Journal of Crop and Weed, 10(2):104-107(2014)

Genetic diversity of wheat genotypes based on principal component analysis in Gangetic alluvial soil of West Bengal

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Received: 31-07-2014, Revised:19-09-2014, Accepted: 28-09-2014

ABSTRSCT

The present investigation was planned to assess genetic diversity for yield, yield contributing traits and quality traits in forty nine germplasm of bread wheat along with 4 checks and two triticale variety collected from DWR, Karnal were evaluated in randomized block design with two replication in Nadia district of West Bengal during rabi season in two consecutive years 2010-2011 and 2011-2012. Principal component analysis (PCA) indicated that five components (PC1 to PC5) accounted for about 75 % of the total variation among traits in bread wheat cultivars. Out of total principal components retained PC1, PC2 and PC3 with values of 25.9%, 17.1% and 13.3% respectively contributed more to the total variation. The first principal component had high positive loading for 9 characters out of 16 viz. weight of grains spike^{-1}, number of grains spike^{-1}, number of spikelets spike^{-1}, spike length, plant height, days to heading, days to flowering, grain protein content and yield plant^{-1} which contributed more to the diversity. The result of present study could be exploited in planning and execution of future breeding programme in wheat.

***Keywords*:** Principal component analysis, *Triticale*, wheat

Wheat (*Triticum aestivum* L.) is the most important cereal crop for the majority of world's populations. It is the most important staple food of about two billion people (36% of the world population). Approximately one-sixth of the total arable land in the world is cultivated with wheat. Whereas paddy is mainly cultivated in Asia, wheat is grown in all the continents of the world. India is one of the principal wheat producing and consuming countries in the world. The annual production of wheat in India during 2011-12 was 94.88 million tonne (MT) (Sharma, 2013) unfortunately fall by 2.47 MT in 2012-13. Wheat provides a large fraction of the dietary protein and total food supply, and is grown all throughout the world, in a wide variety of climates. Wheat is a staple crop, grown as a primary food product and for other uses as well. Wheat is cultivated over a wide range of climatic conditions and therefore understanding of genetics is of great value for genetics and plant breeding purposes.

One of the important approaches to wheat breeding is hybridization and subsequent selection. Parents' choice is the first step in plant breeding program through hybridization. In order to benefit transgressive segregation, genetic distance between parents is necessary (Joshi *et al*., 2004). The higher genetic distance between parents, the higher heterosis in progeny can be observed (Anand and Murrty, 1968). Estimation of genetic distance is one of appropriate tools for parental selection in wheat hybridization programs. Appropriate selection of the parents is essential to be used in crossing nurseries to enhance the genetic recombination for potential yield increase (Islam, 2004). Some appropriate methods, cluster analysis, PCA and factor analysis, for genetic diversity identification, parental selection, tracing the pathway to evolution of crops, centre of origin and diversity, and study interaction between the environment are currently available (Eivazi *et al.,* 2007). Principal component analysis helps researchers to distinguish significant relationship between traits. This is a multivariate analysis method that aims to explain the correlation between a large set of variables in terms of a small number of underlying independent factors. The cluster analysis is also an appropriate method for determining family relationships but the main advantage of using PCA over cluster analysis is that each genotype can be assigned to one group only (Mohammadi, 2002). The main objective of this study is to assess the potential genetic diversity among wheat genotypes by using cluster analysis and cluster analysis-PCA-based methods for selection of parents in hybridization programme to obtain desirable segregants in advanced generation.

MATERIALS AND METHODS

The wheat germplasm consisted of forty nine genotypes including four checks and two triticale varieties collected from DWR, Karnal through All India Coordinated Wheat & Barley Integrated Project

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of Kalyani centre, BCKV The experiment was conducted in randomized block design with two replication at 2 locations, District Farm, AB Block, BCKV. Kalyani, West Bengal and Instructional Farm, BCKV, Jaguli, Nadia, West Bengal during *rabi* seasons in two consecutive years 2010-2011 and 2011-2012. The gross plot was divided in two blocks and passages of 1 m width were left between the blocks. The blocks were taken as the replications and each block in turn was divided into 49 equal plots. There were six rows of 6 m length in each plot at spacing of 23cm between the rows for each genotype. Data on different characters *viz.* days to heading, days to flowering, days to maturity, plant height (cm), number of tillers plant^{-1}, spike length (cm), number of spikelets spike^{-1}, number of grains spike^{-1}, weight of grains spike^{-1}, flag leaf area, chlorophyll-a content, chlorophyll-b content, total chlorophyll content, thousand grain weight, grain protein content and yield plant^{-1} were taken from ten randomly selected plants from each replication. The principal component analysis method explained by Harman (1976) was followed in the extraction of the components. Principal Component Analysis was performed using Minitab 14 software.

Table 1: Studies on Principal component for 49 varieties on 18 characters in wheat

Variables	PC_1	PC_2	PC_3	PC_4	PC_5
Days to heading	0.365	-0.223	0.192	0.234	-0.160
Days to flowering	0.364	-0.224	0.193	0.238	-0.162
Days to maturity	0.148	-0.080	0.270	0.368	-0.176
Plant height (cm)	0.329	0.005	-0.173	0.091	0.389
No. of tillers plant^{-1}	0.044	0.096	-0.377	0.302	-0.527
Spike length (cm)	0.326	0.220	-0.006	0.045	0.038
No. of spikelets spike^{-1}	0.339	0.005	0.322	-0.125	0.279
No. of grains spike^{-1}	0.296	0.158	0.121	-0.475	-0.219
Wt. of grains spike^{-1}	0.376	0.221	-0.104	-0.147	0.177
Flag leaf area (cm^2)	0.072	0.068	-0.490	-0.170	-0.008
Chlorophyll- a (mg g^{-1})	-0.152	0.450	0.285	0.103	0.037
Chlorophyll-b (mgg^{-1})	0.000	0.449	0.062	0.157	-0.081
Total chlorophyll (mgg^{-1})	-0.128	0.513	0.256	0.129	-0.022
1000 grain wt. (g)	-0.011	0.064	-0.241	0.439	0.535
Grain protein (%)	0.113	0.097	-0.040	-0.315	-0.059
Yield plant^{-1} (g)	0.307	0.275	-0.317	0.127	-0.178
Eigenvalue	4.138	2.732	2.135	1.599	1.378
Individual percentage	25.9	17.1	13.3	10.0	8.6
Cumulative percentage	25.9	43.0	56.3	66.3	74.9

RESULTS AND DISCUSSION

Principal component analysis (PCA) reflects the importance of the largest contributor to the total variation at each axis of differentiation (Sharma, 1998). The eigenvalues are often used to determine how many factors to retain. The sum of the eigenvalues is usually equal to the number of variables. Therefore, in this analysis the first factor retains the information contained in 4.138 of the original variables. PCA for the first five principal components of these data are given in table1.

Five principal components PC_1 to PC_5, which are extracted from the original data and having latent roots greater than one, accounting nearly 75% of the total variation. Suggesting these principal component scores might be used to summarize the original 16 variables in any further analysis of the data. Out of the total principal components retained, PC_1, PC_2 and PC_3 with values of 25.9%, 17.1% and 13.3% respectively contributed more to the total variation.

According to Chahal and Gosal (2002), characters with largest absolute value closer to unity within the first principal component influence the clustering more than those with lower absolute value closer to zero. Therefore, in the present study, differentiation of the genotypes into different clusters was because of relatively high contribution of few characters rather than small contribution from each character.

Accordingly, the first principal component had high positive component loading from weight of grain spike^{-1}, days to heading, days to flowering, number of spikelets spike^{-1}, plant height, spike length and yield plant^{-1}; and high negative loading from chlorophyll-a and total chlorophyll content. The positive and negative loading shows the presence of positive and negative correlation trends between the components and the variables. Therefore, the above mentioned characters which load high positively or negatively contributed more to the diversity and they were the ones that most differentiated the clusters.

Hence, the major contributing characters for the diversity in the second principal component (PC_2) were total chlorophyll content, chlorophyll-b content and days to flowering; number of tillers plant^{-1}, number of spikelets spike^{-1} and yield plant^{-1} grain filling period and days to heading in principal component three (PC_3).

Usually it is customary to choose one variable from these identified groups. Hence, for the first group weight of grains spike^{-1} is best choice, which had the largest loading from component ones, total chlorophyll content for the second and number of tillers plant^{-1} for the third group.

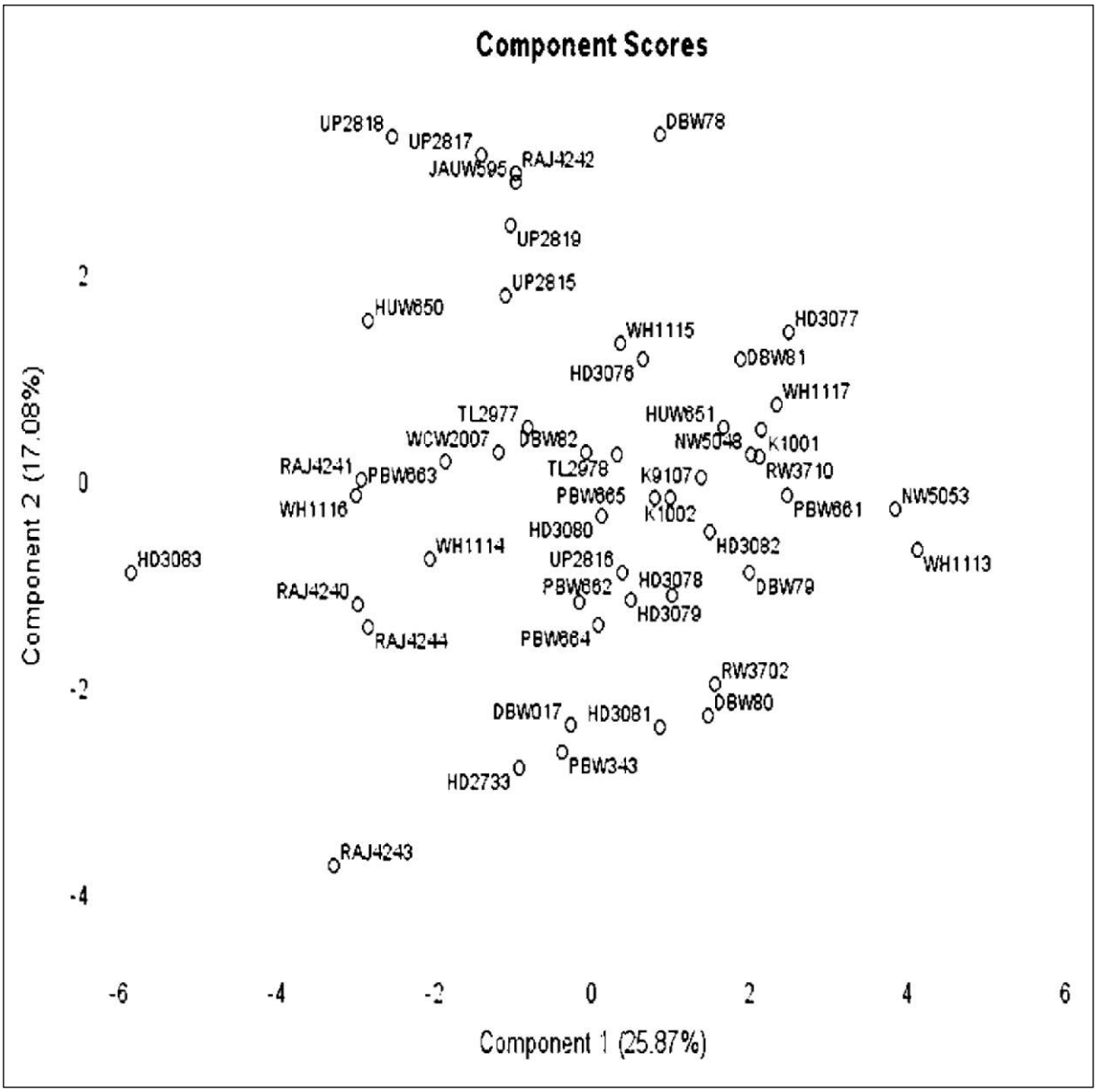

Fig 1: Score plot of 49 genotypes of *Triticum aestivum* L

These findings revealed that first three principal components were related to various morphological and physiological traits in wheat mostly associated with early genotypes and also these traits can identify the diverse genotypes which could be employed in hybridization programme for improvement of wheat.

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