Original Research Article

Evaluate the genetic diversity and Principal component analysis in Bread wheat (*Triticum aestivum* L.)

Abstract

The current investigation was carried out on bread wheat (*Triticum aestivum* L.) crop during rabi season with the aim ofanalysis of genetic diversity among late sown/terminal heat tolerant condition wheat genotypes with the help of principal component analysis. The experimental included 60 genotypes, in an augmented block design with three replications. Observation was based upon twenty-six quantitative characteristics.For all characteristics Cluster I had highest number of genotypes (56) followed by cluster II to cluster V whereas clusterhad presented one entry in each group.The minimum intra cluster distance (0.00)was found for II to V and maximum was found for cluster I (57.879).The maximum inter-cluster distance was found between cluster II to III (267.377).The minimum inter- cluster D^2 value found in case of cluster I to II (86.469). Cluster I showed earliest mean value for day to 50 per cent flowering (76.689 day) and most important character grain yield per plantcluster III showed maximum mean value for (27.664). Principal component analysis (PCA) indicated that the five principal components (PC1 to PC5) showed 65.61 per cent of the total variability. PC1 accounted for 11.51 % of the total variance and almost all studied characters showed positive loading in this principal component. The factor loading of principal component showed that, PC1 accounted maximum variability for characters like harvest index, grain yield per plant, flag leaf width, leaf rolling.As a result of the foregoing data, it is possible to conclude that there is great potential for effective crop improvement yield and yield-attributing traits in present wheat germplasm.

Key word: Wheat; genetic diversity; cluster analysis; morphological traits.

INTRODUCTION

Wheat (Triticum *aestivum* L., 2n=42) is the most important cereal in the world.Wheat belongs to the family Poaceae (Gramineae) and tribe Triticeae containing more than 15 genera and 300 species including wheat and barley.T. *aestivum* is a segmental allohexaploid (2n = 6x = 42, AABBDD) originated in the Fertile Crescent area of South-Western Asia its geographical centre of origin and spread globally for cultivation and consumption. Allohexaploid wheat possesses three genomes and A, B, and Dare three genomes.

The nutritional composition of the wheat grain varies somewhat with differences in climate and soil. On an average, the kernel contains 10-12 per cent water, 65-70 per cent carbohydrates, 9-12 per cent protein, 1-2 per cent fat, 1-1.8 per cent minerals, and 2-2.2 per cent crude fibres. Thiamine, riboflavin, niacin, and small amounts of vitamin A are present, but the milling processes removes most of those nutrients with the bran and germ.

The yield and productivity of wheat are seriously threatened by high temperatures. In India, wheat cultivation suffers significant injuries each year due to high tempreature stress (Kumar et al.2013). As wheat is a crop grown in the winter, it needs an extended period of low temperatures to produce its highest yield. According to Wahid *et al.* (2007) and Sareen *et al.* (2015), high temperature stress is the outcome of a temperature increase that lasts longer than a threshold and has the potential to permanently harm plant growth and physiological development.

In the hybridization programme, D2 statistics analysis is used to select genetically dissimilar parents. P.C. Mahalanobis introduced the concept of D2 statistics in 1936. Rao utilised this approach to estimate genetic diversity in plant breeding. It is used to assess the degree of diversity and identify the relative contribution of each component characteristic to overall divergence. Genetic variety is important in plant breeding because hybrids from different lines exhibit more heterosis than closely related parents. The PCA analysis is a multivariate method of statistical analysis that seeks to evaluate the relationships between an extensive range of variables in terms of a relatively small number of variables or components while retaining all of the important features from the original data set. The PCA lowers the relatively significant series of data into a smaller number of components by looking for groups with very high inter-correlation in an assortment of variables, with each component explaining percent (%) variance in overall variability. This experiment was undertaken with the goals of assessing the possible genetic diversity among wheat genotype using cluster analysis and principal component analysis for the selection of desirable parents in hybridization programmes.

MATERIALS AND METHODS

The current investigation entitled was conducted at three different locations; namely:

1. Crop research farm, Nawabganj (UP)

2. Crop research farm, Araul(UP)
3. Crop research farm, Daleep Nagar (UP).

during crop season of Rabi 2021-2022 and 2022 2023 under normal (non-stressed) and late sown (heat-stressed) conditions. The field experiments were planted comprising 60 germplasm of bread wheat. Therefore, our experimental trials were conducted in 12 environments (E1 to E12), which included six non-stressed (NS) and six heat-stressed (HS) environments. The field experiments were laid out in Augmented Block Design (ABD). Each experimental plot consisted of three rows of 2m length with 20 cm spacing between rows covering an area of 2 m x 0.20m (1.2 m^2) under irrigated condition. The observations on 26 physio-morphological and yield related traits were recorded *viz.*, Days to 50% flowering, Number of spikelets per spike, Plant height (cm), Physiological maturity (days), Spike bearing tillers per plant, Plant biomass (g), Peduncle length (cm), Number of grains per spike, Flag leaf length (cm), Number of grains per plant, Flag leaf width (cm), Grain length(mm), Flag leaf area (cm2), Grain width(mm), Chlorophyll content, L/W ratio of grains, Canopy temperature depression (0C), Grain yield /plant(g), Plant waxiness (0-10), Harvest index (%), Leaf rolling (0-10 scale), 1000- grain weight(g), Grain filling period (days), Protein content (%), Spike length (cm), Gluten content (%).The analysis of variance for 26 quantitative traits among 60 genotypes showed significant variation for all the traits studied. This indicates the presence of high degree of variability among the genotypes and ample scope of improvement by selection.

List 1 :Details of bread wheat accessions used in the study.

Sr. No.	Genotypes	Sr. No.	Genotypes
1.	K-1711	31.	K-2105
2.	K-1903	32.	K-2109
3.	K-1805	33.	K-0307
4.	K-1907	34.	K-0607
5.	K-1910	35.	K-1803
6.	K-2003	36.	K-1317
7.	K-0306	37.	PBW-852
8.	K-0402	38.	DBW-173
9.	K-2107	39.	HD-3388
10.	K-2121	40.	HD-2359
11.	K-8962	41.	K-9644
12.	K-9351	42.	K-2101
13.	K-9465	43.	KRL-213
14.	K-8027	44.	KRL-19
15.	K-2103	45.	PBW-826
16.	K-1006	46.	DBW-187
17.	K-1616	47.	HD-3392
18.	K-1905	48.	HD-2967

19.	K-1809	49.	DBW-107
20.	K-1908	50	DBW-222
21.	K-2001	51.	PBW-833
22.	K-2007	52.	HD-3399
23.	K-9107	53.	PBW-835
24.	K-9162	54.	KRL-210
25.	K-9533	55.	KRL-1-4
26.	K-2108	56.	K-2010
27.	K-9423	57.	KRL-283
28.	K-8434	58.	DBW-350
29.	K-7903	59.	HD-3086
30.	K-2104	60.	WH-1142

RESULT AND DISCUSSION

Genetic Divergence:

The non-hierarchical Euclidean cluster analysis was employed to study the genetic divergence existing among 60 bread wheat germplasm collection based on twenty-six characters. The pseudo-F-test revealed that cluster arrangements was most appropriate for grouping the 60 genotypes. Therefore, the 60 genotypes were expected to be grouped into 5 non-overlapping clusters. The distribution of 60 bread wheat germplasm in 5 clusters is presented in Table 1

The clustering pattern of the sixty genotypes were grouped into five different non-overlapping cluster. Cluster I had highest number of genotypes (56) followed by cluster II (1), cluster III (1), cluster VI (1), cluster V (1).This indicated presence of considerable diversity in the genotype. The main groups in the genetic divergence analysis typically comprised genotypes of different origins. However, genotypes from the same origin or geographical area were also shown to be clustered together. The instance of grouping of genotypes of different origin or geographic region in same cluster were frequently observed. This implied that there is no correlation between genetic and geographic diversity.The estimates of intra and inter- cluster distance represented by D^2 values are given in table 2The minimum intra cluster distance (0.00) was found in cluster II, cluster III, cluster IV, cluster V and maximum was found for cluster I (57.879). The maximum inter-cluster distance was found between cluster II to III (267.377) followed by cluster III to IV (201.540), cluster II to V (172.747), cluster I to I (142.980), cluster IV to V (137.586). The minimum inter- cluster D^2 value found in case of cluster I to II (86.469) followed by cluster I to IV (86.769), cluster I to IV (88.334), cluster II to IV (101.141), cluster III to V (112.853). The higher inter- cluster distance indicated greater genetic divergence between the genotypes of those clusters, while lower inter-cluster values between the clusters suggested that the genotypes of the clusters were not much genetically diverse from each other.

These results are in close conformation with the findings of Rahman *et al.* (2013)and Kumar *et al.* (2016),Pandey *et al*. (2021)and Abdelghany*et al.* (2023).

A perusal of table 3 showed that cluster means for the different traits indicated considerable differences between the clusters. The entire cluster from cluster I to cluster V had average mean performance for most of the characters.

Cluster I showed earliest mean value for day to 50 per cent flowering (76.689 day), cluster II showed earliest mean value for the grain filling period (29.536 day), cluster II showed maximum mean value for flag leave length (23.579), cluster III showed maximum mean value for flag leave width (1.988), cluster II showed maximum mean value for flag leave area (46.832) cluster IV showed maximum mean value for plant height (101.590), cluster III showed maximum mean value peduncle length (36.941), cluster V showed maximum mean value for spike bearing tiller per plant (12.415), cluster III showed maximum mean value for chlorophyll content (30.244), cluster I maximum mean value for canopy temperature depression (7.864), cluster III showed maximum mean value for plant waxiness (5.694), clusterII showed maximum mean value for leave rolling (5.596), cluster I showed maximum mean value for spike length (10.768), cluster I showed maximum mean value for no. of spikelet per spike (20.413), cluster III showed maximum mean value for physiological maturity (117.984), cluster I showed maximum mean value for plant biomass (51.717), cluster V showed maximum mean value for no. grain per spike (46.519), cluster III showed maximum mean value for no. of grain per plant (489.685), cluster I showed maximum mean value for grain length (6.778), cluster V showed maximum mean value for grain width (2.869), cluster I showed maximum mean value for length/width ratio (2.439), cluster I showed maximum mean value for testweight (39.125), cluster III showed maximum mean value for grain yield per plant (27.664), cluster III showed maximum mean value for harvest index (55.976), cluster IV showed maximum mean value for protein content (12.203), cluster III showed maximum mean value for gluten content (7.263). These results are in close conformation with the findings of Khalid *et al*. (2022), Abdelghany*et al*. (2023) and Khalid *et al.* (2023)

PRINCIPAL COMPONENT ANALYSIS

In the present study, 26 original interrelated variables were transformed to five independent principal components by getting loaded on common principal factors, indicating that these five components contributed maximum towards variation of the data s*et* the first five principal components having eigen values altogether explained 65.61 per cent of the total variation and were retained for further studies. The relative contribution to the variation by different principal components was proportional to their eigen values and it decreased progressively.

PC1 accounted for 11.51 % of the total variance and almost all studied characters showed positive loading in this principal component. The factor loading of principal components showed that, PC1 accounted maximum variability for characters like harvest index, grain yield per plant, flag leaf width, leaf rolling, protein content, chlorophyll content, grain L/W ratio, days of 50% heading, grain length, gluten content and grain yield per plant. These results agreed in Khodadadi *et al.* (2011),Rymuza*et al.* (2012),Sareen *et al.* (2014), Hamam *et al.* (2015), Adilova *et al.* (2020), Farheen *et al.* (2021), Bhatti *et al.* (2022), Khalid *et al.* (2023) and Kumar *et al.* (2024).

Principal Component Analysis (PCA) is a valuable technique which is used to classify the relationships among the traits in a complete multi-trait system and helps in identification of data pattern by reducing the number of dimensions. PCA accomplishes this reduction by identifying directions, called principal components (PCs), along which the variation in the data is maximal. By using a few components, each sample can be represented by relatively few numbers instead of by values for thousands of variables. In the present investigation, PCA was performed for twenty-six yield and yield component traits in wheat lines. The principal components with eigen values more than 1 and which explained at least 5 per cent of the variation in the data should be considered. Eigen value measures the amount of variation explained by a particular factor out of the total variation. The factor loadings, also known as component loadings, are the correlation coefficients between the original variables and the factors obtained. The eigen values from PCA determines the number of factors to be retained which accounts for most of the variability in the original data set. The principal components with higher eigen values and variables which had high factor loading were considered as best representative of system attributes. The sum of all eigen values is always equal to the number of variables.

In our study, first eight principal components had eigen value greater than one and they cumulatively explained 65.61 per cent of the total variation present in the original data set. So, these eight principal components were considered important for further explanation. The first principal component explained 11.51 per cent while, the second, third, fourth, fifth, sixth, seventh and eighth principal component exhibited 10.03 per cent, 9.65 per cent, 8.81 per cent, 7.81 per cent, 6.48 per cent, 5.99 per cent and 5.30 per cent variability, respectively among the lines for the traits under study (Table 4). The first principal component accounts for as much of the variability in the data as possible, and each succeeding component accounts for as much of the remaining variability as possible.

Scree plot explains the percentage of variation associated with each principal component and is obtained by drawing a graph between principal component numbers (X-axis) and percentage of variation explained (Y-axis). The Principal Component 1 showed 11.51 per cent variability with eigen value 2.99 which then declined gradually. From the graph, the maximum variation was observed in Principal Component 1.

The result of the PCA explained the genetic diversity of wheat lines. Eigen values assess the importance and role of each component to total variation, while the factor loading indicates the scale of contribution of every origin variable with which each principal component is associated. Within each principal component, only highly loaded factors or traits were retained for further explanation. Component matrix revealed that Principal Component 1 showed high positive loading for harvest index (0.435), grain yield per plant (0.293), flag leaf width (0.214), leaf rolling (0.195), protein content (0.174) and chlorophyll content (0.159). Principal Component 2 enabled high positive loading for grain L/W ratio (0.499), days of 50% heading (0.351), grain length (0.245), gluten content (0.268) and grain yield per plant (0.231). The prominent traits contributing maximum variability and desegregating in different principal components have the tendency to remain together which may be kept into consideration during utilization of these characters in crop improvement programme as a donor for the associated traits.

Table: 1 Cluster analysis:

Clusters	Size	Genotypes

I	**56**	DBW-350, PBW-833, HD-3399, KRL-213, KRL-1-4, DBW-173, K-0402, WH-1142, KRL-19, K-2104, K-2108, KRL-283, K-1908, HD-2359, K-8962, K-9533, K-1907, DBW-107, PBW-826, K-1711, K-2109, K-0607, K-0306, K-1809, PBW-852, K-2101, K-1805, PBW-835, K-1317, K-2105, KRL-210, DBW-187, K-1910, K-2103, HD-3086, K-2010, K-9644, K-9351, HD-3388, HD-2967, K-1905, K-2007, DBW-222, K-9162, K-1616, HD-3392, K-2107, K-2001, K-1006, K-1903, K-7903, K-1803, K-9423, K-8027, K-0307, and K-9107
II	**1**	K-2003
III	**1**	K-2121
IV	**1**	K-8434
V	**1**	K-9465

Table: 2 Average inter and intra cluster distance

	cluster 1	**cluster 2**	**cluster 3**	**cluster 4**	**cluster 5**
cluster I	**57.879**	86.469	142.980	88.334	86.769
cluster II		**0.000**	267.377	101.141	172.747
cluster III			**0.000**	201.540	112.853
cluster IV				**0.000**	137.586
cluster V					**0.000**

Table: 3 Average cluster mean for 26 traits

	Cluster I	**Cluster II**	**Cluster III**	**Cluster IV**	**Cluster V**
D50H	76.689	76.931	77.027	76.774	76.856

GFP	29.685	29.536	29.573	29.560	29.555
FLL	23.033	23.579	23.249	22.882	23.009
FLW	1.981	1.964	1.988	1.950	1.973
FLA	45.790	46.832	46.788	45.154	45.999
PH	100.009	100.288	100.975	101.590	99.925
PL	36.309	35.957	36.941	36.451	35.704
SBTPP	12.305	12.272	12.212	12.294	12.415
CC	29.556	29.317	30.244	29.534	29.935
CTD	7.864	7.783	7.557	7.756	7.581
PW	5.446	5.631	5.694	5.626	5.726
LR	5.425	5.596	5.583	5.335	5.375
SL	10.768	10.726	10.483	10.662	10.661
NSPS	20.413	20.202	20.098	20	20.057
PM	117.199	117.559	117.984	117.841	117.705
PB	51.717	50.657	50.987	51.604	50.077
NGPS	44.391	44.793	44.343	43.901	46.519
NGPP	425.896	441.773	489.685	455.669	467.843
GL	6.778	6.746	6.710	6.740	6.716
GW	2.813	2.835	2.849	2.844	2.869
GLWR	2.439	2.411	2.383	2.398	2.365
TW	39.125	38.555	38.568	38.863	38.413
GYPP	27.006	27.364	27.664	27.401	27.142
HI	53.767	55.777	55.976	54.923	55.722
PC	11.998	12.083	12.175	12.203	12.226
GC	7.255	7.252	7.263	7.257	7.247

Table: 4 Principal Component analysis for yield and yield related traits

	Eigen value	**Variance percent**	**Cumulative variance percent**
PC1	2.993	11.513	11.513

PC2	2.608	10.033	21.547
PC3	2.509	9.653	31.200
PC4	2.291	8.814	40.015
PC5	2.032	7.818	47.833
PC6	1.687	6.489	54.323
PC7	1.557	5.992	60.315
PC8	1.378	5.302	65.618
PC9	1.199	4.611	70.229
PC10	1.101	4.237	74.467
PC11	1.001	3.853	78.320
PC12	0.811	3.119	81.439
PC13	0.809	3.113	84.553
PC14	0.673	2.588	87.142
PC15	0.612	2.354	89.497
PC16	0.565	2.173	91.670
PC17	0.499	1.920	93.591
PC18	0.397	1.529	95.120
PC19	0.357	1.376	96.496
PC20	0.292	1.126	97.623
PC21	0.274	1.057	98.680
PC22	0.197	0.759	99.440
PC23	0.116	0.446	99.886
PC24	0.014	0.055	99.942
PC25	0.011	0.041	99.984
PC26	0.004	0.015	100.000

Table: 5 Factor loadings of principal components

	PC1	PC2	PC3	PC4	PC5
D50H	0.000	0.351	0.000	0.128	0.000
GFP	0.123	0.000	0.000	0.152	-0.144
FLL	0.313	0.000	0.393	0.000	0.000
FLW	0.214	0.000	0.129	-0.278	0.184
FLA	0.371	0.000	0.380	-0.181	0.117
PH	-0.265	0.000	-0.146	-0.349	0.000
PL	-0.107	-0.119	0.000	-0.527	0.000
SBTPP	0.000	0.000	0.117	0.000	-0.103
CC	0.159	-0.242	0.000	0.000	0.000
CTD	-0.109	-0.185	0.286	0.000	-0.288
PW	0.000	0.000	-0.135	0.000	-0.211
LR	0.195	0.000	0.000	0.161	-0.207
SL	-0.141	0.000	0.247	0.274	0.000
NSPS	0.000	0.000	0.415	0.171	0.270
PM	0.000	0.122	-0.309	0.238	0.000
PB	-0.312	0.126	0.187	0.213	0.241
NGPS	0.195	0.000	-0.161	0.000	0.307
NGPP	0.167	-0.128	-0.216	0.000	0.281
GL	0.000	0.245	0.169	0.000	-0.367
GW	0.000	-0.447	0.000	0.249	0.000
GLWR	0.000	0.499	0.000	-0.224	-0.174
TW	-0.190	0.104	0.000	-0.214	0.228
GYPP	0.293	0.231	-0.119	0.141	0.000
HI	0.435	0.000	-0.210	-0.111	-0.235
PC	0.174	0.166	0.000	0.000	0.123
GC	0.000	0.268	0.000	0.000	0.340

CONCLUSION:

Based on the above result of genetic diversity with the help of principle component analysis it could be concluded for all characteristics Cluster I had highest number of genotypes (56).The minimum intra cluster distance (0.00)was found for II to V and maximum was found for cluster I (57.879).The maximum inter-cluster distance was found between cluster II to III (267.377).The minimum inter- cluster D^2 value found in case of cluster I to II (86.469). Cluster I showed earliest mean value for day to 50 per cent flowering (76.689 day) and most important character grain yield per plant cluster III showed maximum mean value for (27.664). Principal component analysis (PCA) indicated that the five principal components (PC1 to PC5) showed 65.61 per cent of the total variability. Thus, this finding indicated that these traits could utilize in various breeding as well as improvement programmes. The information may further help the breeder in formulation appropriate strategy aimed at getting higher yield and character improvement in wheat.

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