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Genetic Diversity Based on Cluster and Principal Component Analyses for Yield and its Contributing Characters in Wheat (*Triticum aestivum* L.)

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An experiment was carried out to assess genetic diversity by cluster and principal component analysis (PCA) for yield and its nine contributing characters in 24 bread wheat genotypes at BHU Agricultural Research Farm during Rabi 2010-11. The cluster analysis grouped all the 24 wheat genotypes into four major clusters. Extreme divergence was observed among clusters. Second cluster with two genotypes (WH 542 and ATTILA) had better yield potential as compared with fourth cluster which had also two genotypes (WL 711 and MALAVIYA 206). The result of PCA revealed that all the 4 principal components (PC1, PC2, PC3 and PC 4) contributed 89.68% of the total variability and accounted with values of 45.38, 20.69, 12.43 and 11.17 respectively. The third principal component had high positive component loading for all variables except spike length and grain spike^{-1}. The result of present study could be exploited in planning and execution of future breeding programme in wheat.

Key words: PCA, Cluster analysis, Dendrogram, Eigen vector, wheat.

Germplasm diversity analysis has opened new realm of crop improvement. Recent crop improvement efforts result in narrow genetic diversity of elite germplasm pool leads to problematic in breeding for biotic stresses, abiotic stresses as well as adaptation (Rao and Hodgkin, 2002; Zhang et al., 2005). So, it is mandatory to identify genetically diversified lines for future wheat breeding. Information on genetic diversity among elite germplasm is beneficial for identifying lines for desirable traits (Ali et al., 2008) and estimating genetic relatedness among parents. Therefore, concise information about nature and magnitude of genetic diversity present in wheat gene pool would be helpful regarding parents selection for deriving superior cultivars.

Cluster analysis and principal component analysis (PCA) are major genetic diversity analysis tools having relative differences with each other. The cluster analysis is an appropriate method for assessing family relationships (Mellingers, 1972) and the merit of using PCA over cluster analysis is that each germplasm line can be assigned to one group only (Mohammadi, 2002). The objective of current study is to find out the fruitful genetic diversity between wheat genotypes grown in India by using the tools i.e., cluster analysis and PCA.

Materials and Methods

The current experiment was conducted at the Agricultural Research Farm of Institute of Agricultural Sciences, Banaras Hindu University, Varanasi during Rabi season of 2010-11. The experimental site was situated at in South- Eastern part of the city at 25$_o$ 18' North latitude and 82$_o$ 09' East longitude at an elevation of 75.5 m above the mean sea level. The experimental site belongs to sub-tropical climate and north eastern plains zone (NEPZ). Soil pH ranged from7.0- 7.5. Genetically pure and physically healthy seeds of 24 diverse wheat germplasm collections were obtained from Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University Varanasi (Table 1). The experiment was carried out in Randomized Complete Block Design (RCBD) with three replications and individual plot was 3 m × 1 min size. The distance between row to row and plant to plant was maintained were 23 cm and 10 cm respectively. Recommended agronomic practices and protective measures were followed to grow a healthy crop. Data were recorded on 10 characters, viz., days to heading, chlorophyll content,

Table 1. List of 24 Wheat Genotypes.

S. No.	Genotypes	S. No.	Genotypes
1	A 068	13	LOK 1
2	A 115	14	36896//CJ54./K65*SKA
3	NIPHAD 4	15	HD 2329
4	KENPHAD 32	16	MALAVIYA 206
5	HY 65	17	HUW 234
6	K 65	18	RAJ 1972
7	NP 846	19	HD 2402
8	KALYANSONA	20	WH 542
9	SONALIKA	21	UP 2338
10	WL 711	22	ATTILA
11	UP 262	23	HP 1744
12	HP 1209	24	HUW468

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plant height, tillers meter^{-2}, grains spike^{-1}, 1000-grain weight (g), plot yield^{-1}(g), sheath length (cm), peduncle length (cm) and spike length (cm). Data of randomly selected five plants of each germplasm line were averaged replication wise and mean data was used for statistical analysis. The statistical tool SAS (Statistical Analyses Software) was utilized for genetic divergence, principal component and cluster mean analysis including dendogram.

Results and Discussion

Genetic divergence analysis

Data analysis by using Statistical analyses software (SAS) results 4 distinct clusters in 24 bread wheat genotypes, reveals the presence of wide genetic diversity among the experimental material (Table 2) as similar reported by Auvuchanon, A. (2010). The genetic distance (degree of similarity)

Table 2. Clustering pattern of genotypes based on Dendrogram (Cluster Analysis tree chart).

Cluster	No. of Genotypes	Genotypes
1.	14	A 068,KENPHAD 32,UP262, HD 2329, 36896// CJ54./K65*SKA, HD 2402, HP 1744, LOK 1, HP 1209, HUW 234, RAJ 1972, HUW468,UP 2338 and KALYANSONA
2.	2	WH 542 and ATTILA
3.	6	A 115, NIPHAD 4, SONALIKA, HY 65, K 65 and NP 846
4.	2	WL 711 and MALAVIYA 206

among 24 genotypes is represented by dendrogram (obtained from cluster analysis) (Fig.1). It represents below 1 similarity coefficient in cluster 1 and 3 while below 0.75 similarity coefficient in cluster 2 and cluster 4 having below 0.25 similarity coefficient (Fig.1) as similar reported by Khan A.A. et al., (2010).

Genotypes of the first cluster

Fourteen genotypes were classified in first cluster accounting for 58.33 per cent of total genotypes (Table2). The average value of genotypes in the cluster for days to heading, plant height, tiller meter^{-2}, 1000- grain wt. and spike length are below the mean of all genotypes representing earlier maturity but relatively low yield potential (Table3) as similar reported by Khodadadi, et al., 2011. Based on CV, the cluster represents poor yield potential than remains.

Genotypes of the second cluster

Two genotypes (WH 542 and ATTILA) were classified in second cluster accounting for 8.33 per cent of total genotypes (Table2). The average value of genotypes in the cluster for days to heading, tiller meter^{-2} and plot yield are above the mean of all genotypes representing better yield potential (Table3).

Genotypes of the third cluster

Six genotypes were classified in third cluster accounting for 25 per cent of total genotypes (Table2). The average value of genotypes in the cluster for plant height, grain spike^{-1} and peduncle length are above the mean of all genotypes but below for days to heading, tiller meter^{-2}, plot yield, 1000- grain wt. and spike length (Table3). Based on CV, third cluster represents higher yield potential than remains.

Table 3.The Mean, Standard Deviation and CV (in per cent) of variables for each cluster.

Clusters		Daystoheading(Days)	ChlorophyllContent	PlantHeight (cm)	Tillerspermeter^{-2}	GrainsperSpike	1000-grainweight(g)	Plot Yield(g)	Sheath Length(cm)	PeduncleLength(cm)	Spike Length(cm)
	Mean	80.64	44.51	86.62	354.67	53.45	32.31	1059.48	16.58	30.40	9.46
1	SD	-2.30	-0.62	-5.55	-41.94	5.09	-3.11	-66.91	-2.15	-6.13	-1.37
	CV	2.85	1.39	6.40	11.83	9.52	9.64	6.32	12.98	20.17	14.54
	Mean	89.83	44.60	77.67	460.67	68.13	34.68	1287.00	17.67	27.17	10.00
2	SD	6.89	-0.53	-14.50	64.06	-9.60	-0.74	160.60	2.18	-9.36	-0.83
	CV	7.67	1.18	18.67	13.90	14.09	2.13	12.48	12.34	34.46	8.33
	Mean	82.50	44.02	108.83	368.22	46.74	33.72	927.84	22.00	44.22	10.67
3	SD	-0.44	1.11	16.67	-28.39	11.79	-1.70	-198.56	1.68	7.69	-0.17
	CV	0.54	2.52	15.31	7.71	25.23	5.04	21.40	7.64	17.40	1.56
	Mean	86.83	53.30	95.50	356.67	66.50	30.75	970.38	21.50	35.33	12.33
4	SD	3.89	8.18	3.33	-39.94	-7.96	-4.67	-156.01	-3.24	-1.19	1.50
	CV	4.48	15.34	3.49	11.20	11.98	15.19	16.08	15.05	3.38	12.16

Genotypes of the fourth cluster

Two genotypes (WL 711 and MALAVIYA 206) were classified in fourth cluster accounting for 8.33 per cent of total genotypes (Table2). The average value of genotypes in the cluster for days to heading, chlorophyll content, plant height and spike length are above the mean of all genotypes but below for tiller meter^{-2}, grain spike^{-1}, 1000- grain wt. and plot yield representing poor yield potential (Table3) as similar

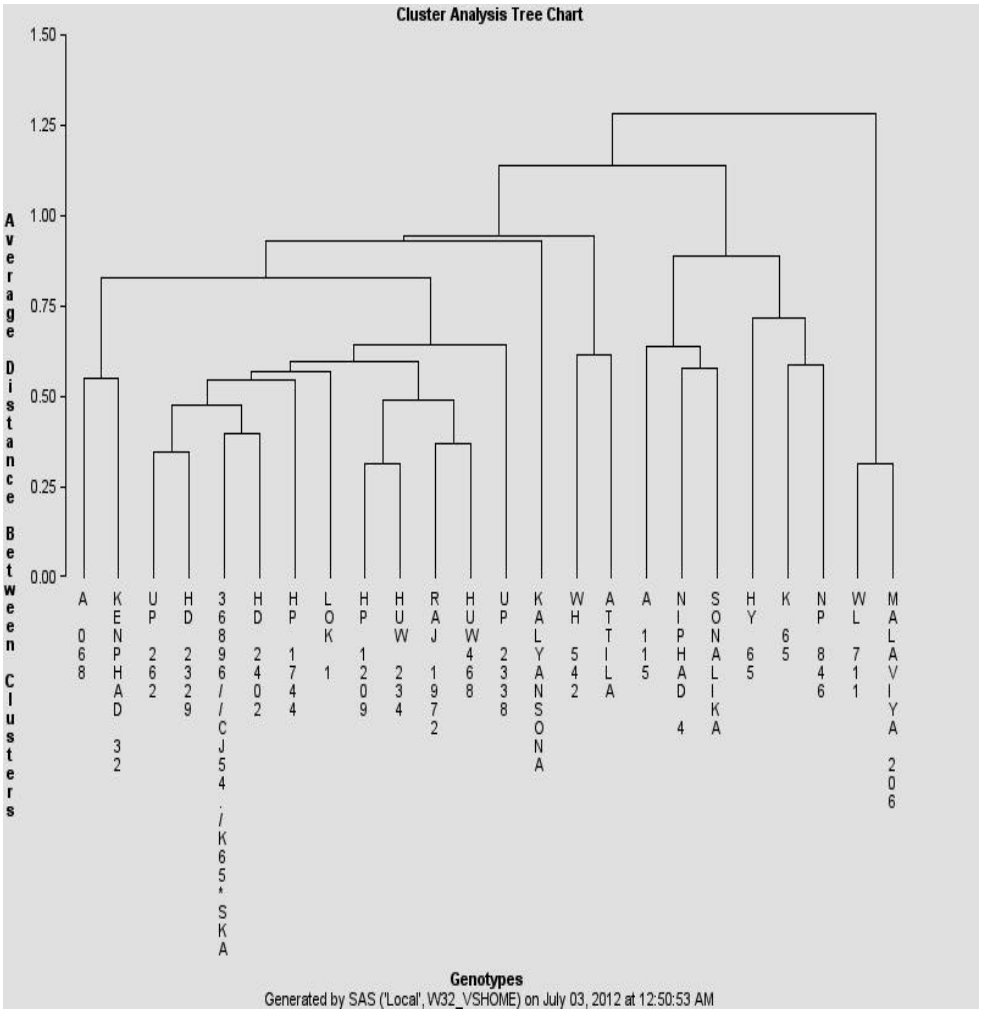

Fig. 1. Dendrogram (Cluster Analysis tree chart) depicting genetic relationships among 24 wheat genotypes.

reported by Khodadadi, M. et al., 2011. Based on CV, fourth cluster represents relatively higher yield potential than cluster first and second except third cluster.

Principal components analysis (PCA)

Principal components analysis (PCA) represents the largest contributor to the total variation at each axis of differentiation. The Eigen values are often used to fix the number of major principal components to be explained. The total of Eigen values is usually equal to the number of variables. Four principal components (PC1 to PC4) are extracted from the original data and having latent roots greater than one, accounting nearly 89.68 per cent of the total variation (Table.4) as similar reported by Maqbool, R, et al., 2010 and Hailegiorgis, et al., 2011. Out of the total 4 principal components (PC1, PC2, PC3 and PC 4) account with values of 45.38, 20.69, 12.43 and 11.17 per cent respectively, contributed 89.68 per cent of the total variation. Two dimensional ordinations of 24 wheat genotypes on principal component axis 1 and 2 are represented in four clusters following clustering pattern of genotypes in Table.2 (Fig.2). The first principal component has high positive component loading from chlorophyll content, plot yield, sheath length and grain spike^{-1} and high negative loading from tillers meter^{-2},1000-grain wt. and plant height. The positive and negative loading represents existence of positive and negative correlation between the components and the character. Aforesaid characters which load high positively or negatively contributed more to genetic diversity and they became important in representing the clusters. The second principal

Table 4. Vector loadings and per cent explained variation by the Major four PCs.

	Eigen Vectors			
Characters	PC1	PC2	PC3	PC4
Days to Heading	-0.078	-0.077	0.334	-0.340
Chlorophyll Content	0.473	-0.159	0.205	0.102
Plant Height(cm)	-0.152	-0.216	0.474	0.584
Tillers per meter^{2}	-0.24	0.152	0.340	-0.436
Grains per Spike	0.120	-0.143	-0.037	0.161
1000-grain weight(g)	-0.442	-0.112	0.444	0.143
Plot Yield (g)	0.459	0.076	0.340	0.186
Sheath Length(cm)	0.495	0.073	0.176	-0.158
Peduncle Length(cm)	0.086	0.525	0.382	-0.211
Spike Length(cm)	-0948	0.759	-0.112	0.436
Eigen value	4.409	2.0106	1.207	1.085
Individual per cent	45.38	20.69	12.43	11.17
Cumulative per cent	45.38	66.08	78.50	89.68

component has high positive component loading from sheath length, peduncle length and tillers meter^{-2}; and high negative loading from chlorophyll content, plant height, grain spike^{-1} and1000- grain wt. The third principal component has high positive component loading for all variables except spike length and grain spike^{-1}. The fourth principal component has high positive component loading from plant height, spike length, 1000- grain wt. and grain spike^{-1}; and high negative loading from days to heading, tillers meter^{-2},

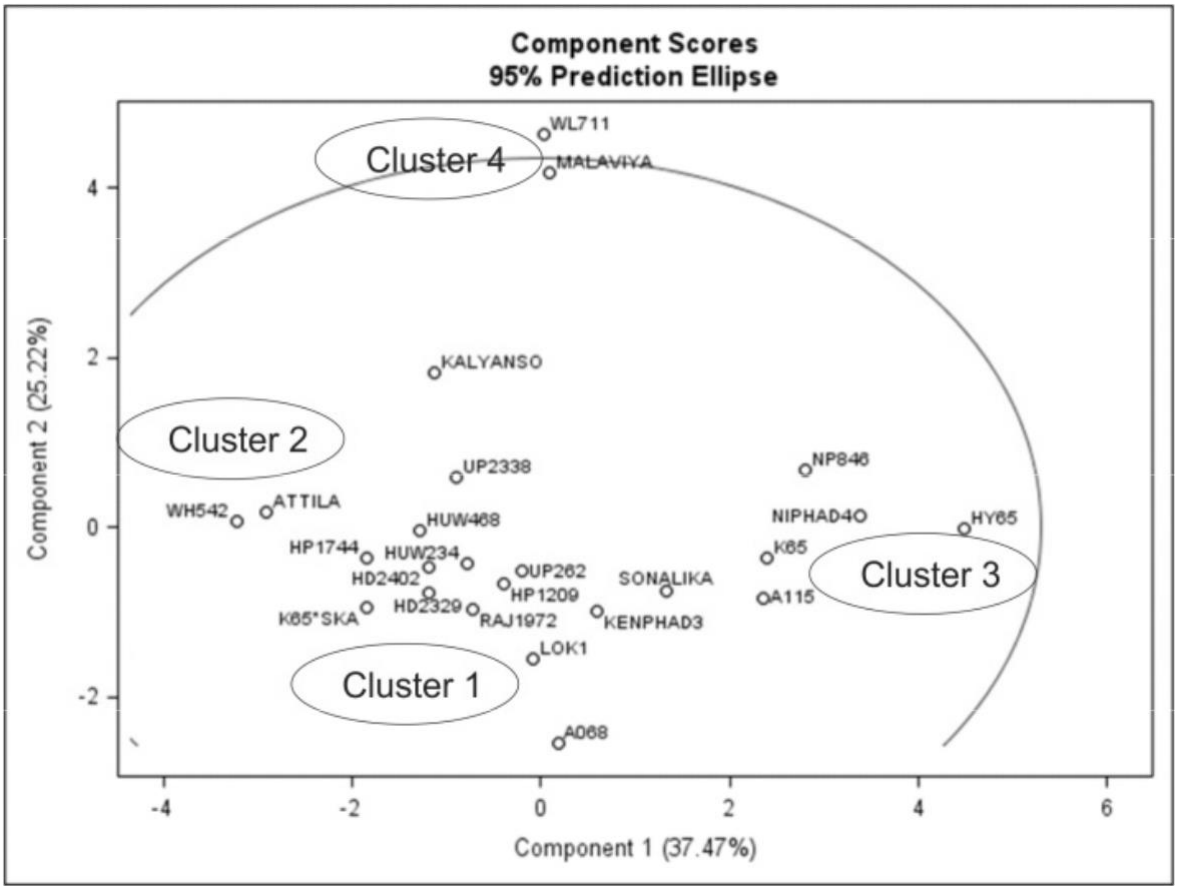

Fig. 2. Two dimensional ordination of 24 wheat genotypes on principal component axis 1and 2.

sheath length and peduncle length (Table.4) as similar reported by Hailegiorgis et al., 2011.

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