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Study of genetic diversity in wheat (*Triticum aestivum* L.) genotypes by using principle component analysis

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Abstract
Fifty genotype of wheat were evaluated to access the genetic diversity by using principle component analysis for eleven quantitative traits in wheat viz. days to 50% flowering, days to reproductive phase, days to maturity, plant height (cm), number of reproductive tillers per plant, spike length (cm), number of spikelets per spike, number of grains per spike, grain weight per spike (gm.), test weight (gm.) and grain yield per plant (gm.). Principal component analysis (PCA) indicated that four components (PC1 to PC4) accounted for about 77% of the total variation among traits in bread wheat genotypes. Out of total principal components retained PC1, PC2 and PC3 with values of 34.49%, 20.63% and 13.06% respectively contributed more to the total variation. The first principal component had high positive loading for 9 characters out of 12 viz. days to 50% flowering, days to maturity, spike length, number of spikelets per spike, test weight, grain yield per plant (gm.), grain weight per ear (gm.), days to reproductive phase, number of grains per spike. The result of present study could be exploited in planning and execution of future breeding programme in wheat.

Keywords: Genetic diversity, wheat (*Triticum aestivum* L.) genotypes, principle component analysis

Introduction
Wheat with scientific name *Triticum aestivum* L. em. Thell, is the first cereal and most important crop in the world. It is a member of *Graminae* family (Sub-family *Poaceae*) and genus *Triticum*, and the world leading cereal grain. It has been described as the 'King of cereals' because of the acreage it occupies, high productivity and the prominent position it holds in the international food grain trade. Wheat is a cereal grain (botanically, a type of fruit called caryopsis) and is a self-pollinated C3 plant with cleistogamous condition. The optimum temperature for wheat growth is 25 °C with minimum and maximum growth temperatures of 30 °C to 40 °C and 30 °C to 32 °C, respectively. Wheat is a major diet component because of wheat plants agronomic adaptability, ease of grain storage and ease of converting grain into flour for making edible, palatable and satisfactory foods.

Wheat provides 20% dietary calories of the world. Wheat is the most important source of carbohydrate in majority of countries. Wheat contains minerals, vitamins and fats and with a small amount of nutrition's. It contains 70% carbohydrates, 22% crude fibers, 12% protein, 12% water 2% fat, and 1.8% minerals. A predominately wheat-based diet is higher in fiber than a meat-based diet.

The United States Department of Agriculture (USDA) estimates that the World Wheat Production 2017-2018 will be 757 million tonnes. India is the largest wheat producing country in the world after China and account for more than 13.06 percent of the world's wheat production. During the crop year 2017-18, India harvested 98.4 million tonnes of wheat in an area of 30.6 million hectares with productivity of 3216 kg/ha). U.P is the leading state in wheat production.

Bread wheat (*Triticum aestivum*) 2n=42, Macaroni wheat (*Triticum durum*) 2n=28 and emmer wheat (*Triticum dicoccum*) 2n= 28 occupy the place of prominence among the seven cultivated species of wheat grown in the world. Among these, first two occupies maximum acreage and production and have great significance for human and animal consumption. Bread and Macaroni wheat's are widely cultivated under different agro climatic condition due to their versatile genotype which has wider adaptation in diverse agro ecological condition. Nevertheless, the crop offer sizeable opportunities of quantum jump by accelerating its yield potential through genetic manipulation. These gains could be realized by utilizing vast and enormous magnitude of genetic variability available in these species.

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Grain yield is a complex polygenic character with great genetic, physio-morphological, ecological and Pathological dependence. The hereditary potential of a genotype depends upon stability and yielding. Genetically, yield contributing attributes there genetic nature and magnitude of association are responsible for realization of yield potential influenced by changing edaphic, agro climatic condition. Therefore, it is highly important to investigate the genetic variation of the varities and lines of this plant in breeding programme.

One of the important approaches to wheat breeding is hybridization and subsequent selection. Parent's 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) [6]. The higher genetic distance between parents, the higher heterosis in progeny can be observed (Anand and Murrty, 1968) [1]. 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) [4]. 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) [3]. 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) [7]. 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 experimental materials comprised of 50 wheat genotypes from Indian origin was carried out during *rabi* 2015-16 at research farm Nawabganj of Chandra Shekhar Azad University of Agriculture and Technology, Kanpur (U.P). All the genotypes were sown in Randomized Complete Block Design with three replications. The present research is based on eleven characters namely days to 50% flowering, days to reproductive phase, days to maturity, plant height, spike length, number of reproductive tillers per plant, number of spikelet per spike, number of grains per spike, grains weight per spike, test weight and grain yield per plant was taken to obtain sufficient information about characters and thereby to make significant improvement in yield. Each genotype was sown in two lines in 5.0 m long and 1.38 m broad plots and space planted at 23 x 5 cm between row to row and plant to plant distance respectively. The principal component analysis method explained by Harman (1976) was followed in the extraction of the components. Principal Component Analysis was performed using software

Table 1: Studies on Principal component for 50 genotypes on 12 characters in wheat

Variables	PC1	PC2	PC3	PC4	PC5
Days to 50% Flowering	0.069	0.432	0.553	0.209	0.029
Days to Maturity	0.279	0.495	-0.136	0.151	-0.314
Plant Height (cm)	-0.435	0.259	-0.111	0.068	-0.209
Spike Length (cm)	0.203	-0.372	0.163	-0.014	-0.339
Reproductive Tillers/ Plant	-0.428	-0.073	-0.295	-0.137	0.010
Spikelets/ Spike	0.449	0.135	0.054	0.057	-0.054
Test Weight (1000)	0.046	0.453	-0.124	-0.273	0.550
Grain Yield/ Plant(gm)	0.370	-0.338	0.098	-0.062	0.322
Grain Weight/ Ear (gm)	0.241	0.073	-0.220	-0.604	0.089
Days to Reproductive Phas	0.311	0.074	-0.568	0.046	-0.362
Grains/ Spike	0.086	-0.092	-0.388	0.678	0.437
Eigene Value (Root)	3.794	2.269	1.438	1.021	0.745
% Var. Exp.	34.491	20.630	13.069	9.288	6.769
Cum. Var. Exp.	34.491	55.121	68.191	77.479	84.249

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) [8]. 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 3.794 of the original variables. PCA for the first five principal components of these data are given in table 1. Four principal components PC1 to PC4, which are extracted from the original data and having latent roots greater than one, accounting nearly 77% of the total variation. Suggesting these principal component scores might be used to summarize the original 12 variables in any further analysis of the data. Out of the total principal components retained, PC, PC and PC 1 2 3 with values of 34.49%, 20.63% and 13.06% 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 days to 50% flowering, days to maturity, spike length, number of spikelets per spike, test weight (1000gm.), grain yield per plant (gm.), grain weight per ear (gm.), days to reproductive phase, number of grains per spike and high negative loading from plant height and number of reproductive tillers per plant. 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 (PC2) were days to 50% flowering, days to maturity and test weight(1000gm.); days to 50% flowering in principal component three (PC3). Usually it is customary to choose one variable from these identified groups. Hence, for the first group number of spike lets per spike is best choice, which had the largest loading from component ones, days to maturity for the second and days to 50% flowering for the third group.

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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