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Pavan Devesh
Research Scholar
Department of Genetics and
Plant Breeding, Institute of
Agricultural Sciences, Banaras
Hindu University, Varanasi,
Uttar Pradesh, India

PK Moitra
Principal Scientist
Department of Genetics and
Plant Breeding, Jawaharlal
Nehru Krishi Vishwa Vidyalaya,
Jabalpur, Madhya Pradesh,
India

RS Shukla
Principal Scientist
Department of Genetics and
Plant Breeding, Jawaharlal
Nehru Krishi Vishwa Vidyalaya,
Jabalpur, Madhya Pradesh,
India

Suneeta Pandey
Assistant Professor
Department of Genetics and
Plant Breeding, Jawaharlal
Nehru Krishi Vishwa Vidyalaya,
Jabalpur, Madhya Pradesh,
India

Genetic diversity and principal component analyses for yield, yield components and quality traits of advanced lines of wheat

Pavan Devesh, PK Moitra, RS Shukla and Suneeta Pandey

Abstract
The present research work comprises sixty advanced lines of wheat, collected from Wheat Improvement Project, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur. These genotypes were evaluated in a randomized complete block design (RCBD) with three replications at Seed Breeding Farm, Department of Genetics and Plant Breeding, College of Agriculture, Jabalpur during *Rabi* 2016-17. The presence of genetic divergence among these lines was observed by Mahalanobis's D^2 statistic. All the accesses were grouped into five distinct clusters. The highest number of genotypes appeared in cluster I (45) followed by cluster III (8) and cluster IV (5) while the lowest numbers of entries were reported in cluster II (1) & V (1). Principal component analysis (PCA) indicated that the seven principal components (PC1 to PC7) showed 66.22% of the total variability. The highest value of yield and its attributing traits were present in PC3, PC2, and PC1 respectively, whereas PC4 & PC7 were related to quality traits.

Keywords: Cluster analysis, PCA, protein%, Hectolitre weight, yield, and wheat

Introduction
Wheat is the most important cereal crop for the majority of the world's populations. It contributes substantially to national food security by providing more than 50% calories to the people who mainly depend on wheat. The Food and Agriculture Organization of the United Nations (FAO) gracefully project the worldwide acclaim sticking with wheat as human food. Wheat is a rich source of carbohydrate and it provides about 20% of the food resources of the world (Farzi and Bigloo 2010) [5].

There are seventeen different species of wheat, out of which only three (*i.e. Triticum aestivum, Triticum durum* and *Triticum dicoccum*) are cultivated in the world. *Triticum aestivum* (bread wheat) is occupying more than 90% area followed by *Triticum durum* (9- 10%); however, very limited area of wheat is under *Triticum dicoccum.* India is the second largest wheat producer in the world and produced 86.50 million metric tonnes of wheat as per (FAO, 2016). Due to the high adaptation to varied environments, wheat is cultivated in almost all the states of India. The production of wheat has been increased manifold from 6.60 million tonnes at the time of independence to 97.44 million tonnes in 2016-17. The productivity has observed an increase of 473 per cent *i.e.* from 670 kg ha^{-1} to 3172 kg ha^{-1} during the above time period. Even with delayed sowing, the country recorded 30.71 million hectares acreage during *rabi* 2016-17 (Annual Report 2016-17, ICAR-IIWBR).

Genetic diversity (D^2 statistic) developed by Mahalanobis (1928) [7] 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) [10, 9]. Mahalanobis D^2 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 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
Sixty advanced lines of wheat (10 *Triticum durum* and 50 *Triticum aestivum*) depicted in (Table 1) obtained from Wheat Improvement Project JNKVV, Jabalpur, were grown in

Correspondence
Pavan Devesh
Research Scholar
Department of Genetics and
Plant Breeding, Institute of
Agricultural Sciences, Banaras
Hindu University, Varanasi,
Uttar Pradesh, India

randomized complete block design (RCBD) with three replications at Seed Breeding Farm, Department of Genetics and Plant Breeding, College of Agriculture Jabalpur, during *Rabi* 2016-17.

Each plot consists of two rows of 2.5 m length and 20 cm apart. The experimental area occupied was quite uniform with respect to topography and fertility. Jabalpur region has a semi-humid and subtropical climate. It is situated at 23.90^0 North latitude and 79.58^0 East longitudes at the altitude of 411.87 m above mean sea level. The minimum and maximum temperature varies between 8^{0C} in January to 45 ^{0C} in May. The crop was grown under normal crop season.

Table 1: List of advanced lines of wheat

S. No.	Advanced line	S. No.	Advanced line
1	N5B 801	31	PYT 86
2	N5B 803	32	PYT 100
3	N5B 804	33	PYT 64
4	N5B 805	34	PYT 33
5	N5B 806	35	PYT 44
6	N5B 807	36	PYT 56
7	N5B 808	37	PYT 31
8	N5B 809	38	PYT 85
9	N5B 810	39	PYT 88
10	N5B 811	40	PYT 70
11	GW 366	41	PYT 13
12	Lok 1	42	PYT 89
13	JW 3173	43	PYT T$_3$ 24
14	MP 4010	44	PYT 6
15	GW 322	45	PYT 91
16	MP 1106	46	PYT 19
17	MP 1201	47	PYT 87
18	GW 173	48	PYT 32
19	MP 3288	49	PYT 69
20	JW 3269	50	PYT 98
21	HI 1544	51	PYT 18
22	WH 147	52	PYT 9
23	JW 3020	53	PYT 62
24	MP 1142	54	PYT 1
25	MP 3336	55	PYT 3
26	JW 3211	56	PYT 10
27	MP 1202	57	PYT 66
28	GW 273	58	PYT 68
29	JW 17	59	PYT 45
30	MP 3382	60	PYT 20

Observations recorded
The observations were recorded on five randomly selected competitive plants from each plot and from each replication for the nineteen traits *viz.* days to 50% heading, days to maturity, plant height (cm), number of tillers plant^{-1}, number of spikes plant^{-1}, spike length (cm), peduncle length (cm), number of spikelets spike^{-1}, number of grains spike^{-1}, thousand grain weight (g), biological yield plant^{-1} (g), grain yield plant^{-1} (g), harvest index (%), canopy temperature (ºC), chlorophyll content (SPAD unit), protein (%), wet gluten (%), hectolitre weight (kg hectolitre^{-1}), sedimentation value (SDS value in ml).

The protein content of each genotype was estimated using the micro-Kjeldahl method (Markham, 1942). Wet gluten was estimated using automatic gluten washer. Sedimentation value measures the quality of proteins and is based on the fact thatgluten protein absorbs water and swells considerably

when treated with lactic acid in the presence of Sodium Dodecyl Sulphate (SDS). The hectolitre weight of the samples was measured by Hectolitre machine developed by ICAR-IIWBR, Karnal, which gives the weight in terms of kg hectolitre^{-1}.

Data analysis
The data collected were subjected to multivariate analysis utilizing Mahalanobis D^2 statistic as suggested by Mahalanobis (1936) and Rao (1952) using statistical software WINDOSTAT Version 9.2 developed by INDOSAT services Ltd. Hyderabad, India. Accessions were grouped into five clusters following Tocher's method as suggested by Rao (1952). The necessity of the principal component analysis (PCA) for measuring the degree of divergence has been established by XLSTAT 2017.

Results and discussion
Cluster analysis
The existence of genetic divergence among the sixty wheat advanced lines was examined by employing Mahalanobis's D^2 statistic. The clustering pattern of these genotypes on the basis of D^2 analysis has been presented in (Table 2). The entries were grouped into five distinct clusters. The highest number of genotypes appeared in cluster I, which possessed 45 genotypes, cluster III comprised of 8 genotypes, cluster IV comprised of 5 genotypes and the lowest number of entries *i.e.* one-one accession was found in cluster II & V. Dendrogram of these sixty wheat genotypes was constructed by Tocher's clustering method (Fig 1).

The maximum intra-cluster distance was obtained for cluster III (65.68) followed by cluster IV (62.91) and cluster I (47.40) respectively. The lowest intra cluster D^2 value was shown by cluster II (0.00) and cluster V (0.00) which had only one-one genotype. The highest inter cluster D^2 values was observed between cluster IV and cluster V (298.15) followed by cluster I and IV (239.48), cluster III and cluster V (137.21), cluster II and cluster IV (130.88), cluster III and cluster IV (124.50), cluster I and cluster III (101.78), cluster I and cluster V (82.99), cluster II and cluster V (77.67), cluster I and cluster II (75.06). The lowest inter-cluster distance was found between cluster II and cluster III (48.48). It suggests that the crossing between genotypes of these clusters may yield better recombinant and superior segregants.

The percent contribution of nineteen traits towards total genetic divergence presented in (Table 3) which showed that thousand grain weight exhibited highest percent contribution towards total genetic divergence (41.30%), followed by plant height (17.97%), sedimentation value (16.38%), days to 50% heading (8.7%), peduncle length (4.46%), number of grains spike^{-1} (3.67%), canopy temperature (2.6%), biological yield plant^{-1} (1.24%) and number of spikelets spike^{-1} (1.13%). Chlorophyll content possessed lowest contribution (0.85%) followed by hectolitre weight (0.40%), grain yield plant^{-1} (0.34%), protein% and wet gluten% (0.28%), number of tillers plant^{-1} (0.17%) and days to maturity and spike length (0.11%). Sangwan (2004) [12], Dwivedi and Pawar, (2005) the genotypes of cluster I, II and IV were identified as divers and higher mean value. Sultana and Malik (2005) [13], Jaiswal *et al.* (2010) [6], reported the formation of the cluster representing the availability of wide genetic diversity in wheat lines studied.

Table 2: Clustering pattern of sixty wheat genotypes based on D² analysis

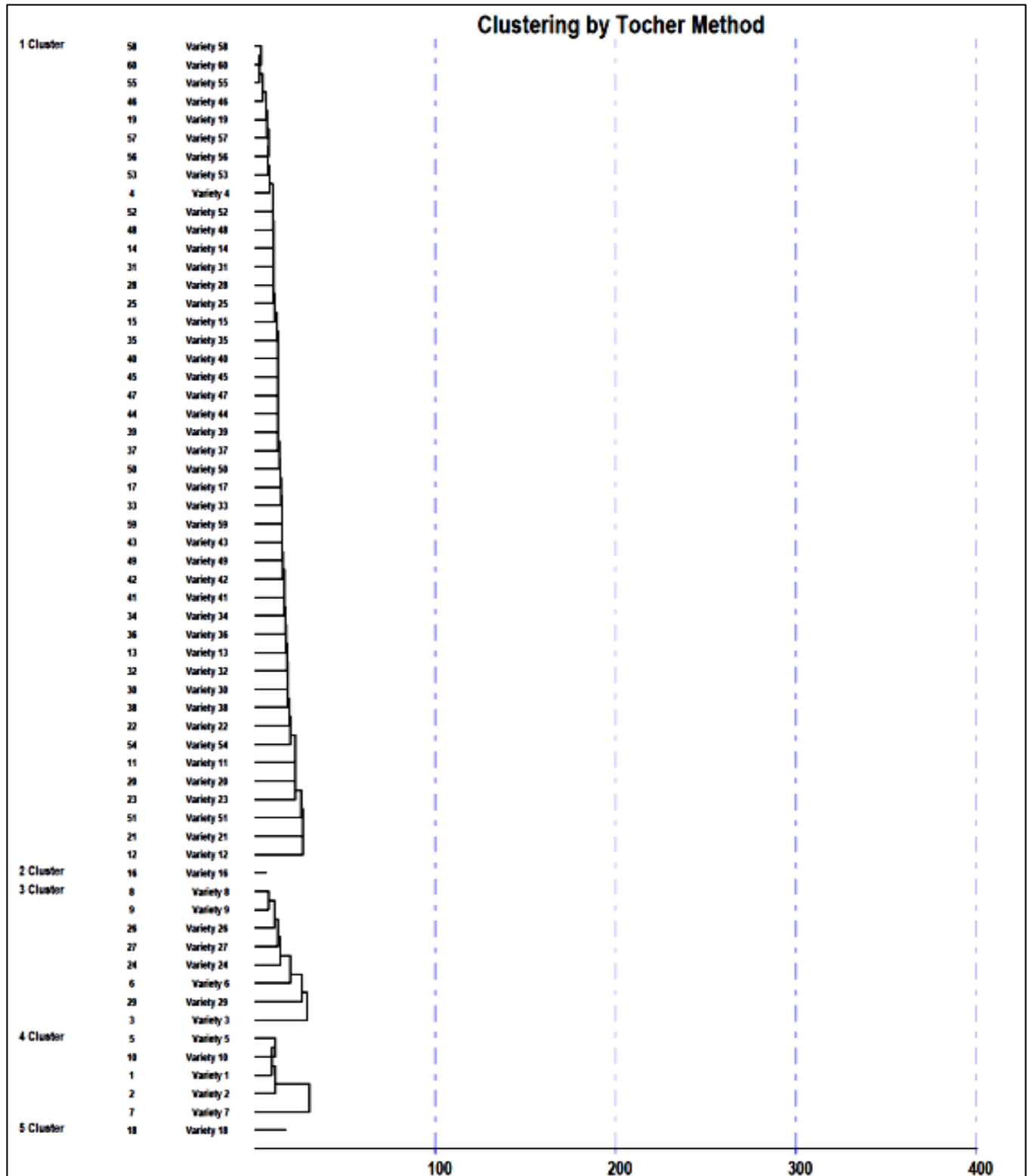| Cluster	Genotypes	Name of genotypes
I	45	PYT 68, PYT 20, PYT 3, PYT 19, MP 3288, PYT 66, PYT 10, PYT 62, N5B 804, PYT 9, PYT 32, MP 4010, PYT 86, GW 273, MP 3336, GW 322, PYT 44, PYT 70, PYT 91, PYT 87, PYT 6, PYT 88, PYT 31, PYT 98, MP 1201, PYT 64, PYT 45, PYT T₃ 24, PYT 69, PYT 89, PYT 13, PYT 33, PYT 56, JW 3173, PYT 100, MP 3382, PYT 85, WH 147, PYT 1, GW 366, JW 3269, JW 3020, PYT 18, HI 1544 and Lok 1
II	1	MP 1106
III	8	N5B 808, N5B 809, JW 3211, MP 1202, MP 1142, N5B 806, JW 17 and N5B 803
IV	5	N5B 805, N5B 810, N5B 801, N5B 802 and N5B 807
V	1	GW 173

Fig 1: Dendrogram of wheat genotypes

Table 3: Percent contribution of nineteen traits towards total genetic divergence

Traits	No. of times ranked first	Percent Contribution (%)
Days to 50% heading	154	8.70
Days to maturity	2	0.11
Plant height (cm)	318	17.97
Number of tillers plant[-1]	3	0.17
Number of spikes plant[-1]	-	0.00
Spike length (cm)	2	0.11
Peduncle length (cm)	79	4.46
Number of spikelets spike[-1]	20	1.13
Number of grains spike[-1]	65	3.67
Thousand-grain weight (g)	731	41.30
Biological yield plant[-1] (g)	22	1.24
Grain yield plant[-1] (g)	6	0.34
Harvest Index (%)	-	0.00
Canopy temperature (ºC)	46	2.60
Chlorophyll content	15	0.85
Protein (%)	5	0.28
Wet gluten (%)	5	0.28
Hectolitre weight (kg hl[-1])	7	0.40
Sedimentation value (ml)	290	16.38

Principle component analysis (PCA)

Principle Component Analysis was performed for nineteen traits of wheat. Out of nineteen traits, only first seven principal components (PCs) exhibited more than 1.00 eigenvalue (Table 4, Fig 2), and showed maximum variability about 66.22% among the traits studied. The PC1 had the highest variability (15.30%) followed by PC2 (12.19%), PC3 (11.04%), PC4 (8.01%), PC5 (7.73%), PC6 (6.26%) and PC7 (5.67%).

Rotated component matrix revealed that the first seven PCs (Table 5) are representing maximum variability hence, the traits falling to these seven PCs may be given due importance in wheat improvement programmes. The PC1 was mostly associated with traits such as, thousand-grain weight, plant height, hectolitre weight, canopy temperature, and peduncle length. In PC2 the traits *viz.*, number of grains spike[-1], number of spikelets spike[-1] and spike length whereas, PC3 was consisting of mainly four traits *viz.*, number of spikes plant[-1], number of tillers plant[-1], grain yield plant[-1], and biological yield plant[-1]. Quality traits *viz.*, protein% and sedimentation value were reported in PC4 whereas, PC5 was related with days to maturity and days to 50% heading. PC6 was related to chlorophyll content and harvest index. Wet gluten% was reported in PC7. On the basis of PCA, most of the important yield and yield attributing traits were present in PC3, PC2, and PC1. High PC score for a particular genotype in a particular component denotes high values for the variables in that particular genotype. In PC1 genotypes *viz.*, N5B 808 had

the highest PC score followed by N5B 806, N5B 801 and N5B 803 for traits *viz.*, 1000-grain weight, plant height, hectolitre weight, canopy temperature and peduncle length, whereas in PC2 genotype N5B 808 scored maximum followed by PYT 68, PYT 69 and N5B 807, for number of grains spike[-1], number of spikelets spike[-1] and spike length. In PC3 highest PC scores was obtained by PYT 85 followed by PYT 100, PYT 89 and N5B 811, for characters *viz.*, number of spikes plant[-1], number of tillers plant[-1], grain yield plant[-1] and biological yield plant[-1]. PC4 has the highest value for characters *viz.*, protein (%) and sedimentation value was noted for PYT 31 followed by PYT 64, N5B 801 and PYT 9. In PC5 characters *viz.*, days to maturity and days to 50% heading PYT 1 showed the highest score followed by JW 3173, N5B 809 and MP 1202. In PC6 characters *viz.*, chlorophyll content and harvest index GW 173 score highest followed by PYT 100, GW 366 and HI 1544, while in PC7 N5B 809 score highest for wet gluten% followed by PYT 62, N5B 810, MP 1142, GW 173, PYT 88, MP 3336 and PYT 64.

High PC score for a particular genotype in a particular component denotes high values for the variables in that particular genotype. Similar findings for plant height were reported in PC1 by Bhanupriya *et al.* (2014) [2], but in contradiction Meena *et al.* (2014) obtained a higher value for plant height and 1000-grain weight in PC2. It can be concluded from the above results that yield contributing traits were having the highest variation in PC3 followed by PC2 and PC1.

Table 4: Principle component, eigenvalue, percentage of total variation and cumulative percentage of nineteen traits of advanced lines of wheat

Principal component	Eigenvalue	Percentage of total variation	Cumulative percentage
PC1	2.907	15.301	15.301
PC2	2.317	12.194	27.494
PC3	2.098	11.043	38.538
PC4	1.523	8.017	46.554
PC5	1.470	7.734	54.289
PC6	1.190	6.266	60.554
PC7	1.077	5.670	66.224
PC8	0.929	4.891	71.114
PC9	0.873	4.594	75.708
PC10	0.831	4.371	80.079
PC11	0.748	3.936	84.016
PC12	0.692	3.641	87.657
PC13	0.551	2.899	90.556

PC14	0.498	2.620	93.176
PC15	0.448	2.359	95.535
PC16	0.433	2.278	97.813
PC17	0.222	1.167	98.980
PC18	0.104	0.548	99.528
PC19	0.090	0.472	100.000
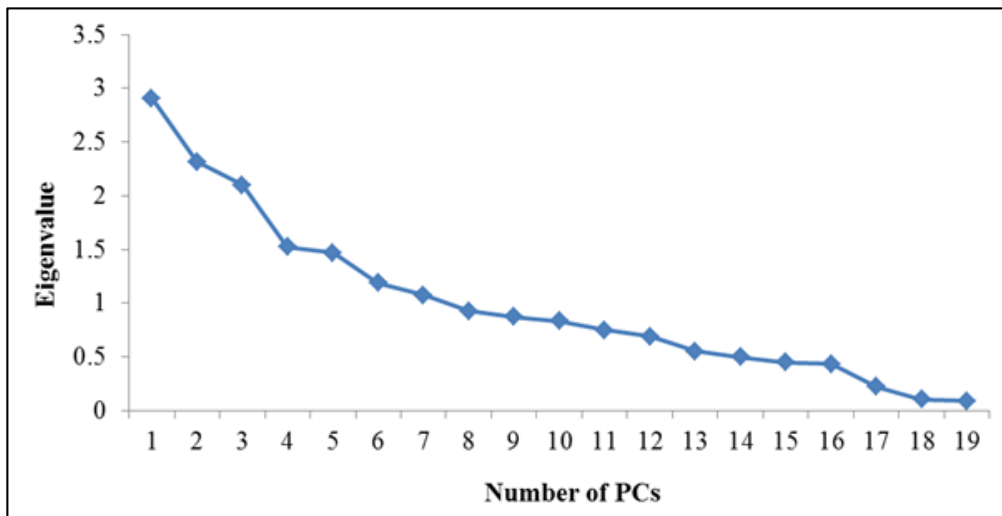
Fig 2: PCA Scree plot

Table 5: Rotated component matrix of seven PCs

PC1	PC2	PC3	PC4	PC5	PC6	PC7
1000-grain weight (g)	No. of grains spike^{-1}	No. of spikes plant^{-1}	Protein%	Days to maturity	Chlorophyll content (SPAD unit)	Wet gluten%
Plant height (cm)	No. of spikelets spike^{-1}	No. of tillers plant^{-1}	Sedimentation value (ml)	Days to 50% heading	Harvest Index (%)	
Hectolitre weight (kg hl^{-1})	Spike length (cm)	Grain yield plant^{-1} (g)				
Canopy temperature (°C)		Biological yield plant^{-1}(g)				
Peduncle length (cm)						

Conclusion
From the present study, it was concluded that thousand-grain weight exhibited the highest percent contribution towards total genetic divergence, followed by plant height. The maximum cluster distance reported between cluster IV & V followed by cluster I & IV. It suggests that the crossing between genotypes of these clusters may lead to better recombinant and superior segregants for wheat improvement programmes. On the basis of PCA the promising genotypes *viz.*, PYT 64, N5B 801, PYT 9, PYT 89, MP 4010, PYT 1, JW 3173, PYT 69, PYT 56 and PYT 31 were identified for yield and quality attributing traits.

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