, these findings provide a robust framework for wheat improvement, identifying elite, stable genotypes and key traits to enhance yield stability and resilience under changing climatic conditions.

Author's contribution:

AK and YS designed and performed the experiment; AK, SG and AT have done analysis and compiled result. SV, HK, AG and AT drafted and reviewed the manuscript.

Data availability:

Yield and related traits were recorded. In separately plan, five competitive plants were haphazardly tagged for observations across the three environments. The mean values for each treatment were premeditated, and the traits studied along with the methods used for their measurement. The traits recorded included: (a) days to 50% flowering, (b) days to maturity, (c) plant height, (d) spike length, (e) spikelets per spike, (f) effective tillers, (g) grains per spike,

(h) 1000-seed weight, (i) grain yield (kg/ha), (j) biological yield (kg/ha), and (k) harvest index. The collected data were averaged and subjected to analysis.

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REFERENCES

- Baye A, et al. (2020). Genotypic and phenotypic correlation and path coefficient analysis in bread wheat (Triticum aestivum L.). Cogent Food Agric 6:1752603. https://doi.org/10.1080/23311932.2020.1752603
- Bhandari RK, Nyaupane S, Poudel MR (2023). Expression and association of quantitative traits of wheat under different environments. Cogent Food Agric 9. https://doi.org/10.1080/23311932.2023.2288394
- Bita CE, Gerats T (2013). Plant tolerance to high temperature in a changing environment: scientific fundamentals and production of heat stress-tolerant crops. Front Plant Sci 4:273. https://doi.org/10.3389/fpls.2013.00273
- Cifci EA (2012). Estimation of heterosis, correlation and path analysis for grain yield in durum wheat (Triticum durum Desf.). J Anim Plant Sci 22:747-752
- Dagade SK, Dodake SS, Magar NM (2020). Genetic variability and path coefficient analysis in bread wheat (Triticum aestivum Desf.). J Pharmacogn Phytochem 9:2149-2155
- Fellahi Z, et al. (2013). Genetic variability, heritability and association studies in bread wheat (Triticum aestivum L.) genotypes. Electron J Plant Breed 4:1161-1166
- Hyles J, et al. (2020). Phenology and related traits for wheat adaptation. Heredity 125:417-430. https://doi.org/10.1038/s41437-020-0320-1
- Irfan M, Khan I (2018). Effect of heat stress on morpho-physiological traits of wheat (Triticum aestivum L.) genotypes. Spec J Agric Sci 4:13-23
- Jan N, Rumisa S, Subhash CK (2020). Interrelationship and path analysis in wheat (Triticum aestivum L.) for yield traits. Plant Arch 20:1483-1486
- Kaur SJ, et al. (2023). Genetic profiling of bread wheat (Triticum aestivum L.): analyzing variation and diversity. J Food Chem Nanotechnol 9:S21-S27
- Khan A, et al. (2018). Comparative performance of spring wheat (Triticum aestivum L.) through heat stress indices. Pak J Bot 50:481-488
- Kumar A, et al. (2021). Assessment of genetic variability, heritability and genetic advance in wheat (Triticum aestivum L.) under salt-affected soil

- Kumar A, et al. (2025). Assessment of genetic variability, heritability and genetic advance in wheat (Triticum aestivum L.) under salt-affected soil Kumar R, et al. (2023). Stability analysis for yield and yield contributing traits in wheat (Triticum aestivum L.) 53:13477-13485
- Kushwaha AK (2019). Studies on genetic variability, correlation, path coefficient and divergence analysis in wheat
- Mamrutha HM, et al. (2020). Impact of high night temperature stress on different growth stages of wheat. Plant Physiol Rep 25:707-715
- Mishra SK, et al. (2024). Studies on genetic variability, correlation and path coefficient analysis for yield and yield contributing traits in bread wheat (Triticum aestivum L.). J Exp Agric Int 46:389-397
- Patil P, et al. (2024). Genetic variability, heritability, genetic advance and divergence analysis in wheat (Triticum aestivum L.). Indian J Agric Res 58:209-214
- Rajput RS (2019). Path analysis and genetic parameters for grain yield in bread wheat (Triticum aestivum L.). Annu Res Rev Biol 31:1-8
- Rathod ST, Pole SP, Gawande SM (2019). Correlation and path analysis for quality and yield contributing traits in wheat (Triticum aestivum L.). Int J Curr Microbiol Appl Sci 8:456-461
- Reddy BSK, et al. (2021). Agronomic evaluation of wheat (Triticum aestivum L.) genotypes under north eastern plain zones. Int J Chem Stud 9:200-202. https://doi.org/10.22271/chemi.2021.v9.i1c.11234
- Saini PK, et al. (2025). Genetic assessment of quantitative trait variation in bread wheat (Triticum aestivum L.). J Sci Res Rep 31:871-880
- Saleem B, et al. (2016). Estimation of heritability and genetic advance for metric traits in wheat (Triticum aestivum L.). J Agric Sci 61:1-9
- Saxena DC, et al. (2016). Phenotypic characterization of specific adaptive physiological traits for heat tolerance in wheat. Indian J Plant Physiol 21:318-322
- Shyam C, et al. (2018). Evaluation of genetic divergence analysis in wheat for yield and component traits. Int J Agric Environ Biotechnol 11:829-834
- Wani SH, et al. (2018). Genetic variability study in bread wheat (Triticum aestivum L.) under temperate conditions. Curr Agric Res J 6
- Waqas M, et al. (2014). Estimation of heritability and genetic advance for yield traits in F2 populations of wheat (Triticum aestivum L.). Sci Lett 2:43-47
- Zhang D, et al (2023) Future climate change impacts on wheat grain yield and protein in the North China region. Sci Total Environ 902:166147. https://doi.org/10.1016/j.scitotenv.2023.166147