

# Genetic diversity assessment in bread wheat (*Triticum aestivum* L.) using multivariate biplot analysis for yield and its components

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## Abstract

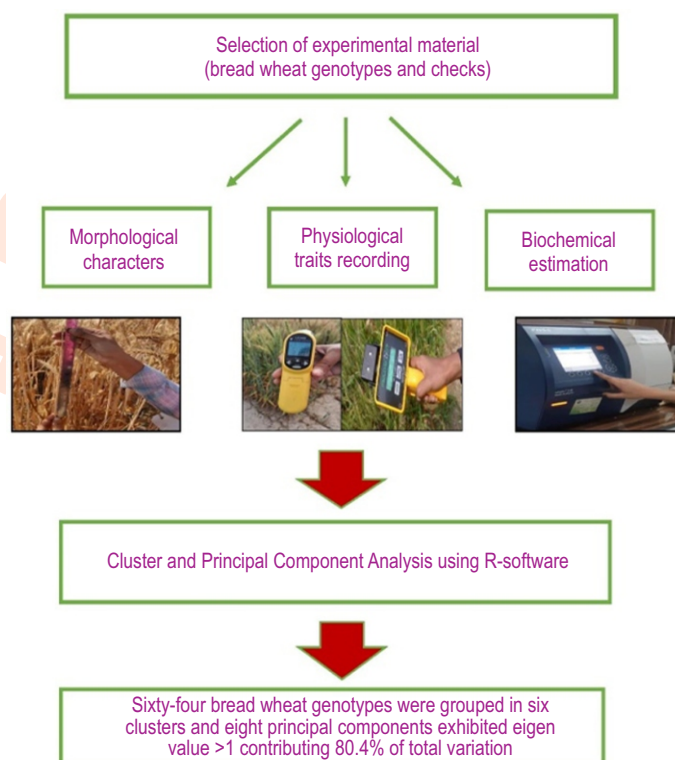
**Aim:** Evaluation of genetic diversity among 64 bread wheat genotypes for morpho-physiological and biochemical traits to select better parent for wheat breeding programme.

**Methodology:** Multivariate analysis was done for 25 morpho-physiological and biochemical traits. ANOVA, cluster and principal component analysis were performed to evaluate genetic diversity between the genotypes for selected traits.

**Results:** Significant variability was observed for all the traits under study. Hierarchical clustering grouped 64 bread wheat genotypes into six clusters. Cluster II had maximum 19 genotypes while cluster III had least three genotypes. Cluster IV exhibited the highest intra-cluster distance genotypes whereas cluster II and V showed maximum inter-cluster distance. PCA revealed that first eight components exhibited eigenvalues >1 and accounted for 80.4% variance. Biplot depicted that CTD-II, biological yield/plot, grain yield/plot, days to maturity, crude protein, gluten content, and days to anthesis contributed most to PC-I and PC-II.

**Interpretation:** Genotypes of cluster II and V showed high genetic diversity and can be utilized in hybridization programs. Simultaneous selection of these traits can improve wheat crop performance, aiding future improvement programs.

**Key words:** Genetic diversity, Grain yield, Principal component, *Triticum aestivum*, Wheat genotypes



## Introduction

Bread wheat (*Triticum aestivum* L. em. Thell), an allohexaploid ( $2n = 6x = 42$ , AABBDD), belongs to family *Poaceae*, genus *Triticum*. It is the second most cultivated crop globally, and used as staple food by one-third of world's population. The grains are high in carbohydrates, providing an excellent source of energy (Sallam *et al.*, 2024). During 2022-23, wheat production was 788.95 million tonnes with an acreage of 222.88 million hectares globally, while in India, it covers 31.78 million hectares, yielding 112.92 million tonnes (ICAR-IIWBR, 2023-24). However, several factors including extreme environmental conditions, gradual climate change, urbanization-driven loss of arable land, and population growth pose significant threat to wheat production and quality. India is particularly vulnerable to yield losses due to its reliance on subsistence farming, outdated technology and inadequate adaptation strategies (Baig *et al.*, 2023). To ensure food stability and security amidst continuous global population growth, wheat production needs to increase by 2–3% annually (Al-Ashkar *et al.*, 2023a).

By 2050, the global wheat production must increase by 60% compared to present levels to meet the growing supply demands (Majidmehr *et al.*, 2024). The primary aim of wheat breeding is to produce high-yielding, adaptable and resistant varieties and pre-requisite for any breeding program is the presence of genetic diversity because it provides traits to enhance resilience, productivity and quality (Dashora *et al.*, 2022). Multivariate analysis tools like cluster and principal component analysis examine data with multiple variables, to reveal diversity patterns and relationships among genotypes (Lal *et al.*, 2019). Cluster analysis is a tool for grouping similar genotypes into different clusters based on values of multiple variables used so that the genotypes with similar characters are gathered in same cluster (Al-Ashkar *et al.*, 2023b). The genotypes in same cluster exhibited high internal homogeneity and genotypes in different clusters exhibit high external heterogeneity (Phougat *et al.*, 2022a). When plotted geometrically, the genotypes within a cluster shall be closer and in different clusters shall be farther apart.

Principal component analysis (PCA) is a multivariate statistical technique that evaluate relationships among a large number of variables by reducing them to a smaller set of components, while retaining critical information of the original data set (Kumar *et al.*, 2024a). PCA assigns genotypes to groups, evaluates variance contributions, and identifies highly correlated variables. This makes PCA a valuable tool for prioritizing traits, differentiating genotypes and understanding variance structures, providing crucial insights for targeted breeding strategies (Hussain *et al.*, 2024). It helps the breeders to focus on key target traits rather than on all traits under study, lowers the field costs and simplifies the data, making it easier to analyze and interpret the relationships among the original variables (Kumar *et al.*, 2022). In a hypothetical scenario, Cluster and Principal Component Analysis (PCA) can identify the best wheat genotypes for cultivation by analyzing 50 genotypes across traits

like grain yield, days to maturity, plant height, spike length, spike weight, gluten content and protein content. Cluster analysis groups genotypes based on performance, like, Cluster I includes high-yield, high-protein genotypes, while Cluster II includes moderate-yield, high-protein genotypes. PCA reduces data complexity by focusing on key traits, such as grain yield and protein content (PC1) or earliness and plant height (PC2), which explain most variance. These methods prioritize genotypes for specific conditions, streamline selection, guide breeding strategies, and offer precise recommendations to farmers. In view of the above, the aim of this study was to evaluate genetic variability among bread wheat genotypes using multivariate biplot analysis methods for identification and selection of superior genotypes which can further be used to develop improved varieties.

## Materials and Methods

A field trial was conducted at Research area of Wheat and Barley Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar (29.1503° N, 75.7056° E, and 215.2 m above mean sea level). The experimental material used in the study comprised 60 genotypes and four checks viz. WH 1105, HD 3086, DBW 222, DBW 187 grown during *Rabi* season of 2022-23 in RCBD with four replications. Each genotype was planted in a plot measuring 6 m × 1.20 m with a spacing of 20 cm × 10 cm following recommended practices for optimal crop growth (Directorate of Extension Education, 2021).

**Data recording:** The data was recorded on 10 randomly selected plants of each genotype in each replication for 25 morpho-physiological and biochemical traits. Morphological traits included days to 50% heading (DH), anthesis (DA) and physiological maturity (DM) measured from sowing to specific growth stages. Plant height (PH in cm) was recorded from ground level to apex, excluding awns and number of effective tillers per meter (NT/M) was counted at physiological maturity. Spike length (SL in cm) was measured from the base to the end of mature spike, while the peduncle length (PL in cm) was recorded from the first node to spike bottom. The number of spikelets (NS/S) and grains per spike (NG/S) was calculated from ten spikes per genotype, and the main spike weight (SW in g) was measured using an electric balance. Biological and grain yield per plot (BY and GY in g/plot) were recorded post-harvest, and grain filling duration (GFD) was noted from anthesis to maturity. Harvest index (HI in %) was calculated as the ratio of grain yield to biological yield, and 1000-grain weight (TGW) was measured for each genotype.

Physiological traits viz., chlorophyll fluorescence (CFC), canopy temperature depression (CTD) and Normalized Difference Vegetation Index (NDVI) measured by using handheld OS-30p fluorometer, infrared thermometer and FIELDSCOUT NDVI meter respectively at anthesis (I) and 15 days after anthesis (II). Biochemical traits viz., crude protein (CP in %), gluten content (GC in %), sedimentation value (SV in ml) in grain were determined by using Infratec 1241 Grain Analyzer and hectolitre weight (HW in kg hl<sup>-1</sup>) by using the hectolitre weight instrument.

Mean values across the selected plants were utilized for data analysis. The data was first subjected to analysis for ANOVA (Panse and Sukhatme, 1978). Different libraries of R-software were used for performing statistical data analysis. Cluster analysis suggested by Ward (1963) was performed with appropriate procedure by using “ggplot2” and “factoextra” packages of R-software. Similarly, Principal component analysis (Hotelling, 1933) was computed using R- software with “ggplot2”, “agricolae” and “factoextra” packages.

### Results and Discussion

The mean sum of squares due to genotypes was found highly significant (at 1% level of significance) for all the traits indicating a considerable amount of genetic variation present among the genotypes (Table 1). Based on 25 morpho-physiological and biochemical traits, Euclidean distance was measured between different bread wheat genotypes. Multivariate hierarchical clustering grouped sixty-four bread wheat genotypes in six clusters so that the genotypes within each cluster exhibited smaller D<sup>2</sup> value compared to distances between the clusters, i.e., genotypes within the cluster had higher similarity than the genotypes that fell in distinct clusters. Cluster II consisted of

maximum 19 genotypes whereas Cluster III had only three genotypes. High yielding check varieties viz., WH1105, HD3086 and DBW222 grouped in Cluster VI. Genotypes of cluster II and V exhibited maximum inter-cluster distance (6155.86), while Cluster V and VI showed minimum inter-cluster distance (2446.10) (Table 2). This indicated that Cluster II and V genotypes exhibited maximum diversity and could be utilized in hybridization programmes to generate variability and attain maximum heterosis. The average intra-cluster distance was maximum within the genotypes of Cluster IV (4303.32) and minimum within the genotypes in Cluster VI (1156.10) (Fig. 1).

Niyazi et al. (2023) reported that crossing between genotypes of cluster II and IV could be used for developing potential hybrids. In their study while categorizing 20 genotypes in five clusters the highest inter-cluster distance was found between genotypes of cluster II and IV indicating wide genetic diversity. Singh et al. (2022) also grouped thirty bread wheat genotypes in seven clusters where Cluster I contained maximum genotypes and cluster VII had the least. Cluster VII and Cluster IV exhibited the maximum inter-cluster distance whereas the intra-cluster distance was maximum in Cluster VII. Similarly, Chaudhary et al. (2023) grouped 45 genotypes in 12 clusters and reported that

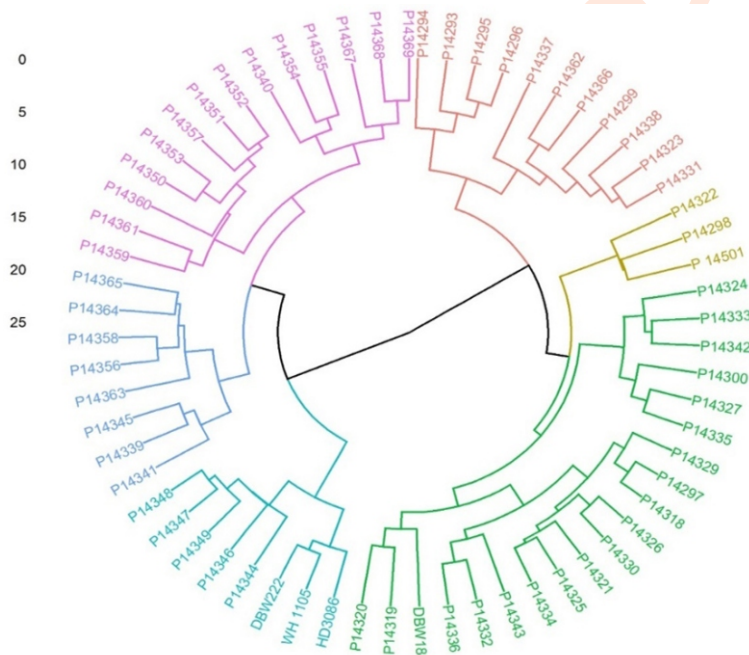
**Table 1:** ANOVA for 25 morpho-physiological and biochemical traits among sixty-four bread wheat genotypes

Character	Mean sum of squares			CD at 5 %	CV (%)
	Replication	Genotypes	Error		
	df (3)	df (63)	df (189)		
DH	12.2	32.7**	1.1	1.4	1.1
DA	12.5	31.4**	1.1	1.5	1.0
DM	17.1	50.5**	2.8	2.3	1.2
PH	2.2	97.7**	3.5	2.6	1.8
NT/M	117.6	619.9**	92.4	13.4	8.3
SL	0.0	2.6**	0.2	0.6	3.5
PL	21.3	25.6**	2.0	2.0	3.6
NS/S	1.1	9.1**	0.5	1.0	3.5
NG/S	27.6	256.9**	13.2	5.1	6.6
SW	1.1	1.4**	0.2	0.6	11.5
BY	8408437.5	4625873.0**	769760.3	1223.8	7.4
GFD	14.1	25.5**	3.5	2.6	4.4
HI	47.9	26.8**	2.7	2.3	4.4
TGW	10.5	94.8**	0.6	1.1	1.7
CFC-I	0.0	0.0**	0.0	0.0	3.1
CFC-II	0.0	0.0**	0.0	0.0	3.1
CTD-I	0.2	4.560**	0.4	0.8	11.0
CTD-II	1.1	9.9**	1.0	1.4	20.9
NDVI-I	0.0	0.0**	0.0	0.0	3.3
NDVI-II	0.0	0.0**	0.0	0.1	7.2
CP	1.2	4.0**	0.1	0.5	2.9
GC	7.2	85.8**	0.2	0.7	1.2
SV	8.3	336.7**	0.4	0.9	1.3
HW	15.1	52.0**	0.6	1.1	1.1
GY	89534.8	1337951.9**	82491.0	400.6	6.6

\*\* = Significant at p=0.01 and \* = Significant at p=0.05

**Table 2:** Average inter-cluster and intra-cluster (diagonal) distances among different clusters for sixty-four bread wheat genotypes for morpho-physiological and biochemical traits

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	3735.04	4144.50	2579.96	5214.36	5718.41	4422.93
Cluster II		4084.51	2786.87	5690.12	6155.86	4849.61
Cluster III			1167.19	4509.94	4558.89	3264.05
Cluster IV				4303.32	4760.06	3453.57
Cluster V					2171.75	2446.10
Cluster VI						1156.10



**Fig. 1:** Dendrogram depicting clustering pattern of sixty-four bread wheat genotypes

Cluster VI (7.12) showed the maximum intra-cluster distance, while Cluster II and XII (15.94) exhibited the maximum inter-cluster distance.

The wide inter-cluster distances suggest potential for selecting diverse parents in hybrid breeding to improve grain yield. In the current study, among six clusters, the highest mean values for maximum traits were present in Cluster III for eleven traits viz., SL, NS/S, BY, GFD, HI, CTD-I, CTD-II, NDVI-I, SV and GY, followed by Cluster II for eight traits viz., DH, DM, PH, NT/M, NG/S, SW, NDVI-II, GC and HW, Cluster I for two traits viz., CFC-I and CFC-II, Cluster VI for two traits viz., DA and CP, and Cluster V for TGW (Table 3). Genotypes of cluster III and I can be exploited for direct release as a variety after testing or can be used as parents in hybridization programme to develop high-yielding varieties as it showed higher cluster mean for yield and important yield attributing traits.

Using  $D^2$  statistics, Singh *et al.* (2024) categorized 30 genotypes into five clusters and found that Cluster II showed the maximum intra-cluster distance and Clusters III and IV (6.062) showed the highest inter-cluster distance. Cluster means of 13 characters were highest in Clusters IV and V and lowest in Clusters III and II. Thus, crosses between Cluster III and IV are expected to exhibit high heterosis and provide new recombinants with desired characters. Similarly, 68 bread wheat genotypes were categorized in five clusters by Reddy *et al.* (2022) who reported that Cluster III (150.64) exhibited maximum intra-cluster distance and Clusters II and III (488.73) showed maximum inter-cluster distance. Therefore, they suggested that cluster pairing exhibiting maximum inter-cluster distances can produce the highest amount of hybrid vigour and maximum number of useful segregants. On the basis of genetic divergence and cluster mean, Yasin *et al.* (2024) advised crossing the genotypes of Cluster VI and Cluster X, while grouping 40 bread wheat lines into ten

**Table 3:** Cluster mean values for 25 morpho-physiological and biochemical traits for six clusters of sixty-four bread wheat genotypes

Traits	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
DH	96.91	98.15	91.00	94.25	95.00	98.50
DA	100.55	102.10	94.67	98.75	98.57	102.50
DM	141.91	145.20	142.33	139.88	139.43	144.25
PH	104.90	108.50	105.03	105.88	100.49	106.13
NT/M	120.27	126.15	117.33	105.63	107.71	113.88
SL	11.65	11.69	12.13	11.75	10.21	11.23
PL	39.36	38.64	39.93	38.76	37.84	38.35
NS/S	19.91	20.30	20.33	19.88	17.71	19.75
NG/S	57.64	59.70	59.67	46.63	52.29	53.75
SW	3.79	4.01	3.83	3.31	3.17	3.01
BY	12095.45	12686.25	13000.00	11475.00	10950.00	11140.63
GFD	41.55	43.22	47.80	41.38	40.77	41.84
HI	39.74	36.72	40.57	35.89	35.27	35.01
TGW	48.03	47.70	45.93	50.45	43.96	44.34
CFC-I	0.711	0.682	0.673	0.660	0.674	0.661
CFC-II	0.668	0.638	0.628	0.603	0.637	0.627
CTD-I	5.01	6.16	6.30	5.60	4.87	5.65
CTD-II	4.30	6.11	7.83	4.04	3.46	4.03
NDVI-I	0.73	0.78	0.79	0.73	0.73	0.74
NDVI-II	0.63	0.65	0.60	0.51	0.52	0.59
PC	12.80	13.41	13.67	12.84	12.33	14.10
GC	37.57	41.93	39.30	35.04	34.08	39.94
SV	49.45	55.12	56.00	43.00	37.99	55.20
HW	75.39	76.01	73.73	73.76	72.19	68.64
GY	4797.82	4650.60	5261.33	4109.25	3851.43	3895.50

clusters since this might result in the development of wide range of beneficial genetic diversity for yield improvement in wheat. Yadav *et al.* (2023) grouped 34 bread wheat genotypes in seven clusters and suggested that genotypes from Cluster VI and VII (maximum inter-cluster distance) can be selected as a parent in hybridization to get maximum number of transgressive recombinants from segregating generations to improve wheat yield and also suggested that genotypes of cluster VII can be directly released as a variety or used as a parent in hybridization because it exhibited the highest mean for traits like tillers per plant, spike length, spike weight and grains per spike.

Principal component analysis of 25 traits is presented in Table 4. Out of 25 components, the first eight components exhibited eigenvalues >1, showing 80.04% of the total variability and were considered principal components. This indicated that these eight components played an important role in classifying genotypes based on variability while the remaining 17 components contributed insignificantly. The first PC had an eigenvalue of 7.778 and explained 31.1% of total variation. PC-2, PC-3, PC-5, PC-5, PC-6, PC-7 and PC-8 attributed 12.2%, 9.7%, 7.1%, 6.3%, 5.4%, 4.5% and 4% proportion of the variability with eigenvalues of 3.005, 2.428, 1.764, 1.578, 1.360, 1.128 and 1.005, respectively (Table 4). The factor loading of different traits in each PC is present in Table 5. It helps in interpreting correlation between the variables and principal components. Traits with highest absolute factor loading value contributed more to PC

variability. Positive or negative values indicated the direction and strength of the relationship. PC-1 exhibited the highest positive loading value for CTD-II (0.274) followed by BY (0.273), SV (0.270) and GY (0.266) whereas PC-2 had the highest positive factor loading value for DM (0.296) followed by CTD-I (0.269), CP (0.243) and DA (0.241). In contrast, CFC-I (-0.324) had the highest negative factor loading. It shows that these traits are of great importance, as they have maximum involvement in the total variation and should be considered as a selection-criteria for genetic improvement.

Similarly, Atsbeha *et al.* (2023), examined 180 genotypes of bread wheat for PCA based on 12 morphological traits and found that PC1 accounts for 31.59% variation and PC2 and PC3 for 18.98% and 9.57%, respectively. Furthermore, the findings showed that traits contributed most to PC1 such as total spike weight, number of kernels per spike, 1000-kernal weight and grain yield whereas days to heading, days to flowering and days to maturity contributing most to PC2 were valuable traits, had higher contribution to the total variation and can be focused while selecting parents for hybrid breeding. Zewdu *et al.* (2024) also reported that the first four PCs had eigen values >1 and accounted for 76.76% of the variations. PC-I accounted for 42.55% of the total variation most by associated with plant height, number of kernels per spike, head weight, grain yield and biomass yield, PC-II had about 14.69% of total variation with major contributing characters viz., days to heading and days to

**Table 4:** Eigenvalues for different morpho-physiological and biochemical traits in sixty-four bread wheat genotypes

	Eigenvalue	Proportion of Variability explained	Cumulative Proportion
PC1	7.778	31.1	31.1
PC2	3.055	12.2	43.3
PC3	2.428	9.7	53.0
PC4	1.764	7.1	60.1
PC5	1.578	6.3	66.4
PC6	1.360	5.4	71.9
PC7	1.128	4.5	76.4
PC8	1.005	4.0	80.4
PC9	0.713	2.9	83.2
PC10	0.647	2.6	85.8
PC11	0.593	2.4	88.2
PC12	0.555	2.2	90.4
PC13	0.433	1.7	92.1
PC14	0.412	1.6	93.8
PC15	0.360	1.4	95.2
PC16	0.272	1.1	96.3
PC17	0.226	0.9	97.2
PC18	0.194	0.8	98.0
PC19	0.169	0.7	98.7
PC20	0.131	0.5	99.2
PC21	0.087	0.3	99.5
PC22	0.064	0.3	99.8
PC23	0.045	0.2	100.0
PC24	0.003	0.0	100.0
PC25	0.001	0.0	100.0

maturity. PC-biplot elaborates the interaction between traits, genotypes and their respective principal components, and are widely used to dissect the correlation of traits in various crop plants. The biplot based on PC 1 and PC 2 elaborated their diversity in terms of spatial distance (Fig. 2, 3). Biplot depicted 43.3 percent of the total variation, where dim 1 explained 31.1% variance and dim 2 explained 12.2% variance.

The direction and length of arrow indicate the contribution of each variable to the principal component. The vector of traits viz., CTD-II, BY, GY, DM, CP, GC and DA showed longer lengths, indicating positive contribution to both components. Traits with narrower acute angle were more strongly correlated while traits with obtuse angle were inversely (negatively) correlated. The vector of all the traits were arranged at acute angle with GY suggesting positive correlation with all the traits under study. Smaller angles between the vectors such as GY and BY, DA and DM, CFC-I and CFC-II etc., pointed in same direction indicating a higher positive correlation between the traits. The vectors of traits such as CFC-I and CFC-II were at obtuse angle with CTD-I, which indicated negative correlation between the traits. Phougat *et al.* (2022b) observed high positive correlation between days to heading and spike length, grains per spike and plant height in a biplot analysis. Similarly, Kumar *et al.* (2024 b) found that days to anthesis, heading and maturity, tiller per meter and germination percent were arranged at acute angles in the biplot revealing a positive correlation between them, suggesting that improvement in one character will lead to direct improvement of another.

**Table 5:** Factor loading of different morpho-physiological and biochemical traits for sixty-four bread wheat genotypes

Traits	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
DH	0.152	0.230	-0.454	0.186	0.123	0.111	0.058	-0.022
DA	0.155	0.241	-0.445	0.178	0.089	0.111	0.109	-0.046
DM	0.239	0.296	-0.102	0.076	0.213	0.021	-0.111	-0.273
PH	0.211	0.044	-0.099	-0.218	-0.137	-0.421	-0.007	-0.165
NT/M	0.235	-0.015	-0.148	-0.253	0.070	0.152	0.106	-0.221
SL	0.223	0.007	0.184	-0.010	0.049	-0.356	-0.033	-0.187
PL	0.058	-0.192	-0.239	-0.486	0.157	-0.180	0.004	-0.121
NS/S	0.214	0.023	0.120	0.049	0.046	-0.368	0.032	0.006
NG/S	0.188	-0.162	-0.114	-0.105	0.259	-0.035	-0.352	0.438
SW	0.223	-0.229	-0.125	0.018	0.201	-0.139	-0.112	0.391
BY	0.273	-0.178	0.097	0.101	0.014	0.066	-0.014	-0.091
GFD	0.164	0.136	0.344	-0.078	0.193	-0.079	-0.261	-0.340
HI	0.149	-0.299	0.113	-0.065	-0.053	0.239	0.355	-0.083
TGW	0.103	-0.113	-0.050	0.349	0.007	-0.428	0.393	0.230
CFC-1	0.103	-0.324	-0.156	0.308	-0.267	-0.095	-0.282	-0.127
CFC-II	0.063	-0.292	-0.139	0.277	-0.305	0.100	-0.448	-0.224
CTD-I	0.151	0.269	0.283	0.379	-0.062	-0.023	0.105	0.003
CTD-II	0.274	0.046	0.194	0.010	0.142	0.149	-0.003	0.142
NDVI-I	0.202	0.123	0.257	0.042	0.173	0.244	-0.241	0.261
NDVI-II	0.260	0.020	-0.164	0.095	0.097	0.113	0.109	-0.081
PC	0.166	0.243	0.003	-0.162	-0.505	-0.054	0.031	0.257
GC	0.246	0.132	-0.009	-0.220	-0.351	0.173	-0.059	0.164
SV	0.270	0.126	-0.018	-0.149	-0.353	0.014	0.016	0.053
HW	0.157	-0.284	0.068	-0.017	0.027	0.182	0.280	-0.020
GY	0.266	-0.279	0.133	0.029	-0.018	0.171	0.174	-0.107

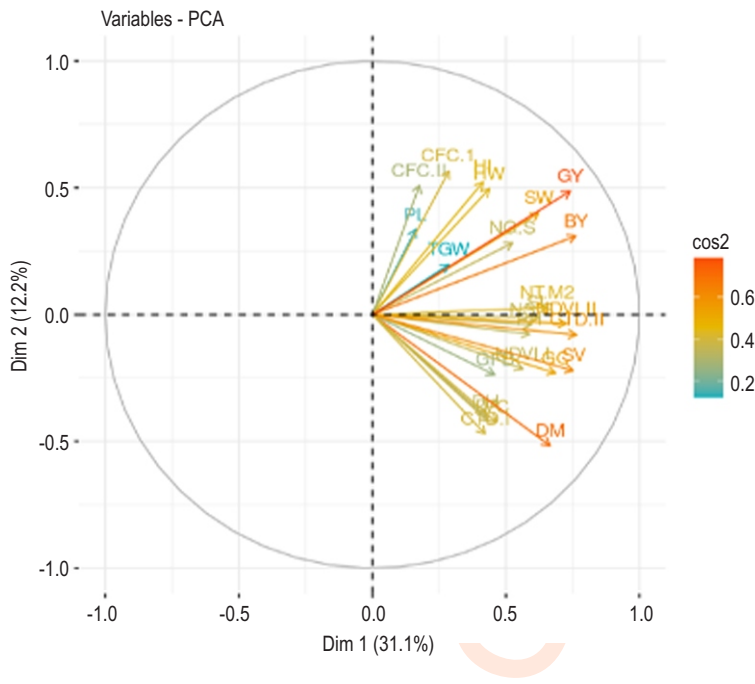


Fig. 2: Biplot of morpho-physiological and biochemical traits based on PCA analysis of sixty-four bread wheat genotypes.

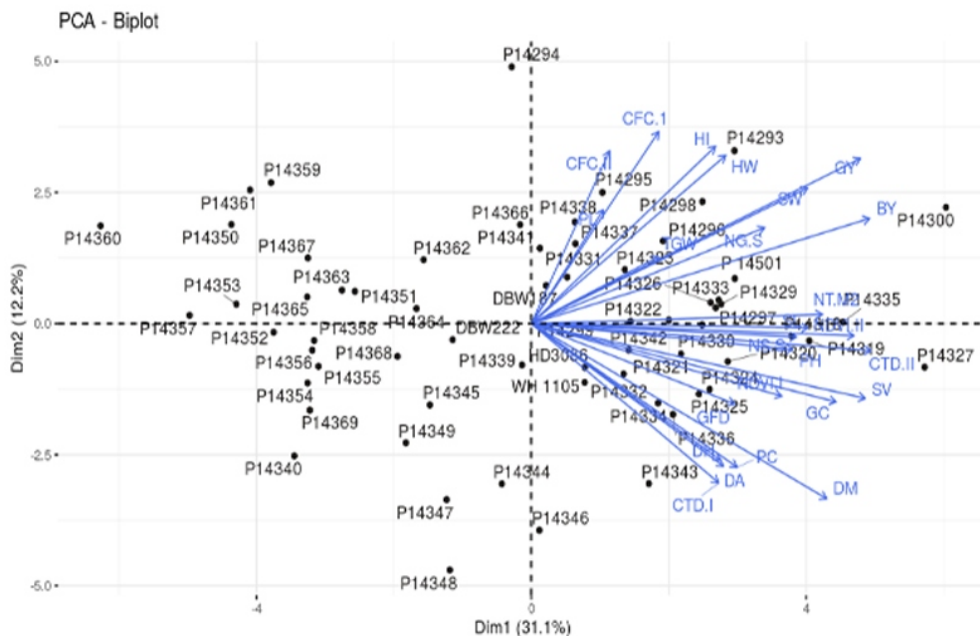


Fig. 3: Biplot of morpho-physiological and biochemical traits along with sixty-four bread wheat genotypes based on PCA.

The biplot revealed different grouping pattern among genotypes, indicating variation in trait expression. It categorized the genotypes in groups present in different quadrants based on PC scores. Genotypes with higher PC1 and lower PC2 scores are represented in quadrant (+,+) viz., P14300, P14293, P14335,

P14341, P14298, P14329 and P14501 etc., in the biplot were high-yielding and stable, while genotypes with lower PC1 and higher PC2 scores in quadrant (-,-) viz., P14369, P14365, P14340, P14348 and P14344 etc., were low-yielding and unstable (Khan et al., 2023). A high PC score for a specific

genotype in a particular PC indicates high values for variables associated with that genotype. These identified genotypes with outstanding traits can serve as valuable candidates for further studies and can be potentially used in breeding programs for improved yield in bread wheat (Hussain *et al.*, 2024). Kumar *et al.* (2024 b) also revealed that Genotype G7 exhibited high positive PC scores indicating a strong contribution to genetic diversity whereas G20, G5, G18 and G4 possessed negative scores and showed lower contributions, providing crucial insights for improving breeding strategies and wheat cultivars.

The biplot dispersion indicated considerable genetic diversity among them. The vector length between the genotype position and biplot origin represents its distinctiveness from other genotypes. Closely placed genotypes showed minimal differences in grain yield whereas distant genotypes showed greater variability. Phogat *et al.* (2022 b) found that DWAP1108, GW1348, DWAP1608, HS 628, MACS 5052 were arranged distant from other genotypes in the biplot, revealing high diversity among them and can be used as diverse parents for wheat hybridization. Siddique and Hoque (2023) also evaluated 70 genotypes and found that out of total 13, first four PCs accounted for 82.81% total variation having eigen value more than one. It was observed that the genotypes present on first PC's positive side viz., 3, 5, 7, 8, 10, 15, 20, 26, 33 *etc.*, produced higher yield than mean yield of the studied genotypes, suggesting their utilization in yield improvement.

The results of cluster analysis and principal component analysis complement each other. The biplot derived from the PC1 and PC2 almost confirmed the results of cluster analysis. The genotypes present in cluster III and cluster I exhibited higher cluster mean values for grain yield and the same genotypes were found in quadrant (+, +) which exhibited higher grain yield than the average grain yield. The position of genotypes is also comparable in both dendrogram of cluster analysis and biplot of PCA whether they are nearer or farther to each other.

The study revealed significant genetic diversity for all the traits among sixty-four bread wheat genotypes. Cluster and Principal component analysis effectively identified superior genotypes such as P14300, P14293, P14335, P14341, P14298, P14329 and P14501, located in the (+,+) quadrant of the PCA biplot and belonging to cluster I and cluster III and key yield-related traits such as grain yield, biomass, and canopy temperature depression. These genotypes can be prioritized for direct selection or used as parents in breeding programs to develop high-yielding, climate-resilient wheat varieties.

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