Original Research Article

Estimate the genetic diversity and relationship of various factor in Bread Wheat with PCA or estimate the genetic diversity in Bread wheat with PCA

(*Triticum aestivum* L.)

Abstract

The present investigation was carried out on breadwheat (*Triticum aestivum* L.) crop during rabi season with the aims of analysis of genetic diversity with the help of principle component analysis. The experimental sample size included 80 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 (28) followed by cluster II (5), cluster IV, cluster V and cluster VI had presented (4), cluster VII and VIII (3), cluster III, cluster IX, cluster X, cluster XI and cluster XII (2) whereas clusterhad presented one entry in each group.The minimum intra cluster distance (0.00)was found for XIII to XXXI and maximum was found for cluster XII (2.10).The maximum inter-cluster distance was found between cluster XX to XVII (11.08).The minimum inter- cluster D^2 value found in case of cluster IV to XVI and XXX to XXXI (2.12). Cluster XVII showed earliest mean value for day to 50 per cent flowering (75.24 day) and most important character maximum mean value for yield per plot (536.13).Principal component analysis (PCA) indicated that the five principal components (PC1 to PC5) showed 50.37 per centof the total variability. The five different groups positive maximum variable loaded component PC I for grain yield per plant (23.2542), PC II flag leave area (19.4005), PC III for peduncle length (23.9893), PC IV grain length /width ratio (21.0627), PC V for physiological maturity (16.7492).As a result of the foregoing data, it is possible to conclude that there is great potential for effective crop modification for improved yield and yield-attributing traits in present wheat germplasm.

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

Introduction

Wheat (*Triticum aestivum*L.) is one of the main cereal crops cultivated globally both in terms of area harvested and productivity, after rice and maize. It is major staple food crop. Wheat, commonly referred to as the "king of cereals," feeds more people than any other food crop and is an important component of global food security. It is a self-pollinating, hexaploid (AABBDD) plant with chromosome number of 42 ($2n = 6x = 42$) and estimated genome size of 16 GB. The starchy endosperm of mature wheat grain is composed of carbohydrates (simple starches), which account for 55-75% of the total dry grain weight, and storage protein, which account for the remaining 10-20%. Consuming whole wheat grains provides nutritional fibre and minerals. According to Lafiandra*et al.* (2014) and Shewry*et al.* (2015), it has lipids, vitamins, and minerals. As recommended by World Bank estimates, a 2^0C rise in world average temperature may lead to extreme heat conditions. The yield and productivity of wheat are seriously threatened by high temperatures. In India, wheat cultivation suffers significant injuries each year due to high temperature 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.* (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.The heat-stress reduces the grain yield and yield-related traits by enhancing leaf senescence, reduction in photosynthesis, deactivation of photosynthetic enzymes, assimilate translocation and duration, reduction in grain number and size by affecting grain setting and growth rate of grains **(Akter and Islam, 2017)**. High temperature reduces yield by 3-4% for every 1^0C rise in temperature leading to reduced global wheat productivity by 5%.

Morphological characterization using phenotypic traits associated with heat-stress tolerance is a right approach for underpinning the physiological mechanism involved in wheat crop adaptation to global warming **(Bita and Gerats, 2013; Hyles *et al.*, 2020).**

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 breedingIt 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 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 genotypes using cluster analysis and principal component analysis for the selection of desirable parents in hybridization programmes.

Materials and Methods

The current research work "Unraveling genetic parameters of physio-morphology traits of terminal-heat stress tolerance in bread wheat (*Triticum aestivum* L.) will be conducted at three different locations; namely Crop research farm, Nawabganj, Crop research farm, Araul and Crop research farm, Daleep Nagar during crop season of Rabi 2021-2022 and 2022-2023.These research farms comes under the North Eastern Plain Zone of India having semi-arid and sub-tropical climate. The experiment will be conducted 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 m2) under irrigated condition.To produce a successful harvest, all the necessary agronomic practises and plant protection measures were implemented. The observations on 26 physio-morphological and yield related traits will be recorded on five randomly selected plants in each genotype and their mean values will be used for statistical analysis.Days of 50% Heading, Grain filling period (days), Flag leaf length (cm), Flag leaf width (cm), Flag leaf area (cm^2), Plant height (cm), Peduncle length (cm), Spike bearing tillers per plant, Chlorophyll content, Canopy temperature depression (°C), Plant waxiness (0-10 scale), Leaf rolling(0-10 scale), Spike length(cm), Number of spikelets per spike, Physiological maturity (days), Plant biomass (gm), Grain weight per spike, Number of grain per spike, Number of grain per plant, Grain length (mm), Grain width (mm), Grain L/W ratio, 1000 grain weight (gm), Grain yield / plant (gm), Harvest index (%), Yield per plot (g).

Result and discussion

Genetic Divergence:

The non-hierarchical Euclidean cluster analysis was employed to study the genetic divergence existing among 80 bread wheat germplasm collection based on twenty-six characters. The pseudo-F-test revealed that cluster arrangements was most appropriate for grouping the 80 genotypes. Therefore, the 80 genotypes were expected to be grouped into 31 non-overlapping clusters. The distribution of 80 bread wheat germplasm in 31 clusters is presented in Table 1

The clustering pattern of the eighty genotypes were grouped into thirty-one different non-overlapping cluster. Cluster I had highest number of genotypes (28) followed by cluster II (5), cluster IV, cluster V and cluster VI had presented (4), cluster VII and VIII (3), cluster III, cluster IX, cluster X, cluster XI and cluster XII (2) whereas cluster XIII, cluster XIV, cluster XV, cluster XVI,cluster XVII, cluster XVIII, cluster XIX, cluster XX, cluster XXI, cluster XXII, cluster XXIII, cluster XXIV, cluster XXV, cluster XXVI, cluster XXVII, cluster XXVIII, cluster XXIX, cluster XXX, cluster XXXI had presented one entry in each group. 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 for XIII, cluster XIV, cluster XV, cluster XVI, cluster XVII, cluster XVIII, cluster XIX, cluster XX, cluster XXI, cluster XXII, cluster XXIII, cluster XXIV, cluster XXV, cluster XXVI, cluster XXVII, cluster XXVIII, cluster XXIX, cluster XXX, cluster XXXI and maximum was found for cluster XII (2.10) followed by cluster XI (2.07), cluster II and IV (1.88), cluster I and VII (1.85), cluster VI and VIII (1.84) cluster X (1.72) cluster IX (1.64) cluster V (1.58) cluster III (1.21). The maximum inter-cluster distance was found between cluster XX to XVII (11.08) followed by cluster III to XX (11.05), cluster IX to XX (10.12), cluster III to XXIII (8.06), cluster XX to XXII (7.73), cluster III to XXXI (7.31), cluster III to XXI (7.18), cluster III to XXIX (7.12), cluster XIII to XX (7.10), cluster XXIII to XXVII (7.07), cluster XX to XXV (7.01), cluster XV to XX (6.86) were very high. The minimum inter- cluster D^2 value found in case of cluster IV to XVI and XXX to XXXI (2.12) followed by cluster IX to XXII (2.18), cluster I to X (2.20), cluster I to VIII (2.21), cluster XIV to XXXI and XXV to XXXI (2.31), cluster VI to XXI (2.32), cluster V to XIII (2.36), cluster I to IV (2.37), XVI to XXIX (2.38), cluster XXI to XXX (2.39), cluster I to VII (2.40). 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 Sabar *et al.* (2021), Gebremariam *et al.* (2022), Khalid *et al.* (2022), Khare *et al.* (2022), Abdelghanyet *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 XXXI had average mean performance for most of the characters.

Cluster XVIII showed earliest mean value for day to 50 per cent flowering (75.24 day), cluster XI showed earliest mean value for the grain filling period (28.92 day), cluster V showed maximum mean value for flag leave length (22.55), cluster XVIII showed maximum mean value for flag leave width (1.96), cluster XXXI showed maximum mean value for flag leave area (34.23), cluster XXII showed maximum mean value for plant height (102.2), cluster XXV showed maximum mean value peduncle length (38.96), cluster VIII showed maximum mean value for spike bearing tiller per plant (12.28), cluster XIII showed maximum mean value for chlorophyll content (28.29), cluster XV maximum mean value for canopy temperature depression (7.14), cluster XX showed maximum mean value for plant waxiness (7.04), cluster XII showed maximum mean value for leave rolling (7.00), cluster XII showed maximum mean value for spike length (11.06), cluster XXV showed maximum mean value for no. of spikelet per spike (19.90), cluster XXIV showed maximum mean value for physiological maturity (117.68), cluster XII showed maximum mean value for plant biomass (60.53), cluster XXX showed maximum mean value for grain weight per spike (1.89), cluster XXIII showed maximum mean value for no. of grain per spike (48.00), cluster XXIX showed maximum mean value for no. of grain per plant (588.36), cluster XX showed maximum mean value for grain length (6.91), cluster XII showed maximum mean value for grain width (3.06), cluster XVIII showed maximum mean value for grain length/width ratio (2.48), cluster XXI showed maximum mean value for 1000 grain weight (38.06), cluster VIII showed maximum mean value for grain yield per plant (22.29), cluster VIII showed maximum mean value for harvest index (37.60), cluster XVIII showed maximum mean value for yield per plot (536.13). These results are in close conformation with the findings of Singh *et al.* (2019), Khalid *et al.* (2022), Abdelghany*et al.* (2023) and Khalid *et al.* (2023)

Principal component analysis:

The principal component analysis is a non-parametric approach to obtain a small number of factors that account for maximum variability among the total variability present. The eigen values, variability proportion (per cent) and cumulative proportion (per cent) are displayed in Table 4. Based on the PCA with twenty-six parameters of percent diversity, it formed 5 principal components (PCs) with more than 1 eigen value apart from PC5 (1.88). These components indicate maximum variation among the variables with a diversity percentage of 50.37 per cent. The first PC showed 14.8774 per cent variation, while the second, third, fourth and fifth PCs showed the variation of 10.0803 per cent, 9.3146 per cent, 8.8735 per cent and 7.2336 per cent, respectively. Therefore, the traits coming under the 5 PCs manifest a high degree of genetic variation and they add up the genetic diversity between the genotypes which could be exploited in crop improvement programs.

In PC 1, maximum positive factor loadings were observed in average grain yield per plant (23.2542), followed by harvest index (13.7383), grain weight per spike (12.5796), spike bearing tiller per plant (11.8027), no. of grain per plant (11.2868), plant bio-mass (6.1440) and peduncle length (4.4102).

In PC2, maximum positive factor loadings were observed in flag leave area (19.4005), followed by flag leave length (16.6287), no. of grain per plant (9.3308), spike bearing tiller per plant (8.1034), grain width (6.7537), grain length/width ratio (6.1683) and yield per plant (5.8327).

In PC 3, maximum positive factor loadings were observed in peduncle length (23.9893), followed by plant height (15.7415), plant waxiness (8.7097), flag leave width (7.7486), flag leave area (6.9498), leave rolling (6.0115) and yield per plant (5.5698).

In PC 4, maximum factor loadings were appeared in grain length /width ratio (21.0627), followed by grain length (17.1429), grain width (10.4616), grain filling period (9.9553), no. of grain per spike (9.8609), chlorophyll content (6.3663) and flag leave area (5.3028).

In PC 5, the highest factor loadings were noticed in physiological maturity (16.7492), followed by plant waxiness (15.2796), 1000 grain weight (13.5430), days of 50% flowering (8.8861), plant bio-mass (8.4424), canopy temperature depression (8.1189) and spike length (6.5574).

The study of contribution for diverse trait in principal component analysis among the eighty genotype of wheat was carried out using Harman statistics. The eighty genotypes were group into five different groups positive maximum variable loaded component PC I for grain yield per plant (23.2542), PC II flag leave area (19.4005), PC III for peduncle length (23.9893), PC IV grain length /width ratio (21.0627), PC V for physiological maturity (16.7492). Similar results were also noticed by Devesh *et al.* (2019), Adilova *et al.* (2020), Rufati*et al.* (2022), Khalid *et al.* (2023).

Table 1 Cluster analysis:

Clusters	Size	Genotypes
I	28	K-0402,KRL-283,HD-3392,KRL-213,IC-252794,IC-252772,K-1903,NINGMAI,HI-1612,DBW-187,WH-1142,K-9107,DBW-222,IC-401927,K-2105,IC-574388,KRL-210,K-0607,K-1317,IC-128150,KRL-19,K-2107,HD-3399,K-2007,DBW-107,IC-113734,K-9533,EC-576930
II	5	IC-122126,DBW-316,IC-290186,PBW-835,K-0307
III	2	C-306,HD2967
IV	4	K-2103,K-9423,K-1711,K-1905
V	4	K-1616,K-8027,K-9162,K-2108
VI	4	K-9351,HD-2359,IC-252429,IC-574476
VII	3	KRL-1-4,DBW-175,K-1809
VIII	3	IC-542051,PBW-833,K-9644
IX	2	K-2121,PBW-826
X	2	K-9465,IC-335683
XI	2	K-2010,HD-3086
XII	2	K-1006,K-1910
XIII	1	K-1803
XIV	1	K-1805
XV	1	K-1907
XVI	1	K-1908
XVII	1	K-2001
XVIII	1	K-2003
XIX	1	K-2101
XX	1	K-2104
XXI	1	K-2109
XXII	1	K-7903
XXIII	1	K-8434
XXIV	1	K-8962
XXV	1	IC-35143
XXVI	1	IC-116276
XXVII	1	IC-290195

XXVIII	**1**	IC-449061
XXIX	**1**	HD-3388
XXX	**1**	HI-1563
XXXI	**1**	PBW-852

Table 2 Average inter and intra cluster distance

	1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**	**15**	**16**	**17**	**18**	**19**	**20**	**21**	**22**	**23**	**24**	**25**	**26**	**27**	**28**	**29**	**30**	**31**
1	**1.85**	2.40	3.50	2.37	2.46	2.61	2.40	2.21	3.27	2.20	2.62	2.50	2.64	2.73	3.16	2.37	2.86	3.05	3.04	5.12	3.48	3.15	3.37	2.82	2.91	2.60	3.26	2.55	3.10	3.50	3.25
2		**1.88**	3.90	2.60	3.30	3.21	3.37	2.33	2.66	2.52	3.90	3.01	3.19	3.53	4.01	2.41	3.84	3.82	3.93	6.65	3.44	3.27	3.25	3.93	3.32	3.11	3.37	2.98	3.82	2.53	2.99
3			**1.21**	5.05	2.82	5.82	3.29	3.76	3.30	3.44	4.78	3.63	4.41	6.88	4.34	5.49	4.44	4.51	6.93	11.05	7.18	4.33	8.06	4.85	4.32	4.30	2.66	3.16	7.12	6.54	7.31
4				**1.88**	4.17	2.65	3.53	2.70	2.98	2.82	3.42	3.10	4.30	2.83	4.64	2.12	3.82	2.50	3.31	5.04	3.53	2.30	3.27	3.49	2.58	2.86	4.55	3.35	3.56	2.73	2.18
5					**1.58**	3.93	2.88	2.55	4.50	2.52	2.89	3.61	2.36	3.81	2.44	3.71	3.19	4.83	3.96	6.59	5.29	5.25	5.52	3.22	4.03	2.56	3.55	2.95	4.00	6.06	5.42
6						**1.84**	3.44	2.83	4.62	3.14	3.18	3.43	4.07	2.56	3.94	2.40	2.91	3.89	2.84	3.53	2.32	3.39	2.85	3.22	4.66	3.50	5.86	4.01	2.94	3.20	3.34
7							**1.85**	2.94	3.77	2.39	2.65	2.47	3.45	4.23	3.31	3.60	3.46	4.31	4.68	5.89	4.72	3.73	4.11	3.36	3.40	4.39	3.38	2.66	3.55	4.43	5.13
8								**1.84**	3.96	2.69	2.93	3.82	3.67	3.20	3.78	2.76	2.52	4.14	3.00	5.30	4.42	4.27	3.87	3.11	4.24	3.50	4.13	3.47	3.20	4.25	4.13
9									**1.64**	3.13	4.99	2.99	4.16	5.96	5.04	3.56	6.40	3.25	6.13	10.12	4.40	2.18	5.76	5.33	2.61	3.47	2.55	2.61	5.17	3.81	4.12
10										**1.72**	2.96	2.67	3.24	3.88	2.82	2.89	3.23	3.64	4.39	6.43	4.56	2.27	4.01	3.84	3.39	2.42	3.24	3.21	4.20	3.78	4.46
11											**2.07**	3.73	3.48	3.81	2.51	3.63	2.96	4.39	3.17	5.23	4.86	4.55	4.54	3.45	4.02	3.21	4.26	4.33	3.59	5.62	4.95
12												**2.10**	2.90	3.69	4.21	3.03	4.24	3.84	5.05	6.50	3.68	2.69	4.08	3.78	2.57	3.20	3.05	2.67	4.31	3.19	3.37
13													**0.00**	3.48	3.19	3.18	4.17	5.21	4.16	7.10	4.17	5.62	5.08	3.84	4.29	2.64	2.45	3.14	3.71	4.95	4.44
14														**0.00**	4.57	2.41	3.73	4.51	2.91	3.43	2.65	4.67	2.67	2.82	4.20	3.47	6.19	4.76	3.02	3.07	2.31
15															**0.00**	3.69	4.03	3.81	3.16	6.86	5.36	5.33	5.15	4.40	4.71	3.30	4.15	4.61	3.42	5.52	5.41
16																**0.00**	3.65	3.35	2.68	4.29	2.46	3.61	2.46	3.05	3.51	2.81	4.52	3.81	2.38	2.69	2.21
17																	**0.00**	4.48	3.03	4.19	5.92	5.44	4.03	2.69	5.37	4.17	6.07	5.39	4.91	5.76	5.50
18																		**0.00**	3.36	6.87	4.70	2.82	3.80	4.71	2.98	3.92	4.85	3.48	4.33	3.95	3.20
19																			**0.00**	3.29	3.75	6.10	2.86	2.45	4.50	4.22	6.73	4.67	2.66	4.97	2.62
20																				**0.00**	4.86	7.73	3.21	4.23	7.01	6.99	11.08	6.89	3.44	5.79	4.36
21																					**0.00**	3.69	2.63	3.86	4.72	4.54	5.71	3.49	2.69	2.39	2.56
22																						**0.00**	4.92	5.14	2.94	3.34	3.78	3.86	5.54	2.72	3.50
23																							**0.00**	4.80	4.65	5.88	7.07	4.04	2.44	2.46	2.58
24																								**0.00**	2.90	3.69	5.98	4.36	4.35	5.01	3.50
25																									**0.00**	2.93	4.14	2.97	5.07	3.74	2.31
26																										**0.00**	3.53	4.09	5.53	4.85	3.47
27																											**0.00**	3.14	5.87	5.38	5.81
28																												**0.00**	3.14	4.27	4.17
29																													**0.00**	4.29	3.67
30																														**0.00**	2.12
31																															**0.00**

Table 3 Average cluster mean for 26 traits

	D50F	GFP	FLL	FLW	FLA	PH	PL	SBTPP	CC	CTD	PW	LR	SL	NSPP	PM	PB	GWPS	NGPS	NGPP	GL	GW	GLWR	TW	GYPP	HI	YPP
1	77.60	29.39	21.84	1.87	30.97	100.44	35.91	11.32	27.30	6.39	6.38	5.82	10.19	19.47	116.35	57.49	1.74	44.30	530.89	6.74	2.93	2.40	36.33	19.79	34.38	502.55
2	77.16	29.34	21.26	1.85	29.72	96.77	35.46	10.53	27.10	6.44	6.36	5.95	10.19	19.10	116.41	54.57	1.83	44.44	493.65	6.75	2.96	2.37	36.13	19.47	35.26	491.54
3	76.03	29.42	22.32	1.85	31.12	100.58	36.89	10.66	27.87	6.71	6.19	5.80	10.50	19.35	114.85	55.01	1.76	39.88	450.57	6.75	2.84	2.44	35.91	18.51	34.69	480.02
4	81.07	29.10	21.49	1.84	29.70	97.25	35.02	10.36	27.72	6.71	6.36	5.61	9.97	18.83	117.03	54.77	1.71	40.78	446.86	6.82	2.93	2.41	35.96	17.15	31.35	457.64
5	76.59	29.11	22.55	1.84	31.48	97.17	35.14	11.31	28.04	6.88	6.33	5.81	10.48	18.66	115.63	55.10	1.72	43.61	517.51	6.82	2.96	2.37	36.59	19.58	35.11	519.03
6	77.62	29.41	22.06	1.86	31.06	100.05	36.77	10.39	26.76	6.26	5.43	6.30	10.33	19.39	116.19	56.03	1.73	43.55	485.77	6.78	2.92	2.40	36.09	18.34	31.80	521.35
7	78.38	29.29	21.33	1.91	30.76	99.05	36.23	10.24	26.61	6.35	6.25	6.33	10.34	18.89	115.92	53.54	1.69	41.55	447.29	6.76	2.92	2.42	37.07	17.16	32.83	497.40
8	78.03	29.11	21.89	1.90	31.21	100.91	36.61	12.28	26.66	6.56	5.28	6.04	10.70	18.68	117.07	58.60	1.78	44.00	570.19	6.71	2.93	2.39	33.76	22.29	37.60	431.24
9	76.96	29.34	21.27	1.87	30.17	97.01	35.49	10.62	26.68	6.45	6.88	6.20	10.19	18.71	116.29	55.10	1.79	42.80	477.90	6.74	2.96	2.33	36.79	19.26	34.82	475.96
10	76.57	29.37	21.20	1.88	30.22	98.84	36.03	10.90	27.42	6.34	6.47	6.11	10.21	18.75	116.03	55.15	1.65	43.06	493.27	6.77	2.93	2.40	35.41	17.88	32.30	437.71
11	75.89	28.92	21.59	1.88	31.19	95.69	34.09	11.91	27.50	6.40	6.43	6.68	10.18	19.36	115.42	59.11	1.82	47.29	573.40	6.88	2.99	2.37	35.20	22.05	35.83	473.00
12	80.39	29.50	21.85	1.85	30.38	95.92	34.74	10.33	26.51	6.48	6.02	7.00	11.06	19.86	116.86	60.53	1.76	39.25	434.12	6.88	3.06	2.37	34.02	18.44	29.59	470.74
13	79.32	29.85	22.40	1.88	31.86	96.29	34.67	10.46	28.29	6.28	6.24	6.62	10.09	19.31	116.32	55.56	1.78	44.59	499.81	6.67	2.89	2.42	38.02	19.36	33.20	523.18
14	77.00	29.53	20.91	1.75	27.72	98.78	34.93	11.89	26.31	6.75	6.02	5.41	10.39	19.00	116.00	55.58	1.70	41.81	525.59	6.78	2.93	2.42	37.81	19.52	34.81	407.98
15	75.31	29.56	21.32	1.75	28.18	95.62	34.65	11.31	26.69	7.14	6.54	5.58	10.04	19.29	117.58	56.70	1.82	47.26	550.67	6.76	2.99	2.32	36.09	20.32	36.11	488.40
16	76.88	29.49	21.03	1.86	29.35	99.67	36.55	10.64	26.95	6.56	6.30	5.78	10.28	19.17	116.03	56.27	1.69	41.64	465.40	6.85	2.94	2.38	35.64	17.87	32.67	517.55
17	79.02	29.46	21.47	1.89	30.56	100.38	36.83	11.95	26.17	6.85	6.03	6.10	10.29	19.52	115.63	58.50	1.80	44.74	556.68	6.87	2.95	2.44	36.28	21.62	36.37	457.33
18	75.24	29.44	20.64	1.96	30.58	97.41	34.76	10.30	26.97	6.18	6.50	5.55	10.08	18.82	117.19	53.47	1.88	42.48	459.17	6.77	2.87	2.48	34.68	19.61	34.55	536.13
19	77.46	29.26	22.25	1.89	31.66	99.49	37.00	10.47	27.27	6.41	6.33	5.67	10.10	18.89	116.40	55.90	1.82	42.24	464.33	6.84	2.89	2.44	35.18	19.37	34.10	483.43
20	75.97	29.31	22.34	1.85	31.29	93.24	33.36	10.79	25.38	6.60	7.04	6.44	10.13	18.43	116.58	56.56	1.85	43.20	482.83	6.91	2.91	2.40	37.35	19.73	34.48	534.49
21	76.49	29.44	22.02	1.87	31.41	98.88	36.00	10.91	27.62	6.88	6.21	6.12	10.15	19.71	115.79	56.09	1.71	45.13	520.04	6.69	2.96	2.33	38.06	18.19	32.35	485.60
22	78.53	29.89	22.22	1.93	32.95	102.92	34.75	11.23	27.68	6.84	5.93	6.57	10.09	18.54	117.11	59.33	1.75	41.28	485.56	6.84	2.98	2.38	34.69	19.72	33.07	455.96
23	78.74	29.42	22.20	1.91	32.40	96.23	35.18	10.64	27.92	6.14	6.21	5.80	10.56	19.00	116.64	54.54	1.82	48.00	536.93	6.76	2.89	2.40	36.18	19.27	34.52	455.03
24	76.50	29.94	21.08	1.82	29.04	98.82	36.36	10.59	27.35	6.44	6.37	5.87	10.24	19.45	117.68	54.18	1.64	43.97	493.72	6.75	2.90	2.38	36.57	17.28	31.75	468.69
25	76.22	29.65	21.45	1.85	30.38	101.44	38.96	11.03	27.39	7.03	6.89	5.76	10.21	19.90	115.83	51.98	1.63	43.13	507.00	6.79	2.95	2.42	37.32	17.74	32.73	458.80
26	77.77	29.11	21.15	1.90	30.53	98.41	36.06	11.06	25.76	6.45	6.24	5.96	9.85	18.18	116.18	57.96	1.77	43.22	506.77	6.85	2.88	2.43	36.12	19.99	34.87	494.26
27	76.05	29.44	21.92	1.91	31.55	100.58	37.99	10.43	28.13	6.66	6.59	5.95	10.16	18.83	115.90	55.94	1.72	43.58	481.46	6.75	2.89	2.42	36.66	17.87	33.10	439.86
28	77.61	29.38	20.71	1.94	30.23	100.50	36.54	11.34	27.18	6.31	6.54	5.56	10.28	18.84	115.83	57.82	1.86	44.54	527.92	6.74	2.93	2.33	35.31	21.41	37.23	470.53
29	76.50	29.56	20.12	1.85	28.00	98.08	35.54	11.93	26.75	6.14	5.41	5.76	10.31	18.37	117.33	60.05	1.75	47.73	588.36	6.72	2.97	2.35	36.10	22.19	33.82	457.45
30	75.78	29.32	20.91	1.88	29.51	98.99	35.08	10.73	26.16	6.36	6.67	5.57	10.53	19.08	116.06	54.94	1.89	45.78	524.53	6.81	2.91	2.43	37.78	19.99	35.42	531.18
31	77.81	29.83	23.27	1.94	34.23	97.86	36.28	11.16	28.01	6.77	5.81	5.96	10.06	19.01	116.50	53.19	1.79	43.51	507.18	6.72	2.85	2.40	35.76	19.74	36.63	476.16

Table 4 Eigen value and percentage of total variance of various principal components

	Eigenvalue	Percentage of variance	Cumulative percentage of variance
PC 1	3.8681	14.8774	14.8774
PC 2	2.6209	10.0803	24.9578
PC 3	2.4218	9.3146	34.2724
PC 4	2.3071	8.8735	43.1459
PC 5	1.8807	7.2336	50.3795
PC 6	1.7557	6.7525	57.1320
PC 7	1.4361	5.5236	62.6557
PC 8	1.3808	5.3106	67.9663
PC 9	1.0750	4.1346	72.1009
PC 10	0.9319	3.5841	75.6850
PC 11	0.8655	3.3288	79.0139
PC 12	0.7986	3.0716	82.0854
PC 13	0.7818	3.0069	85.0923
PC 14	0.6766	2.6022	87.6946
PC 15	0.6451	2.4810	90.1756
PC 16	0.5453	2.0972	92.2727
PC 17	0.4712	1.8125	94.0852
PC 18	0.4069	1.5650	95.6502
PC 19	0.3710	1.4271	97.0773
PC 20	0.3405	1.3095	98.3868
PC 21	0.1675	0.6443	99.0311
PC 22	0.1358	0.5224	99.5534
PC 23	0.0685	0.2634	99.8169
PC 24	0.0333	0.1280	99.9448
PC 25	0.0084	0.0322	99.9770
PC 26	0.0060	0.0230	100.0000

Table 5 Factor loading of nine characters with respect to different principal components

	PC 1	PC 2	PC 3	PC 4	PC 5
D50F	0.0129	0.1305	1.0221	0.0381	8.8861
GFP	0.2557	0.2178	0.0631	9.9553	4.2323
FLL	2.3690	16.6287	2.6230	3.3451	0.5824
FLW	0.6899	5.8032	7.7486	2.6173	2.0270
FLA	2.6016	19.4005	6.9498	5.3028	0.0155
PH	2.2920	5.5357	15.7415	1.1192	0.0899
PL	4.4102	1.2042	23.9893	0.0409	0.6525
SBTPP	11.8027	8.1034	1.9564	1.6450	0.1458
CC	0.9846	1.0142	3.4044	6.3663	3.4449
CTD	0.9486	1.3004	1.6588	0.3135	8.1189
PW	1.5296	0.0071	8.7097	0.2307	15.2796
LR	0.1074	2.6203	6.0115	1.4760	0.2649
SL	1.9332	1.1593	1.3231	0.1535	6.5574
NSPP	0.1181	0.0081	1.1626	3.8353	2.1991
PM	0.3126	1.0117	3.8424	0.9699	16.7492
PB	6.1440	0.7459	0.0468	1.7815	8.4424
GWPS	12.5796	4.6276	1.5875	0.0645	0.0000
NGPS	2.0297	1.7237	0.4422	9.8609	1.1775
NGPP	11.2868	9.3308	0.5041	1.2434	0.6763
GL	0.2512	0.4631	0.0525	17.1429	0.4093
GW	0.2539	6.7537	2.2925	10.4616	0.0556
GLWR	0.0639	6.1683	1.6776	21.0627	0.5004
TW	0.0197	0.1035	1.6161	0.0805	13.5430
GYPP	23.2542	0.0759	0.0005	0.5172	0.0062
HI	13.7383	0.0299	0.0042	0.2693	5.8559
YPP	0.0107	5.8327	5.5698	0.1067	0.0878

CONCLUSION:

Based on the above result of genetic diversity with the help of principle component analysis it could be concluded for all characteristics in this study, 80 genotypes were classified into 31 clusters, with cluster XII exhibiting the highest intra-cluster distance, followed by clusters XI and VII. The greatest inter-cluster distance was observed between cluster XX and XXVII indicating significant diversity. Clusters XVIII and IV demonstrated the highest mean in yield per plot and yield-related traits, making them potential candidates for inter-crossing to develop a base population with desirable characteristics.The five different groups positive maximum variable loaded component PC I for grain yield per plant (23.2542), PC II flag leave area (19.4005), PC III for peduncle length (23.9893), PC IV grain length /width ratio (21.0627), PC V for physiological maturity (16.7492).Thus, this finding indicated that these traits could utilize in various breeding as well as improvement programmes. The information may further help the breeders in formulating appropriate strategy aimed at getting higher yield and character improvement in wheat.

Reference:

Adilova, S.S.; Qulmamatova, D.E.; Baboev, S.K.; Bozorov, T.A. and Morgunov, A.I. Multivariate cluster and principal component analyses of selected yield traits in uzbek bread wheat cultivars. American Journal of Plant Sciences, 2020; 11(06), p.903.

Devesh, P.; Moitra, P.K.; Shukla, R.S. and Pandey, S. Genetic diversity and principal component analyses for yield, yield components and quality traits of advanced lines of wheat. Journal of Pharmacognosy and Phytochemistry, 2019; 8(3), pp.4834-4839.

Khalid, A.; Hameed, A. and Tahir, M.F. Estimation of genetic divergence in wheat genotypes based on agro-morphological traits through agglomerative hierarchical clustering and principal component analysis. Cereal Research Communications, 2023; 51(1), pp.217-224.

Khalid, A.; Hameed, A.; and Tahir, M. F. Estimation of genetic divergence in wheat genotypes based on agro-morphological traits through agglomerative hierarchical clustering and principal component analysis. Cereal Research Communications, 2022; 1-8.

Kumar, S.; Kumari, P.; Kumar, U.; Grover, M.; Singh, A.K.; Singh, R. and Sengar, R.S. Molecular approaches for designing heat tolerant wheat. Journal of plant biochemistry and biotechnology,2013; 22, pp.359-371

Lafiandra, D, Riccardi, G. and Shewry, P.R. Improving cereal grain carbohydrates for diet and health. Journal of cereal science, 2014; 59(3), pp.312 26.

Mondal, S.; Singh, R.P.; Crossa, J.; Huerta-Espino, J.; Sharma, I.; Chatrath, R.; Singh, G.P.; Sohu, V.S.; Mavi, G.S.; Sukuru, V.S.P. and Kalappanavar, I.K. Earliness in wheat: a key to adaptation under terminal and continual high temperature stress in South Asia. Field crops research, 2013; 151, pp.19-26.

Rohith, K.; Talekar, N.; Sree, C. C.; and Pranay, J. Assessment of correlation and path analysis for yield and yield contributing traits in bread wheat (Triticum aestivum L. Em. Thell), 2022.

Sareen, S.; Kundu, S.; Malik, R.; Dhillon, O.P. and Singh, S.S. Exploring indigenous wheat (Triticum aestivum) germplasm accessions for terminal heat tolerance. The Indian Journal of Agricultural Sciences, 2015; 85(2), pp.37 42.

Shewry, P.R. and Hey, S.J. The contribution of wheat to human diet and health. Food and energy security, 2015;4(3), pp.178-202.

Singh, K.P.; Singh, T.; Singh, V.; Verma, O.P. and Singh, S. Divergence analysis in certain genotypes of wheat (Triticum aestivum L.). Journal of Pharmacognosy and Phytochemistry, 2019; 8(1), pp.507-510.

Akter, N. and Islam, M. R. Heat stress effects and management in wheat - A review. *Agronomy for Sustainable Development*,2017; **3**(7), 340-347.

Bita, C. and Gerats, T. Plant tolerance to high temperature in a changing environment: Scientific fundamentals and production of heat stress-tolerant crops. *Frontiers in Plant Science*,2013;**4,** 273-278.

Hyles, J.; Bloomfield, M.T.; Hunt, J. R.; Trethowan, R. M. and Trevaskis, B. Phenology and related traits for wheat adaptation. *Heredity*, 2020;**125**.

Sabar, G.; Jabran, M.; Hussain, A.; Hussain, S.; Sabir, W.; Zulkiffal, M.; Ahmed, M.S.; Joyia, F.A. and Ali, M.A. Field-based assessment of genetic diversity for leaf rust resistance and yield attributes in the locally developed wheat cultivars using multivariate analysis. *Pakistan Journal of Agricultural Sciences*, 2021; ***58(6),*** *1813-1823*

Gebremariam, K.; Alamirew, S.; and Gebreselassie, W**.** Evaluation of Bread Wheat (*Triticum aestivum* L.) germplasm at Kafa Zone, South West Ethiopia. *Advances in Agriculture*, *2022*.

Khalid, A.; Hameed, A.; and Tahir, M. F. Estimation of genetic divergence in wheat genotypes based on agro-morphological traits through agglomerative hierarchical clustering and principal component analysis. *Cereal Research Communications*, 2022;1-8.

Khare, V. Assessment and role of genetic diversity of component traits for improving grain yield in bread wheat (*Triticum aestivum* L.). *Electronic Journal of Plant Breeding*,2022; *13*(2), 447-454.

Abdelghany, M.; Makhmer, K.; Zayed, E.; Salama, Y. and Amer, K. Genetic variability, principal components and cluster analysis of twenty-eight egyptian wheat genotypes. *Scientific Journal of Agricultural Sciences*, (2023); ***5***(1), pp.107-118.