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Vivek Singh
Department of Genetics and
Plant Breeding, CSKHP,
Palampur, Himanchal Pradesh,
India

Alok Kumar Maurya
ICAR-Indian Institute of Pulses
Research Kanpur,
Uttar Pradesh, India

Rajesh Kumar Singh
Narendra Deva University of
Agriculture and Technology,
Kumarganj, Ayodhya,
Uttar Pradesh, India

Anil Kumar Singh
ICAR-Indian Institute of Pulses
Research, Kanpur, Uttar
Pradesh, India

Mohammad Nisar
ICAR-Indian Institute of Pulses
Research, Kanpur,
Uttar Pradesh, India

Runa Singh
ICAR-Indian Institute of Pulses
Research, Kanpur,
Uttar Pradesh, India

Gaurav Sharma
Department of Genetics and
Plant Breeding, CSKHP,
Palampur, Himanchal Pradesh,
India

Corresponding Author:
Alok Kumar Maurya
ICAR-Indian Institute of Pulses
Research Kanpur,
Uttar Pradesh, India

Genetic diversity based on cluster and principal component analyses for yield and its contributing characters of bread wheat (*Triticum aestivum* L.) germplasms

Vivek Singh, Alok Kumar Maurya, Rajesh Kumar Singh, Anil Kumar Singh, Mohammad Nisar, Runa Singh and Gaurav Sharma

Abstract

The present investigation conducted on 80 accessions of wheat during 2018-19 at Main Experiment Station (MES) of A.N.D. University of Agriculture and Technology, Kumarganj, Ayodhya (U.P.) to evaluate genetic divergence based on cluster and principal component analyses for yield and its contributing characters for the identification of most diverse and promising genotypes. The experiment was laid out in Augmented Block Design. The observations were recorded on various phenotypic characters. The varieties of wheat were grouped into 08 distinct clusters by using K mean and Euclidean cluster analysis. Maximum inter cluster distance was found between Cluster VII-IV (7.2631) followed by Cluster VIII-IV (6.0618), Cluster IV-II (5.5329), and Cluster VIII-III (5.02072). Cluster II & I (DFF), cluster III & IV (FLA), cluster II & V (PH), cluster II & V (DM) and cluster IV & VII (TP), were found more diverse clusters based on cluster mean for traits given in parenthesis. Remaining traits had minimum or no contribution in divergence. The result of Principal Component Analysis (PCA) revealed that all 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. The maximum Eigen root value (4.105) was recorded for 1st PC, which explained 37.3% variation. The rest four PCs (2nd, 3rd, 4rd & 5th) explained 17.5%, 14.7%, 11.1% & 5.1% individual variation.

Keywords: Principal component analysis, cluster mean, genetic divergence

Introduction

Ongoing trends in population growth and feeding criteria continue to increase the demand for wheat, a key cereal for global food security. Wheat (*Triticum aestivum* L.) is a crop globally cultivated for its tasty seed grain which is the most important staple food for about two billion people. In recent years, changes in population trends, eating habits, and economic and socio-economic conditions, especially in Africa and Asia, have caused an increase in global wheat demand. Wheat is the most vital cereal crop for the greater part of world's countries. Worldwide, wheat offers about 55% carbohydrates and 20% of the cooking calories consumed globally (Breiman and Graur, 1995), "having a protein content of about 13%, which is relatively high compared to other major cereals". Wheat is cultivated over a broad range of climatic conditions and therefore study of genetics for plant improvement purposes is of great importance.

For several contexts, the assessment of genetic diversity using quantitative traits has been of prime importance, especially for differentiating well-defined populations. For a self-pollinated seed, the germplasm may be regarded as heterogeneous group sets, because each group is homozygous inside itself. Selecting my parents for breeding program in such crops is critical because the success of such program depends on the segregants of hybrid derivatives between parents, particularly when the goal is to improve quantitative characters such as yield. Several methods of divergence analysis based on quantitative characteristics have been suggested to aid the breeder in the process to classify the parents who nick better. Among them, the Non-Hierarchical Euclidean Cluster occupies a unique position and an efficient tool for assessing the degree of genotypic variation, which quantifies the difference between many quantitative traits. The genetic divergence analysis using techniques Non-hierarchical Euclidean Cluster analysis, classify the genotypes into homogenous groups/clusters with similarity of genotypes for different characters within clusters while genotypes between two clusters are more

divergent than the genotypes of the same clusters. Thus, suitable genotypes from diverse cluster can be used for further planning of a successful breeding program. Cluster method is an analysis (CA) that used dendrograms to display how various genotypes were differentiated. Diversity of tetraploid wheat germplasm grouped by cluster analyses (CA) and principal component analyses (PCA) explained the variation among genotypes. As a multivariate statistical technique, the principal components analysis (PCA) has the ability to transform a number of possibly correlated variables into a smaller number of variables called principal components the principal components are linear transformations of the original variables and could be respective of a particular meaning. This approach is very helpful in deciding which agronomic traits of crop contributing most to yield, subsequently, these agronomic traits should be emphasized in the breeding program.

Method and Material

The present investigation conducted on 80 accessions of wheat during 2018-19 at Main Experiment Station (MES) of A.N.D. University of Agriculture and Technology, Kumarganj, Ayodhya (U.P.). The experiment was laid out in Augmented Block Design and plot size was 2.5 m × 0.25m size. The distance between row to row and plant to plant was maintained were 25 cm and 10 cm respectively. Recommended package of practices will be followed to raise the crop. Data will be recorded on the 5 plants/ genotype. Data were recorded on 11 characters, *viz.*, Grain yield/plant (g), Flag leaf area (cm²), Tillers/ plant, peduncle length (cm), 1000-grain weight (g), Biological yield/plant (g), Harvest index (%), Plant height (cm), Spike length (cm), Days to 50% heading, Days to maturity. The statistical tool R software and NTSYS PC with the aid of computer software 'DARwin 6.0' and 'SPSS' 20 for Windows was utilized for genetic divergence, principal component and cluster mean analysis including dendrogram.

Result and Discussion

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. 1). The maximum eigen root value (4.105) was recorded for 1st PC,

which explained 37.3% variation. The rest four PCs (2nd, 3rd, 4rd & 5th) explained 17.5%, 14.7%, 11.1% & 5.1% individual variation. Eigen value and variance associated with each principal component, decreased gradually and stopped at 0.56 and 5.12 respectively.

The first PC was predominantly related to yield and yield contributing traits like peduncle length, biological yield per plant, plant height, spike length and flag leaf area index indicated that these components were proven more important towards the genetic diversity, whereas the second PC contrast variables that related solely to harvest index, grain yield per plant and thousand grain weight 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 and days to maturity. This factor accounted for 13.10% (Table 1 & 2). The fourth principal component, accounted for 11.10% of the variation. In this component, thousand grain weight, flag leaf area and spike length were highly positive. Because of that, this component entitled as reproductive development. 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 1: 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)	4.1056	1.9293	1.6215	1.2164	0.5636
% Var. Exp.	37.32	17.53	14.74	11.1	5.12
Cum. Var. Exp.	37.32	54.86	69.60	80.66	85.78

Table 2: Correlation coefficient of traits with respect to principal components (PCs)

Variable	PC1	PC2	PC3	PC4	PC5
DFP	0.081	-0.061	0.599	-0.277	0.435
FLA	-0.346	0.074	-0.021	-0.377	0.347
PH	-0.436	-0.251	0.005	0.079	0.020
DM	0.014	-0.279	0.584	-0.177	-0.226
TP	0.037	-0.310	0.279	0.661	-0.133
SL	-0.313	-0.151	-0.312	-0.144	-0.159
PL	-0.423	-0.286	-0.002	-0.035	0.199
BYP	-0.445	-0.183	0.069	0.129	-0.132
GYP	0.186	-0.588	-0.264	0.038	0.304
TW	0.180	-0.366	-0.050	-0.515	-0.579
HI	0.374	-0.369	-0.219	-0.033	0.333

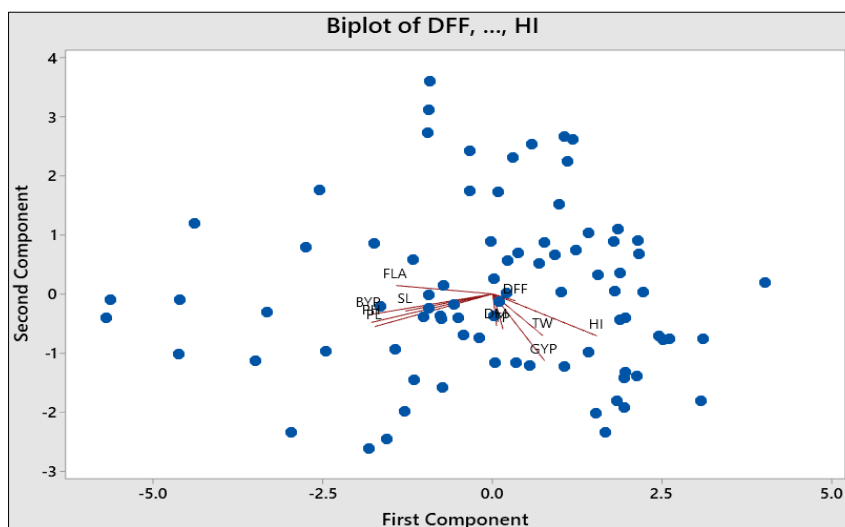


Fig 1: PCA biplot: Grouping pattern of genotypes

Cluster mean analysis

Selection of suitable parents plays a critical role in a successful plant breeding program. Various methods are available for estimating genetic diversity and grouping of breeding material. Eighty genotypes of wheat taken for Euclidian analysis were differed significantly with regard to the characters under study and displayed marked divergence, when taking all 11 characters together. Average intra and inter cluster distances were calculated and presented in Table 3. Intra cluster distance showed divergence among the genotype within a cluster while inter cluster distance expressed relative divergence between the clusters. The cluster mean for eleven characters among the eight clusters are also presented in

Table 3. The detailed descriptions of different cluster are given here under: - K-means clustering of standardized data was used to identify the more significant level of discrimination between the clusters for each of variable. Then dendrogram was constructed based on Ward's method using Euclidean distance (Kumar *et al.*, 2009).

K-mean clustering

After reducing the dimension, eight PCs were transformed into a single index and data were subjected to K mean clustering. Clusters mean for 11 agro-morphological traits are presented in Table 3.

Table 3: Cluster mean based on K-mean method

Variable	Cluster1	Cluster2	Cluster3	Cluster4	Cluster5	Cluster6	Cluster7	Cluster8
DFF	-0.2563	-0.3134	0.4555	-0.0010	-0.2333	-0.4896	-0.7339	0.7739
FLA	0.1313	0.9938	1.1815	0.7280	1.1679	-0.8435	0.1363	-0.6848
PH	0.3966	-0.6906	1.5947	-0.5589	2.1532	-0.7150	0.5214	-0.6263
DM	0.0357	0.1423	0.8396	-0.4397	-0.3475	-1.0275	-0.8373	0.9952
TP	0.4833	-1.8575	-0.4269	-0.8688	0.4881	0.2400	-2.0320	0.4164
SL	0.2137	-0.1819	1.7795	-0.0173	0.7261	-0.4633	0.8588	-0.6648
PL	0.6521	-0.5678	1.6582	-0.5479	1.6245	-0.8423	0.5066	-0.6645
BYP	0.5176	-0.2914	1.6228	-0.4194	1.9005	-0.7684	0.2974	-0.7232
GYP	0.5640	-1.8801	-0.0078	-1.0406	-1.4605	0.2596	0.6853	0.3467
TW	-0.1987	1.0550	-0.0174	-0.2643	-1.0442	-0.2496	0.6326	0.5509
HI	0.0788	-1.4397	-0.8513	-0.5944	-1.9004	0.6204	0.2863	0.6948

The mean characteristics of various clusters have been presented in Table 3. Cluster IV, V, VI and VII (DFF and DM); cluster III & V (FLA), cluster II & VI (PH), cluster I & V (TP), cluster III & VII (SL), cluster III & V (PL), cluster III

& V (BYP), cluster I & VII (GYP), cluster II & VII (TW) and cluster VII & VI (HI) were found more diverse clusters based on cluster mean for traits given in parenthesis.

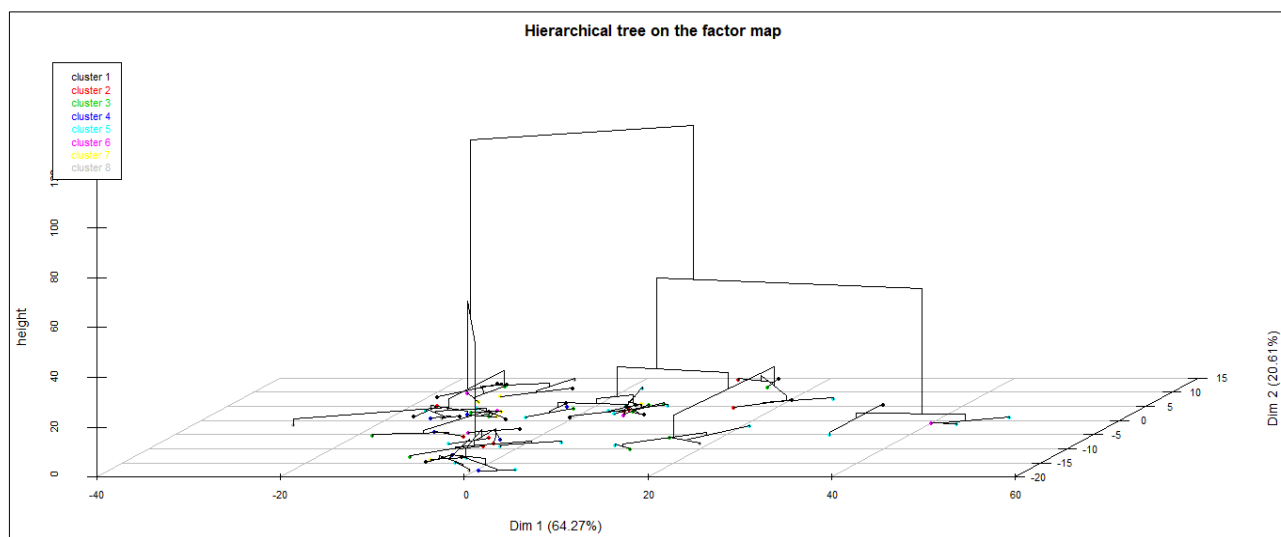


Fig 2: Hierarchical tree on the factor map

Table 4: Intra-and inter-cluster average distances by K-mean analysis

Cluster No.	Cluster1	Cluster2	Cluster3	Cluster4	Cluster5	Cluster6	Cluster7	Cluster8
Cluster1	1.3360							
Cluster2	4.4238	1.7668						
Cluster3	3.2296	5.0843	0.6854					
Cluster4	2.9652	2.1693	4.5104	1.4758				
Cluster5	4.0198	5.3940	2.9131	4.7536	1.8652			
Cluster6	2.8573	4.4813	5.7923	2.8074	6.1179	0.4871		
Cluster7	2.9270	3.9616	3.8956	3.2430	5.1579	3.6770	0.4482	
Cluster8	2.9550	4.4833	5.3818	3.3299	6.3705	2.5457	4.3174	1.3551

The maximum intra cluster distance was recorded for Cluster V followed by Cluster II, Cluster IV, Cluster I, Cluster VIII, Cluster III, Cluster VI and Cluster VII, whereas maximum inter cluster distance was found between Cluster VIII-V (6.3705) followed by Cluster VI-V (6.1179), Cluster VI-III (5.7923), Cluster V-II (5.3940) and Cluster VII-V (5.1579) (Table. 4).

The maximum intra cluster distance was recorded for Cluster I followed by Cluster V, Cluster VII, Cluster II, Cluster III, Cluster VI, Cluster IV and Cluster VIII, whereas maximum inter cluster distance was found between Cluster VII-IV (7.2631) followed by Cluster VIII-IV (6.0618), Cluster IV-II (5.5329), and Cluster VIII-III (5.02072) 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 (2005), Verma *et al.* (2006), Singh *et al.* (2006) and Mittal *et al.* (2008) ^[1, 3].

Hierarchical Euclidean-ward clustering

After reducing the dimension, PCs were transformed into a single index and data were subjected to non-hierarchical Euclidean clustering. Eight well characterized groups were formed on the basis of similarity in agro-morphological traits (Table. 5). The maximum number of genotypes (16) fell in cluster V followed by cluster VI (13) cluster I (13) and cluster VII (12); and forming larger group. Similarly cluster III (10) cluster VIII (7), cluster II (7), and cluster IV (5) comprised variable number of genotypes given in parenthesis.

Table 5: Cluster mean based on Euclidean clustering method

Variable / Cluster No	Cluster1	Cluster2	Cluster3	Cluster4	Cluster5	Cluster6	Cluster7	Cluster8
DFE	-1.12670	-0.65667	0.16719	-0.16922	-0.433542	0.624675	0.44754	1.69477
FLA	0.16560	0.91048	0.92411	1.13181	-0.923159	0.092950	-0.69051	-0.22543
PH	0.34195	-0.65321	1.28440	2.47069	-0.741159	-0.068232	-0.60879	-0.71705
DM	-0.53812	-0.56567	0.32098	-0.19767	-0.750904	0.166716	0.94913	1.02734
TP	-0.48412	-1.79104	0.20124	0.59670	0.337903	0.307707	0.39121	-0.03804
SL	0.55127	0.12154	1.16785	0.55617	-0.566825	0.014586	-0.38364	-1.28477
PL	0.40999	-0.57534	1.47348	1.78359	-0.880623	0.261334	-0.70921	-0.82174
BYP	0.23931	-0.53498	1.38841	2.08570	-0.746003	0.137662	-0.86964	-0.44236
GYP	0.49670	-1.51208	0.41958	-1.55079	0.226269	0.012574	0.91215	-1.00628
TW	-0.19978	-0.16907	-0.12306	-1.21888	-0.219869	0.463542	1.11679	-0.68627
HI	0.18168	-1.01777	-0.45913	-2.02067	0.583981	-0.111939	1.27450	-0.53219

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

Cluster No	Cluster1	Cluster2	Cluster3	Cluster4	Cluster5	Cluster6	Cluster7	Cluster8
Cluster1	1.5634							
Cluster2	3.27183	1.2238						
Cluster3	2.75673	4.71445	0.5884					
Cluster4	4.80032	5.53290	3.23529	0.2943				
Cluster5	2.77165	3.76671	4.82548	6.50382	1.4562			
Cluster6	2.33360	3.50753	2.78547	4.86778	2.62070	0.5490		
Cluster7	3.68101	4.90013	4.87399	7.26311	2.55989	2.61341	1.2465	
Cluster8	4.49921	3.90391	5.02072	6.06180	3.45171	2.87440	3.62999	0.0241

The mean characteristics of various clusters have been presented in Table. 6. Cluster II& I (DFE), cluster III & IV (FLA), cluster II & V (PH), cluster II & V (DM), cluster IV & VII (TP), cluster III & IV (SL), cluster III & IV (PL), cluster III & IV (BYP), cluster I & VII (GYP) and cluster VII & V (HI) were found more diverse clusters based on cluster mean for traits given in parenthesis. 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 (2005), Verma *et al.* (2006), Singh *et al.* (2006) and Mittal *et al.* (2008) ^[1, 3]. To exploit genetic diversity through hybridization program inter-cluster distance must be taken into consideration. Genetic diversity is directly proportional to the inter-cluster distance. Higher the distance between cluster greater the diversity between them and vice-versa.

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