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Dissecting genetic variability for yield components in wheat through multivariate analysis

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Abstract
This study was aimed to evaluate genetic diversity, character associations, and multivariate structure among wheat genotypes to identify key traits for yield improvement. The analysis revealed that phenotypic variation marginally exceeded genotypic variation across traits, indicating a limited environmental influence on trait expression. Relatively higher variability was identified for number of tillers/plant, while moderate for spike length, number of spikelets/ spike, number of grains /spike, biological yield and grain yield/ plant and harvest index, suggesting greater scope for effective selection. High heritability in conjunction with substantial genetic advance was recorded for all major yield-contributing traits, reflecting the predominance of additive gene effects and their responsiveness to selection. Correlation indicates strong positive associations of grain yield with number of tillers /plant, spike length, number of spikelets/ spike, number of grains /spike, test weight biological yield, highlighting their importance as selection criteria. Principal component analysis demonstrated that first four principal components *viz.,* PC1, PC2, PC3, PC4 accounted for a major proportion (69.20 %) of total variation, with the first component primarily representing yield-related traits. The biplot further confirmed strong positive clustering of yield-related traits, while phenological traits exhibited weak associations with yield. These findings suggest that improvement in yield can be achieved through the selection of genotypes possessing favorable yield contributing traits.

Keywords: Wheat, Heritability, Genetic advance,Yield determinants,Multivariate analysis

INTRODUCTION

Wheat (*Triticum aestivum* L.) serves as a major staple crop contributing significantly to global food security, supplying roughly 20 % of the world's caloric intake and protein (FAO, 2022). Global wheat production faces growing pressure from population growth, climate variability, and shifting consumer demands, making the identification and deployment of diverse, high-yielding genotypes, a central priority in modern breeding programs. Hexaploid wheat originated through natural hybridization involving three distinct genomes (A, B, and D); consequently, no extant wild species possesses the similar genomic constitution as hexaploid wheat (Terasawa *et al.,* 2009). *T.urartu, A. spelt0ides, and A. tauschii* are the progenitor species for A, B & D genomes (Nielsen *et al.,* 2014).

Wheat is grown over approximately 222.88 million hectares (Director's Report, ICAR-IIWBR 2023-24). Recent global estimates indicate that world wheat output in 2023-24 is 788.95 million metric tons (USDA, 2023). Productivity has been consistently increasing, currently averaging about 3.5 tons per hectare (International Grains Council, 2023). China, India, the USA, and Russia, which together play a crucial role in overall global production. India ranks among the world's largest wheat producers, with around 31.23 million hectares allocated for wheat cultivation during the 2023-2024 and the average wheat productivity in India has steadily increased, currently reaching about 36.15 q/ hectare .The primary wheat-growing states and their share include Uttar Pradesh (29.82 %), Madhya Pradesh (22.86 %), Punjab (11.23 %), Rajasthan (8.77 %) and Haryana (7.68 %). (Director's Report, ICAR-IIWBR 2023-24).

Wheat is a nutrient-dense food primarily composed of carbohydrates (70-75 %), proteins (10-12%), and low fat (1-2 %). It is rich in essential vitamins (B1, B3, B9) and minerals. Additionally, it offers significant dietary fiber, antioxidants, and beneficial

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phytochemicals like phenolic acids and alkylresorcinols (Sikhwala *et al.,* 2023). Productivity worldwide is significantly affected by multiple biotic (pests and pathogens) and abiotic stresses (drought, high temperature, and salinity) reinforcing the strategic importance of exploring and exploiting phenotypic and genetic diversity in wheat breeding pipelines (Reynolds *et al.,* 2016).Genetic variability is fundamental to wheat breeding, enabling the selection for improved desirable characters (Kumar *et al.,* 2022). Recent studies indicate that intensive modern breeding has progressively narrowed the genetic base for several yield-related traits across many target environments (Wang *et al.,* 2025). Direct selection effectively improves high-yielding genotypes, whereas indirect selection is best for traits with low heritability (Singh *et al.,* 2026).The present study is to assess genetic variability, character associations, and multivariate structure among wheat genotypes to identify key agro-morphological and yield-related traits under typical production conditions for yield improvement.

MATERIALS AND METHODS

The material used in current research comprised of 100 advance breeding lines and four checks (HD2967, HD3086, NW2036, NW5054), **(Table 1)** representing diverse genetic backgrounds, procured from All India coordinated Research Project on wheat and barley, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya. These lines were carefully selected to explore their genetic performance under optimal conditions. The study was undertaken at main experimental station (MES) of ANDUA&T, Kumarganj, Ayodhya, during *Rabi* 2023-24.

The trial was laid out in augmented design to ensure the reliability and reproducibility of results. Each lines row measuring 3 meters in length. The distance between two rows was 22 cm and a plant-to-plant spacing of 10 cm to allow adequate plant growth and minimize competition. Appropriate and uniform cultural practices were adopted during the entire cropping period, including optimal fertilizer application and crop protection measures at key growth stages, ensuring that the environmental conditions were contributing for unbiased evaluation of the breeding lines. The following observations were recorded at appropriate growth stages days to 50% flowering, days to maturity, plant height (cm), number of tillers /plant, spike length (cm), peduncle length (cm), number of spikelets/ spike ,number of grains /spike , test weight (g), biological yield (g/plot), harvest index (%) and grain yield /plant (g). All the morphological traits were recorded from five randomly selected representative plants in each genotype while days to maturity and days to 50 % flowering were recorded on a plot basis. Biological yield was recorded as the total above-ground biomass produced per plant at maturity and expressed in grams. Grain yield per plant was determined by threshing individual plants and recording the grain weight in grams. Harvest index was calculated as the ratio of grain yield to biological yield and expressed as a percentage using the following formula: biological yield plant /Grain yield per plant x 100

Statistical analysis

The observations were recorded on all quantitative traits used for statistical analysis following the procedure appropriate augmented block design as outlined by Federer (1956). Genotypic variance components, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in the broad sense, and genetic advance using standard biometrical procedures (Burton, 1952). Correlation estimation was used to find the association among traits (Pearson, 1901), while principal component analysis (PCA) was done to assess the contribution of individual traits to total genetic variability and to identify the major sources of variation (Pearson, 1895). All statistical analysis were performed using statistical software **R** studio and OPSTAT.

RESULTS AND DISCUSSION

Analysis of variance (ANOVA)

The analysis of variance (ANOVA) revealed significant differences among treatments for most of the traits studied, indicating the presence of substantial genetic variability among the evaluated wheat genotypes **(Table 2)**. The treatment effect was highly significant ($P \leq 0.01$) for plant height, spike length, number of spikelets/spike, number of grains/spike, biological yield, and harvest index, while significant differences ($P \leq 0.05$) were observed for days to 50% flowering, days to maturity, number of tillers/plant, peduncle length, test weight, and grain yield/plant. Block effects were significant for days to 50% flowering, number of tillers/plant, spike length, test weight, biological yield, and grain yield/plant, indicating some environmental variation among blocks. However, non-significant block effects and lower residual mean squares for most of the traits reflected adequate experimental precision. Considerable variability was observed among the wheat genotypes for all the traits studied. The mean values ranged from 6.52 for number of tillers per plant to 124.06 days to maturity. Wide ranges were recorded for grain yield per plant (8.19–18.21 g), biological yield (22.33–49.59 g), number of grains per spike (29.61–56.77), and harvest index (25.12–55.07%), indicating substantial genetic diversity and scope for effective selection in the breeding population.

Genetic variability analysis

Genetic parameters revealed considerable variability among traits **(Table 3)**. In general, phenotypic coefficients of variation (PCV) were slightly higher than the corresponding genotypic coefficients of variation (GCV) across traits, indicates minor influence of environmental on trait expression.The genotypic coefficient of variation (GCV) ranged from 3.88 to 23.03 % and phenotypic coefficient of variation (PCV) varied from 4.06 to 23.56 % for days to maturity and number of tillers/ plant, respectively. High GCV and PCV values were observed for number of tillers/plant (23.03 and 23.56

Table 1. List of plant material used in current study

S. No.	Genotype	S. No.	Genotype	S.No.	Genotype	S.No.	Genotype
1	1SAWYT-EM-1	27	1SAWYT-EM-27	53	22HTWYT-4	79	22HTWYT-30
2	1SAWYT-EM-2	28	1SAWYT-EM-28	54	22HTWYT-5	80	22HTWYT-31
3	1SAWYT-EM-3	29	1SAWYT-EM-29	55	22HTWYT-6	81	22HTWYT-32
4	1SAWYT-EM-4	30	1SAWYT-EM-30	56	22HTWYT-7	82	22HTWYT-33
5	1SAWYT-EM-5	31	1SAWYT-EM-31	57	22HTWYT-8	83	22HTWYT-34
6	1SAWYT-EM-6	32	1SAWYT-EM-32	58	22HTWYT-9	84	22HTWYT-35
7	1SAWYT-EM-7	33	1SAWYT-EM-33	59	22HTWYT-10	85	22HTWYT-36
8	1SAWYT-EM-8	34	1SAWYT-EM-34	60	22HTWYT-11	86	22HTWYT-37
9	1SAWYT-EM-9	35	1SAWYT-EM-35	61	22HTWYT-12	87	22HTWYT-38
10	1SAWYT-EM-10	36	1SAWYT-EM-36	62	22HTWYT-13	88	22HTWYT-39
11	1SAWYT-EM-11	37	1SAWYT-EM-37	63	22HTWYT-14	89	22HTWYT-40
12	1SAWYT-EM-12	38	1SAWYT-EM-38	64	22HTWYT-15	90	22HTWYT-41
13	1SAWYT-EM-13	39	1SAWYT-EM-39	65	22HTWYT-16	91	22HTWYT-42
14	1SAWYT-EM-14	40	1SAWYT-EM-40	66	22HTWYT-17	92	22HTWYT-43
15	1SAWYT-EM-15	41	1SAWYT-EM-41	67	22HTWYT-18	93	22HTWYT-44
16	1SAWYT-EM-16	42	1SAWYT-EM-42	68	22HTWYT-19	94	22HTWYT-45
17	1SAWYT-EM-17	43	1SAWYT-EM-43	69	22HTWYT-20	95	22HTWYT-46
18	1SAWYT-EM-18	44	1SAWYT-EM-44	70	22HTWYT-21	96	22HTWYT-47
19	1SAWYT-EM-19	45	1SAWYT-EM-45	71	22HTWYT-22	97	22HTWYT-48
20	1SAWYT-EM-20	46	1SAWYT-EM-46	72	22HTWYT-23	98	22HTWYT-49
21	1SAWYT-EM-21	47	1SAWYT-EM-47	73	22HTWYT-24	99	41SAWSN-1
22	1SAWYT-EM-22	48	1SAWYT-EM-48	74	22HTWYT-25	100	41SAWSN-2
23	1SAWYT-EM-23	49	1SAWYT-EM-49	75	22HTWYT-26	C1	HD 2967
24	1SAWYT-EM-24	50	22HTWYT-1	76	22HTWYT-27	C2	HD3086
25	1SAWYT-EM-25	51	22HTWYT-2	77	22HTWYT-28	C3	NW2036
26	1SAWYT-EM-26	52	22HTWYT-3	78	22HTWYT-29	C4	NW5054

Table 2. ANOVA showing mean squares for different quantitative traits in wheat genotypes

S.No.	Traits	Block (ignoring Treatments)	Treatment (eliminating Blocks)	Treatment: Check	Treatment: Test and Test vs. Check	Residuals
1	Df	1	103	3	100	3
2	Days to 50% flowering	31.54*	60.56*	9.45	62.09*	2.73
3	Days to maturity	5.49	29.33*	41.38*	28.97*	2.20
4	Plant height	14.04	46.93**	52.85**	46.75**	1.57
5	Number of tillers /plant	2.73*	2.64*	2.88*	2.63*	0.10
6	Spike length	1.79*	4.21**	0.86*	4.31**	0.06
7	Peduncle length	0.22	0.68*	1.86*	0.64*	0.07
8	Number of spikelets/ spike	0.98	6.37**	12.79**	6.18**	0.17
9	Number of grains /spike	0.08	56.63**	130.87**	54.4**	1.93
10	Test weight	32.74**	14.31*	12.61*	14.36*	0.59
11	Biological yield	12.70**	27.44**	29.69**	27.37**	0.27
12	Grain yield/ plant	6.26*	4.68*	3.70*	4.71*	0.24
13	Harvest index	7.82	33.96**	8.94	34.71**	0.99

P > 0.05; * P <= 0.05; ** P <= 0.01

Table 3. Evaluation of genetic parameters for twelve traits in wheat

S.No.	Trait	GCV (%)	PCV (%)	Heritability (%)	GA	GAM	Mean	Range
1	Days to 50% flowering	9.75	9.98	95.37	15.1	19.63	76.92	63.5-87.5
2	Days to maturity	3.88	4.06	91.34	9.5	7.66	124.06	114.49-136.11
3	Plant height (cm)	8.28	8.42	96.68	13.7	16.8	81.59	64.17-94.97
4	Number of tillers /plant	23.03	23.56	95.59	3.03	46.46	6.52	4.1-9.9
5	Spike length (cm)	18.07	18.22	97.37	3.89	36.98	10.53	6.25-14.16
6	Peduncle length (cm)	4.32	4.58	89.05	1.47	8.42	17.51	15.21-19.24
7	Number of spikelets/ spike	12.61	12.82	96.7	4.55	25.58	17.77	11.56-24.65
8	Number of grains /spike	14.07	14.37	95.9	13.56	28.42	47.69	29.61-65.77
9	Test weight (g)	9.68	9.89	95.78	7.42	19.55	37.94	28.08-43.92
10	Biological yield (g)	15.71	15.78	98.03	10.77	32.25	33.38	22.33-49.59
11	Grain yield/ plant (g)	16.43	16.86	94.98	4.3	33.03	13	8.19-18.21
12	Harvest index	14.88	15.1	97.2	11.89	30.27	39.27	25.12-55.07

%, respectively), indicating the presence of substantial genetic variability for this trait. Moderate GCV and PCV were recorded for spike length, number of spikelets/spike, number of grains/spike, biological yield, grain yield/plant, and harvest index.The close correspondence between GCV and PCV estimates for all traits indicated a minimal influence of environmental factors on trait expression and suggest that the observed variability was predominantly genetic in nature. Comparable results were documented by Ahmad and Gupta (2023). Broad-sense heritability was high for all traits, ranged from 89.05 % for peduncle length to 98.03 % for biological yield and the results aligns with the study reported by Makkena and Kulwal (2025).

Days to 50% flowering (15.10) and number of grains/spike (13.56) recorded the highest genetic advance, followed by harvest index (11.89) and biological yield (10.77), indicating significant improvement potential through selection. Moderate GA was observed for days to maturity (9.50), test weight (7.42), number of spikelets/spike (4.55), grain yield (4.30), and spike length (3.89), while number of tillers/plant (3.03) and peduncle length (1.47) showed the lowest values. High GA for traits suggests additive gene action, enabling effective phenotypic selection.

The high genetic advance (GAM) as % of mean values were observed for number of tillers/plant (46.46 %), spike length (36.98 %), grain yield/plant (33.03 %), biological yield (32.25 %), harvest index (30.27 %), number of grains/spike (28.42 %), and number of spikelets/ spike (25.58 %), indicating that these traits are largely governed by additive gene action and can be effectively improved through direct phenotypic selection. In contrast, days to maturity (7.66 %) and peduncle length (8.42 %) exhibited low GAM despite high heritability, suggesting the possible involvement of non-additive gene effects and environmental interactions. Days to 50% flowering (19.63 %), plant height (16.80 %), and test weight (19.55 %) showed moderate GAM coupled with high heritability, indicating moderate scope for genetic improvement through selection. The above results are in consistent with earlier reports by Tolwani and Shukla (2022)and Abebe *et al*. (2024)**.** The combination of high heritability and high genetic advance observed for number of tillers/ plant, spike length, number of spikelets/ spike, number of grains/spike, biological yield, grain yield/plant, and harvest index suggests that these traits are predominantly controlled by additive gene effects and therefore represent reliable selection criteria for the genetic improvement of grain yield and its related components in wheat breeding programs.

Correlation

Based on the correlation matrix **(Fig.1.)** the strong significant positive correlation was observed between grain yield /plant and biological yield (r = 0.56), followed by test weight (r = 0.43), spike length (r = 0.40), number of grains/spike (r = 0.40), number of tillers/plant (r = 0.51), and number of spikelets/spike (r = 0.34) and harvest index (0.50).It indicates that an increase in sink capacity through the production of more productive tillers, spikelets, and grains/spike can substantially improve grain yield. Likewise, the positive relationship between grain yield and test weight reflects the importance of grain size and grain filling in determining final yield performance.

Among the yield component traits, Spike length showed strong positive correlation with number of grains /spike (r = 0.70), number of tillers/plant (r = 0.65), and number of spikelets/spike (r = 0.63), and harvest index (0.26) indicating that longer spikes tend to possess more spikelets and grains. Similarly, number of grains /spike was positively correlated with number of tillers/plant (r = 0.46) and number of spikelets /spike(r = 0.47). Biological yield showed a significant correlation with spike length (0.20) number of grains /spike. (0 .24) number of tillers/plant. (0 .23).These positive interrelationships among yield and related traits suggest that simultaneous selection

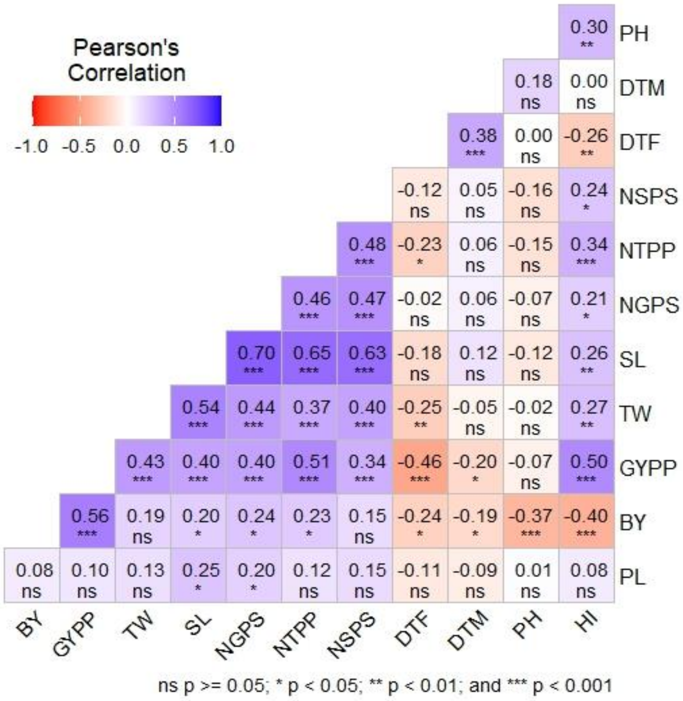

Fig. 1. Pearson's correlation matrix representing interrelationships among yield and associated traits
(DTF Days to 50% flowering; DTM Days to maturity; PH Plant height; NTPP Number of tillers /plant; SL Spike length;PL Peduncle length;NSPS Number of spikelets/ spike;NGPS Number of grains /spike;TW Test weight; BY Biological yield;GYPP Grain yield/ plant;HI Harvest index)

for spike length, productive tillers, spikelets/spike, and grains/spike could effectively enhance biological yield and ultimately improve grain yield in wheat. Test weight is high significantly associated with spike length. (0.54) number of grains/ spike. 0.44. number of tillers/plant (0.37) and number of spikelets/spike. (0.40) and plant height is also positively correlated (0.30) with harvest index. Days to 50% flowering and days to maturity has significant and positive correlation (0.38) Flowering and maturity traits generally displayed negative relationships with most yield-attributing characters.

Spike length, grains/spike, tillers/plant, spikelets/spike, and biological yield showed strong positive associations with grain yield/plant identifying these traits as key yield determinants, in agreement with earlier reports by Khan and Naqvi (2012). Strong intercorrelations among yield components *viz*., number of spikelets/spike, number of grains/spike,number of spikelets/spike, test weight–biomass yield) further indicate coordinated regulation of yield architecture, consistent with the ideotype concept subsequent validation in wheat (Slafer *et al.,* 2014). The weak, non-significant correlations of days to 50 % flowering, days to maturity, and plant height with yield suggest a limited role of phenology and stature under the present conditions, corroborating recent findings by Negash *et al.* (2025).

Principle Component Analysis

Principal component analysis (PCA) of the dataset demonstrate that the first principal component (PC1) showed the highest eigenvalue (λ_1 = 3.93) and accounted for 32.80 % of the total variance (**Table 4**). The cumulative variance explained by the first two PCs reached 47.96 % indicating that these components captured a substantial proportion of the variability present in the population increasing upto 69.20 % for the first four PCs and 81.69 % for the first six PCs **(Fig. 2)**. These findings suggest substantial dimensionality reduction, with subsequent components (PC7–PC12) contributing minimally (18.31 % combined), consistent with typical PCA scree patterns in multivariate genetic or phenotypic datasets.

Table 4. Eigenvalues and variance contribution of principal components

Parameters	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12
Eigen value	3.93	1.81	1.55	0.99	0.80	0.69	0.59	0.52	0.48	0.38	0.19	0.01
Variance %	32.80	15.15	12.96	8.28	6.67	5.81	4.94	4.33	4.01	3.23	1.61	0.16
Cumulative variance %	32.80	47.96	60.92	69.20	75.88	81.69	86.63	90.97	94.98	98.22	99.83	100.00

As shown in **Fig. 3**, spike length, number of spikelets/ spike, number of grains/spike, number of tillers/plant, test weight, and grain yield/plant were located on the positive side of the first principal component and exhibited strong positive associations. Their longer vectors indicated a major contribution to genetic variation and genotype differentiation. Biological yield and harvest index also contributed substantially to overall variability. In contrast, days to 50% flowering was positioned opposite to most yield-related traits, indicating a negative association with these characters. Days to maturity and plant height were mainly associated with the second principal component, whereas peduncle length contributed relatively less to the total variation. The biplot further grouped the genotypes into five distinct clusters, reflecting considerable genetic diversity among the studied genotypes.

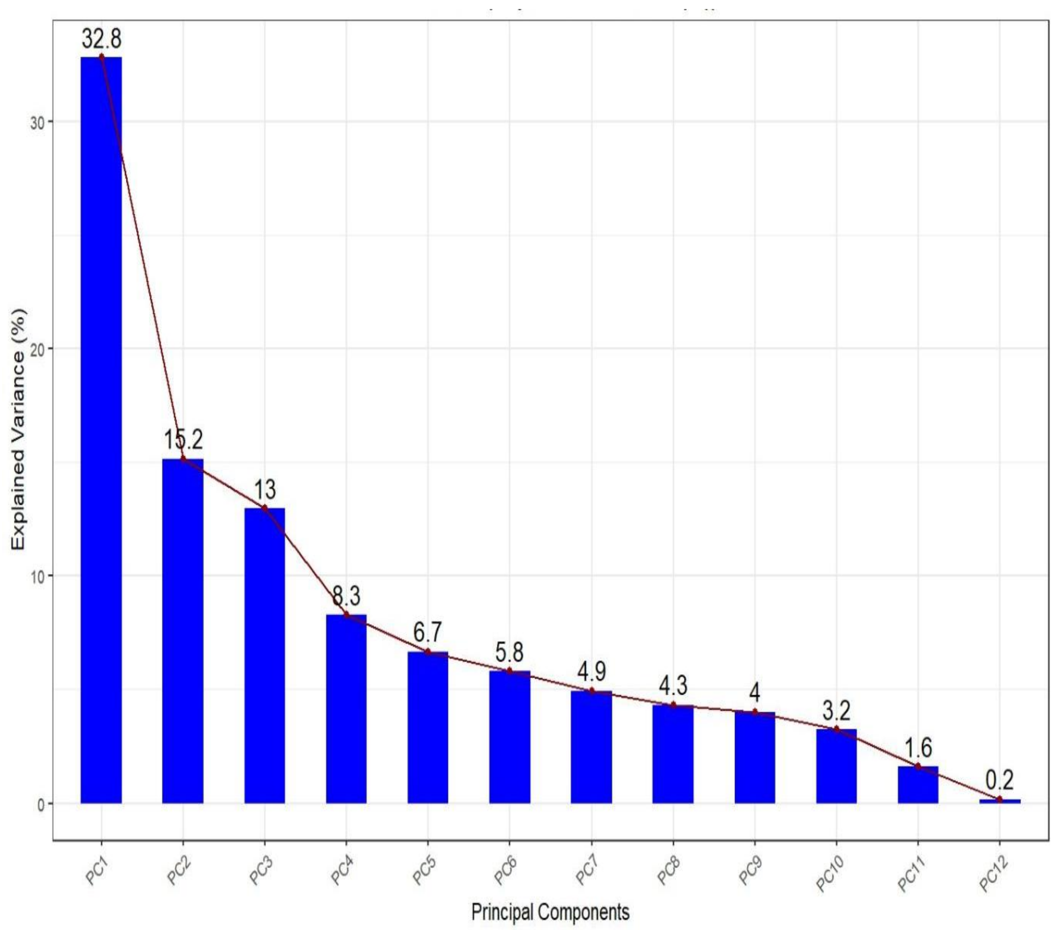

Fig. 2. Scree plot depicting the proportion of total variation explained by each principal component

Table 5. Coordinates table representing the contribution and explained variance of PC1–PC4 for agronomic traits

	Biological yield	Days to 50% flowering	Days to maturity	Grain yield/ plant	Harvest index	Number of grains / spike	Number of spikelets/ spike	Number of tillers / plant	Plant height	Peduncle length	Spike length	Test weight
PC1	0.405	-0.412	-0.085	0.756	0.433	0.720	0.692	0.757	-0.162	0.285	0.832	0.678
PC2	-0.765	0.279	0.544	-0.193	0.592	0.131	0.134	0.092	0.622	0.005	0.178	0.081
PC3	0.159	0.653	0.528	-0.357	-0.536	0.321	0.258	0.096	-0.376	-0.025	0.289	-0.037
PC4	-0.096	-0.004	-0.210	-0.235	-0.112	0.081	0.011	-0.170	0.076	0.907	0.083	-0.011

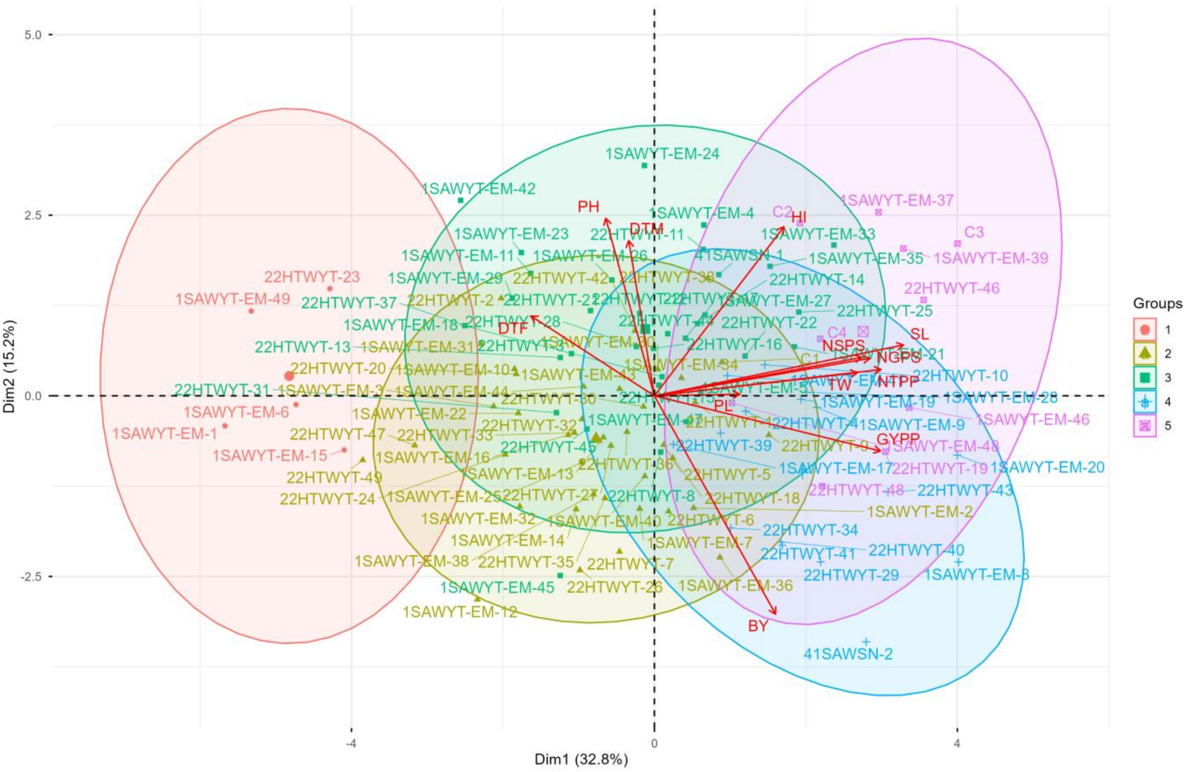

Fig. 3. Principle component analysis (PCA) biplot illustrating contribution and clustering pattern among wheat genotypes based on multiple quantitative traits

The first four principal components explained a substantial proportion of the total variability **(Table 5)**. PC1, accounting for 32.80 % of the total variation, was primarily associated with grain yield per plant (0.756), number of tillers per plant (0.757), spike length (0.832), number of grains per spike (0.720), number of spikelets per spike (0.692), test weight (0.678), harvest index (0.433), and biological yield (0.405). The high positive loadings of these traits indicate that PC1 mainly represented yield potential and yield-contributing characters. In contrast, days to 50% flowering (-0.412) showed a negative loading on PC1, suggesting an inverse relationship between earliness and yield-related traits.

PC2, which explained 15.2 % of the total variation, was largely influenced by biological yield (-0.765), plant height (0.622), harvest index (0.592), and days to maturity (0.544). This component reflected variation associated with plant architecture and phenological development. The contrasting loadings of biological yield and harvest index indicate differences in biomass accumulation and assimilate partitioning among genotypes. PC3 was characterized by high positive loadings for days to 50 % flowering (0.653) and days to maturity (0.528), while harvest index (-0.536) and grain yield per plant (-0.357) exhibited negative loadings. This suggests that PC3 mainly represented variation in crop phenology and its relationship with yield efficiency. PC4 was predominantly influenced by peduncle length (0.907), indicating that this trait contributed independently to genetic variation and was largely uncorrelated with most of the other traits studied.

PCA biplot demonstrated that spike length, number of spikelets/spike, number of grains/spike, number of tillers/plant, grain yield per plant, biological yield, and harvest index were the most influential traits governing genetic diversity in the studied wheat population (Sharma *et al.,* 2012). PCA indicates first four components explained 67.20 % of the variation, confirming effective dimensionality reduction (Kabir *et al.,* 2017). The opposite orientation of days to 50% flowering, days to maturity, plant height indicated limited yield relevance (Ambati *et al.,* 2025). Overall, number of tillers/plant, number of spikelets/spike, number of grains/spike, test weight, spike length, harvest index, and biomass yield were key selection targets.

The research demonstrated considerable variability among wheat genotypes, with key yield-related traits number of tillers/plant, number of spikelets/spike, number of grains/spike, spike length, harvest index, biological yield, and grain yield/plant exhibiting high to moderate GCV and PCV, heritability, and genetic advance, indicating their suitability for effective phenotypic selection. Correlation analysis demonstrated that grain yield/plant was positively associated with biological yield, harvest index, test weight, spike length, number of tillers/plant, number of spikelets/spike, and number of grains/spike. Principal component analysis further identified these traits as the major contributors to phenotypic variation and genotype discrimination.The first four principal components capturing substantial variation and PC1 representing the yield component. The findings support direct selection of these traits for improving grain yield in wheat.

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