The Pharma Innovation

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Genetic diversity and principal component analyses for yield and yield components of advanced lines of wheat (*Triticum aestivum* L.)

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Abstract
The present research work comprises eighty-four advanced lines of wheat including checks, conducted at Main Experimental Station Research Farm of Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya (U.P.) during Rabi 2019-20. The genotypes were evaluated in Augmented Block Design for character association and genetic divergence analysis, divided into 5 blocks of equal size. Each block had 20 plots of test entries along with 4 checks (*viz.* HD-2967, HD-2733.NW-5054 and DBW-187). The presence of genetic divergence among these lines was observed by Mahalanobis's D^2 statistic. All the accesses were grouped into ten distinct clusters. The highest number of genotypes appeared in cluster III (16) followed by cluster X (14) and cluster V (12) while the lowest numbers of entries were reported in cluster VIII (3) & IX (4). Principal component analysis (PCA) indicated that the five principal components (PC1 to PC5) showed 85.8% of the total variability. PC1 to PC3 related to yield and its attributing traits, whereas PC4 was related to reproductive development.

Keywords: Cluster analysis, PCA, augmented block design, yield and wheat

Introduction

Wheat (*Triticum aestivum* L.) is one of the major staple food grains of India and globally as well and good source of energy and nutrition of diet. Wheat is known for its remarkable wide range of adoption to different kind's environment. It forms major portion of Rabi cereals because of its comprehensive adaptation and greater role in human nutrition and also plays vital role in agricultural economy of the country. India is the second largest grower of wheat after China. India contributes about 12 percent to global wheat gene pool. The major importance of wheat is because of its protein called gluten. The cohesive network of clump endosperm protein stretches with the expansion of fermentation dough. Wheat grain contains all major essential nutritional components; kernel contains about 12 percent water, carbohydrates (60-80% mainly as starch), proteins (8-15%) containing adequate amounts of all essential amino acids (except lysine, tryptophan and methionine which generally cereals lack), fats (1.5-2%), minerals (1.5-2%), vitamins (such as B complex, vitamin E) and 2.2% crude fibers (Rathore, 2001) [14]. For maintaining the subsistence and self-sufficiency, the country needs to hit the target of 109 million tonnes by year 2030. In India during 2019-20 rabi season wheat has been cultivated in 30.55 million hectares contributing 24.94% of total crop acreage. India has made another historic achievement in wheat by producing 107.59 mt in 2019-20 with an average national productivity of 3508kg/ha as per the Directorate of Statistics and Economics. During the past year production was also more than 100 mt (103.7mt) and the current year production has observed a change of 3.58 mt (+3.46%). The positive growth in production is contributed by the increase in area by 4.21% in spite of crop yield marginally by 0.72%.

Genetic diversity (D^2 statistic) developed by Mahalanobis (1928) provides a measure of the magnitude of divergence between biological populations and the relative contribution of each component character to the total divergence (Nair and Mukherjee, 1960, Maurya and Singh, 1977). Mahalanobis D2 statistic is more reliable in the selection of potential parents for hybridization programme. The principal component analysis is intended to derive a small number of linear combinations (principal components) of a set of variables that retain many of the existing information in the original variables. Knowledge of Pattern of existing genetic variability, the trend of character association, identification of promising traits and extent of

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genetic divergence will definitely help the researcher to identify high yielding as well as quality attributing traits wheat lines. The objective of this study is to evaluate the potential genetic diversity among wheat genotypes by using cluster analysis and principal component analysis for selection of desired parents in hybridization programmes.

Materials and Methods
The present investigation "Genetic divergence analysis and character association in wheat (*Triticum aestivum* L.)" was carried out during Rabi season (2019-20) on Main Experimental Farm of Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya, (U.P.).

Experimental materials of the study comprised of eighty wheat genotypes of Indian origin. All the genotypes were sown in augmented design with three replications. Plot size of each treatment was 5.0×1.38 m. In each plot, five random plants were tagged to record observations for all the character.

Experimental material
The experimental material for the present investigation comprised 80 accessions drawn from wheat gene pool maintained at this University. These accessions were raised and followed recommended packages and practices during Rabi season, 2019-20 as mentioned below

Table 1: List of Genotypes

S. No.	Genotypes
1	27th SAWYT-302
2	27th SAWYT-303
3	27th SAWYT-304
4	27th SAWYT-305
5	27th SAWYT-306
6	27th SAWYT-307
7	27th SAWYT-308
8	27th SAWYT-309
9	27th SAWYT-310
10	27th SAWYT-311
11	27th SAWYT-312
12	27th SAWYT-313
13	27th SAWYT-314
14	27th SAWYT-315
15	27th SAWYT-316
16	27th SAWYT-317
17	27th SAWYT-318
18	27th SAWYT-319
19	27th SAWYT-320
20	27th SAWYT-321
21	27th SAWYT-322
22	27th SAWYT-323
23	27th SAWYT-324
24	27th SAWYT-325
25	27th SAWYT-326
26	27th SAWYT-327
27	27th SAWYT-328
28	27th SAWYT-329
29	27th SAWYT-330
30	27th SAWYT-331
31	27th SAWYT-332
32	27th SAWYT-333
33	27th SAWYT-334
34	27th SAWYT-335
35	27th SAWYT-336
36	27th SAWYT-337
37	27th SAWYT-338
38	27th SAWYT-339
41	27th SAWYT-342
42	27th SAWYT-343
43	27th SAWYT-344
44	27th SAWYT-345
45	27th SAWYT-346
46	27th SAWYT-347
47	27th SAWYT-350
48	38th ESWYT 121
49	38th ESWYT 132
50	38th ESWYT 138
51	50th IBWSN 1203
52	50th IBWSN 1216
53	16th HTWYT 2

54	16th HTWYT 26
55	16th HTWYT 39
56	16th HTWYT 47
57	25th SAWYT 301
58	25th SAWYT 315
59	25th SAWYT -324
60	25th SAWYT -327
61	25th SAWYT- 328
62	25th SAWYT -340
63	27th SAWYT-350
64	38th ESWYT 121
65	25th HRWYT-206
66	25th HRWYT 241
67	35th SAWAN 3217
68	DWAP-1503
69	WH-1216
70	TL-3007
71	PDW-344
72	DBW-179
73	HI-8759
74	AKAW-3717
75	HTW-9
76	WH-1063
77	AKAW-4901
78	FLW-16
79	HD-3118
80	HI-1609
81	NW-5054 (CH)
82	DBW-187 (CH)
83	HD-2733 (CH)
84	HD-2967 (CH)

Observations recorded

The observations were recorded on five randomly selected competitive plants from each plot and from each replication for the eleven traits *viz*. days to 50% heading, days to maturity, plant height (cm), number of tillers plant-1, flag leaf area, spike length (cm), number of grains spike-1, thousand grain weight (g), biological yield plant-1 (g), grain yield plant-1 (g), harvest index (%). The protein content of each genotype was estimated using the micro-Kjeldahl method (Markham, 1942) [11].

Results and Discussions

Principal Component Analysis (PCA)

Five principal components (PC1 to PC5) are extracted from the original data and having latent roots greater than one, accounting nearly 85.8% of the total variation (Table.2). Similar studies were also reported by Hailegiorgis *et al.* (2011) [8]. The maximum Eigen root value (4.046) was recorded for 1st PC, which explained 33.371% variation. The rest four PCs (2nd, 3rd, 4rd & 5th) explained 12.627%, 12.083%, 9.807%, 8.078% individual variation.

The first PC was predominantly related to yield and yield contributing traits like grain yield per plant, biological yield per plant, test weight, days to maturity and days to 50% flowering indicated that these components were proven more important towards the genetic diversity, whereas the second PC contrast variables that related solely to flag leaf area, plant height, days to 50% flowering, biological yield per plant and thousand spike length with those that are associated with factor seed yield. The third principal component was named of yield component since positively correlated with days to 50% flowering, days to maturity, flag leaf area, and tiller per plant. The fourth principal component, accounted for 9.80%

of the variation. In this component, plant height, days to maturity and spike length were highly positive. Because of that, this component entitled as reproductive development. The fifth principal component was positively correlated with maximum characters as days to flowering, flag leaf area, plant height, days to maturity, grain yield per plant, harvest index and protein content. The results on PCA indicated that these traits are important for trait manipulation and diversity in this population was present due to these traits.

Table 2: Eigen values and variability explained by each principal component (PCs)

Principal components	PC 1	PC 2	PC 3	PC 4	PC 5
Eigene Value (Root)	4.046	1.515	1.449	1.176	0.969
% Var. Exp.	33.716	12.627	12.083	9.807	8.078
Cum. Var. Exp.	33.716	46.344	58.427	68.234	76.313

Table 3: Correlation coefficient of traits with respect to principal components (PCs)

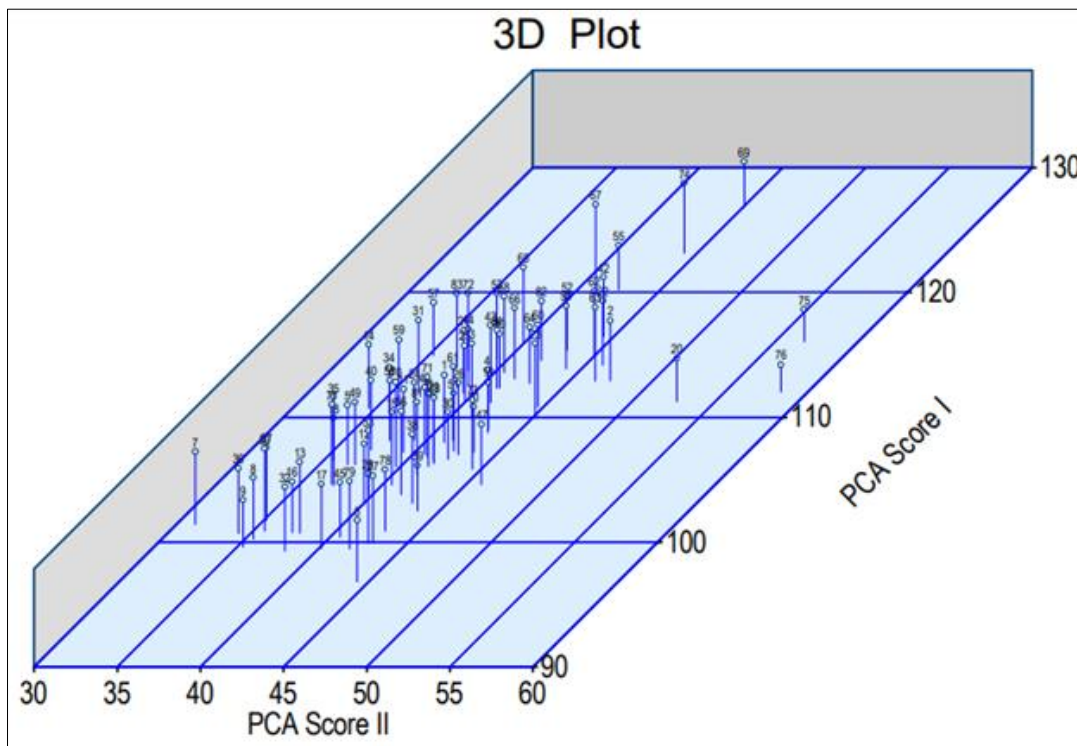| Variable	PC1	PC2	PC3	PC4	PC5
DFF	0.233	0.378	0.121	0.138	0.091
FLA	0.017	0.313	0.029	-0.676	0.264
PH	0.090	0.302	-0.430	0.080	0.518
DM	0.215	0.135	0.547	0.035	0.434
TP	0.415	-0.109	0.114	-0.037	0.053
SL	0.048	0.264	-0.503	0.442	0.086
GS	0.424	-0.177	-0.130	-0.098	-0.093
BYP	0.451	0.126	-0.091	-0.081	-0.180
GYP	0.454	-0.093	-0.067	-0.010	0.052
TW	0.341	-0.329	-0.027	0.142	-0.111
PC	-0.021	-0.321	-0.446	-0.491	0.118
HI	-0.088	-0.546	0.045	0.200	0.618

Fig 1: PCA graph

Cluster Analysis

After reducing the dimension, PCs were transformed into a single index and data were subjected to non-hierarchical Euclidean clustering. Ten well characterized groups were formed on the basis of similarity in agro-morphological traits (Table.4). The maximum number of genotypes (16) fell in cluster III followed by cluster X (14) cluster V (12) and cluster VI (11); and forming larger group. Similarly, cluster VII (8) cluster I (6), cluster II, IV (5), cluster VIII (4) and cluster IX (3) comprised variable number of genotypes given in parenthesis.

Table 4: Distribution of wheat genotypes based on Euclidean clustering method

| Cluster No.	No. of Genotypes	Name of the Genotypes
I	6	27th SAWYT-308, 27th SAWYT-310, 27th SAWYT-338, 27th SAWYT-309, 27th SAWY337, 38th ESWYT-121
II	5	27th SAWYT-314, 27th SAWYT-318, 27th SAWYT-346, 27th SAWYT-317, 27th SAWYT-333
III	16	27th SAWYT-302, 27th SAWYT-304, 27th SAWYT-305, 27th SAWYT-311, 27th SAWYT-320, 27th SAWYT-327, 27th SAWYT-330, 27th SAWYT-331, 27th SAWYT-342, 27th SAWYT-347, 27th SAWYT-349, 38th ESWYT-132, 25th SAWYT -324, TL-3007, PDW-344, HI-8759
IV	5	27th SAWYT-307, 27th SAWYT-328, 27th SAWYT-329, FLW-16, HD-3118
V	12	7th SAWYT-306, 27th SAWYT-312, 27th SAWYT-315, 27th SAWYT-319, 27th SAWYT-325, 27th SAWYT-335, 27th SAWYT-336, 27th SAWYT 341, 27th SAWYT-350, 16th HTWYT 47, 25th SAWYT 301, AKAW-4901
VI	11	27th SAWYT-303, 27th SAWYT-323, 27th SAWYT-324, 27th SAWYT-343, 38th ESWYT 138, 50th IBWSN 1216, 25th SAWYT 315, 25th SAWYT -327, 25th SAWYT- 328, 25th SAWYT -340, DBW-187
VII	8	27th SAWYT-313, 27th SAWYT-316, 27th SAWYT-334, 27th SAWYT-339, 27th SAWYT-340, 27th SAWYT-348, 16th HTWYT -26, NW-5054
VIII	3	27th SAWYT-321, HTW-9, WH-1063
IX	4	16th HTWYT 2, 35th SAWAN 3217, WH-1216, AKAW-3717
X	14	27th SAWYT-322, 27th SAWYT-326, 27th SAWYT-332, 27th SAWYT-344, 27th SAWYT-345, 50th IBWSN 1203, 16th HTWYT 39, 25th HRWYT-206, 25th HRWYT 241, DWAP-1503, DBW-179, HI-1609, HD-2733, HD-2967
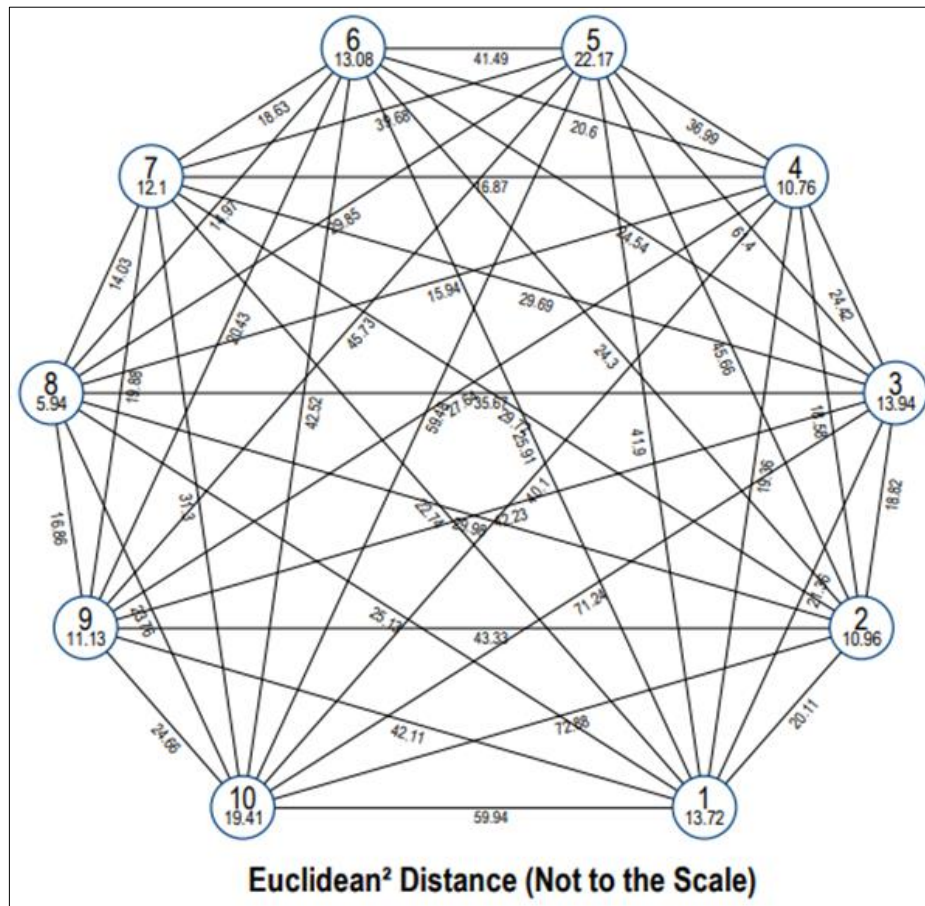
Fig 2: Euclidean Graph

Genetic divergence in bread wheat genotypes also reported by earlier workers (Kashif *et al.*, 2004; Yadav *et al.* 2006; Ali *et al.*, 2008; Chapla *et al.* 2008, Singh *et al.* 2010, Daniel *et al.*, 2011; Degewione and Alamerew, 2013; Fellahi *et al.*, 2013, Amin *et al.*, 2014, Ojha and Ojha, 2020, Iakra *et al.*, 2020) [4, 7, 1, 13].

The maximum intra cluster distance was recorded for Cluster V (22.171) followed by Cluster X (19.409), Cluster III (13.94), Cluster I (13.722), Cluster VI (13.076), Cluster VII (12.104), Cluster IX (11.125), Cluster II (10.97), Cluster IV & VIII whereas maximum inter cluster distance was found between Cluster X-II (72.88) followed by Cluster X-III (71.2), Cluster V-III (61.3), Cluster V-X (59.47) (Table 6). This indicates that strains include in these clusters had high genetic diversity so they can utilization in hybridization program for obtaining desirable recombinants in order to develop high yielding varieties. Same observations were also reported by Singh and Dwivedi (2000), Verma *et al.* (2006) [15], Singh *et al.* (2006) and Mittal *et al.* (2008).

Cluster I: This cluster consist of six genotypes i.e., individuals such as 27th SAWYT-308, 27th SAWYT-310, 27th SAWYT-338, 27th SAWYT-309, 27th SAWY337, 38th ESWYT-121. Genotypes of this cluster had high values for the variable SL (12.322), PH (88.33). Lowest values for the TP (6.667) variables. Cluster II: This cluster consists of five genotypes i.e., individuals such as 27th SAWYT-314, 27th SAWYT-318, 27th SAWYT-346, 27th SAWYT-317, 27th SAWYT-333. Genotype this cluster had high values for the variables FLA (19.41). Low values for the variables TP, SL, GPS & GYP (variables are sorted from the weakest). Cluster III: This cluster consists of sixteen genotypes i.e., individuals such as 27th SAWYT-302, 27th SAWYT-304, 27th SAWYT-305,

27th SAWYT-311, 27th SAWYT-320, etc. This group is characterized by high values for the variable HI (variables are sorted from the highest). Low values for the variables DFF, PH, DM, FLA & BYP (variables are sorted from the weakest). Cluster IV: This cluster consists five genotypes *i.e.,* of individuals such as27th SAWYT-307, 27th SAWYT-328, 27th SAWYT-329, FLW-16, HD-3118. This group is characterized low values for the variables PH, TP and high for DM variable. Cluster V: This cluster consists twelve genotypes *i.e.,* individuals such as, 7th SAWYT-306, 27th SAWYT-312, 27th SAWYT-315, 27th SAWYT-319, 27th SAWYT-325, 27th SAWYT etc. This group is characterized by low values for the variables TW & HI (variables are sorted from the lowest) and high values for FLA, PH & SL. Cluster VI: This cluster consists eleven genotypes *i.e.*, 27th SAWYT-303, 27th SAWYT-323, 27th SAWYT-324, 27th SAWYT-343, 38th ESWYT 138, 50th IBWSN etc. The genotype of this cluster had High values for the variables PC (variables are sorted from the strongest). Moderate values for the variables GYP, FLA. Cluster VII: This cluster consist two genotypes i.e., GJW-463, HW-5207, PBW-756, HI-8777 (d), PDW-344 and UAS-459. It had maximum distance from cluster IV (7.26311) and minimum distance from cluster V (2.55989). Genotype of this cluster had low values for the variables PC (variables are sorted from the strongest). Cluster VIII: This cluster consists three genotypes i.e., 27th SAWYT-321, HTW-9, WH-1063. Genotype of this cluster had moderate values for the variables DFF, PH (variables are sorted from the strongest). Low values for the variables HI, GYP and TW (variables are sorted from the weakest). Cluster IX: This cluster consist of four genotypes16th HTWYT 2, 35th SAWAN 3217, WH-1216, AKAW-3717. Genotype of this

cluster had high values for the variables TW (variables are sorted from the highest). Cluster X: This cluster consist of fourteen genotypes i.e., 27th SAWYT-322, 27th SAWYT-326, 27th SAWYT-332, 27th SAWYT-344, 27th SAWYT-345 etc. Genotype of this cluster had high values for the variables DFF, DM, TP, BYP, GYP, GPS (variables are sorted from the highest).

Table 5: Cluster mean based on Euclidean clustering method

	DFF	FLA	PH	DM	TP	SL	GPS	BYP	TW	HI	PC	GYP
Cluster1	82.778	14.599	88.933	127.111	6.667	12.322	39.144	30.911	39.636	38.286	10.173	11.813
Cluster2	81.167	19.413	82.783	128.083	6.633	10.008	37.575	29.993	36.032	38.013	11.404	11.399
Cluster3	77.400	14.396	82.000	126.800	7.080	10.680	38.872	29.344	37.650	41.768	12.288	12.196
Cluster4	85.684	17.616	82.539	132.368	8.042	10.979	39.554	34.042	38.074	38.316	10.249	13.020
Cluster5	84.333	21.847	113.533	130.667	8.000	12.800	41.627	39.920	35.000	34.533	10.307	13.813
Cluster6	81.769	18.047	83.218	126.538	8.077	10.977	43.589	36.463	39.690	37.815	13.022	13.778
Cluster7	81.667	14.721	83.556	129.333	8.244	11.133	43.079	38.702	40.984	37.388	9.984	14.469
Cluster8	89.143	17.193	88.686	130.571	8.257	11.434	43.706	39.440	40.919	36.171	11.854	14.249
Cluster9	81.000	20.038	88.850	131.500	9.000	10.100	45.375	41.185	44.318	38.817	11.995	15.975
Cluster10	93.333	16.103	88.033	135.000	9.333	11.233	47.293	44.947	44.183	39.267	10.360	17.653

Table 6: Intra-and inter-cluster average distances by Euclidean clustering method

Cluster No	Cluster1	Cluster2	Cluster3	Cluster4	Cluster5	Cluster6	Cluster7	Cluster8	Cluster9	Cluster10
Cluster1	13.722	20.113	21.364	19.363	41.895	25.911	22.735	25.135	42.112	59.944
Cluster2		10.957	18.822	18.579	45.566	24.296	29.717	29.977	43.326	72.881
Cluster3			13.943	24.419	61.395	24.541	29.687	35.667	42.234	71.236
Cluster4				10.757	36.990	20.602	16.871	15.936	27.636	40.101
Cluster5					22.171	41.493	39.680	29.853	45.729	59.479
Cluster6						13.076	18.633	14.970	20.430	42.524
Cluster7							12.104	14.034	19.884	31.303
Cluster8								5.941	16.856	23.765
Cluster9									11.125	24.659
Cluster10										19.409

Conclusion
From the present study, it was concluded that plant height exhibited the highest percent contribution towards total genetic divergence, followed by biological yield per plant and days to maturity. Maximum inter cluster distance was found between Cluster X-II (72.88) followed by Cluster X-III (71.2) It suggests that the crossing between genotypes of these clusters may lead to better recombinant and superior segregants for wheat improvement programmes. Five principal components (PC1 to PC5) are extracted from the original data and having latent roots greater than one, accounting nearly 85.8% of the total variation in which highest variation i.e., 33.71% is accounted for PC1.

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