



## Multivariate analysis of genetic divergence in wheat (*Triticum aestivum*) using yield traits

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### Abstract

The study was conducted to assess genetic divergence in wheat (*Triticum aestivum* L.) using yield traits. The experiment was planted at Mountain Agricultural Research Center, Juglot, Pakistan during 2014-15 following randomized complete block design with three replications. Plant material for the study comprised of 16 lines and four commercial cultivars of bread wheat. The data recorded were days to 50% heading, days to 50% maturity, plant height (cm), Number of grains spike<sup>-1</sup>, grain yield per plot, straw yield per plot, 1000 grain weight and yield per hectare. On the basis of multivariate analysis, genotypes 110, 119, 128, 143 and Pirsabak-2013 were showing maximum divergence from other genotypes. This study has shown the existence of considerable genetic variation among the genotypes considered with may help for further selection and breeding. Parents may be selected from clusters which had significant genetic distance for crossing in order to obtain genetic recombination and transgressive segregation in the subsequent generations. However further study across location and years needs to be done in order to corroborate the results obtained in the present investigation.

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## Introduction

Wheat is the leading food grain of Pakistan occupying the largest area under single crop. Wheat contributes 9.9 percent to the value added in agriculture and 2.0 percent to GDP. Area under wheat has decreased to 9260 thousand hectares in 2015-16 from last year's area of 9204 thousand hectares which shows a decrease of 0.2 percent. The production of wheat stood at 25.4782 million tonnes during 2015-16, showing an increment of 1.6 percent over the last year's production of 25.086 million tonnes (Anon, 2015-16). Genetic diversity of plants determines their potential for improved efficiency and hence their use for breeding, which eventually may result in enhanced food production. Plant uniformity, which can be resulted by the use of modern plant breeding techniques, can produce plants, which are more efficient by means of different goals including enhanced resistance under stress, however much more research must be performed to indicate the most optimized methods that can be used for the production of efficient plants. This is of significance for the production of food for the world increasing population (Fu and Somers, 2009). Accordingly, the increased attention to the production of resistant plant species for prolonged food production under different conditions indicate the necessity of performing breeding experiments (Van de Wouwet *et al.*, 2010).

Genetic diversity could be the result of geographical impact through evolution and hence traits could be considered as a function of variety. 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, center of origin and diversity, and study interaction between the environment are currently available (Eivazi *et al.*, 2007).

Usually before calculating the genetic distance, the variables are standardized so that all variables are of similar.

Germplasm improvement and genetic diversity is a key to reliable and sustainable production of the food crops. For effective evaluation and utilization of germplasm, measure of extent of available genetic diversity is of utmost importance (Zubair *et al.*, 2007). The use of multivariate statistical algorithms is an important strategy for classification of germplasm and analysis of genetic relationships among breeding material (Mohammadi and Prasanna, 2003).

The present study was conducted to decipher the extent of genetic variation and relationships among wheat genotypes based on quantitative traits using multivariate analysis and to identify the set of morpho-agronomic attributes which could be further utilized in breeding programs.

## Material and methods

Plant material for the study comprised of 16 lines and four commercial cultivars of bread wheat (Table 1). The experiment was planted at Mountain Agricultural Research Center, Juglot, Pakistan during 2014-15 following randomized complete block design with three replications. Each plot consists of rows, 5m long and 25 cm apart. Fertilizer was applied at the rate of 90:90kg NP respectively with no irrigation.

### Parameters studied

The data recorded were days to 50% heading, days to 50% maturity, plant height (cm), Number of grains spike<sup>-1</sup>, grain yield per plot, straw yield per plot, 1000 grain weight and yield per hectare.

### Statistical analysis

The combined data of grain yield and its components were then subjected to analysis to estimate the simple statistic i.e., simple correlation. Quantitative traits were analyzed by cluster and principal component analysis with the help of software program 'Past' for windows. Cluster analysis identifies variable which are further clustered into main group and subgroups using Ward's method.

The genotypes in each cluster were also analyzed for basic statistics. Principal component analysis simplifies the complex data by transforming number of correlated variables into a smaller number of variables called principal components. The first principal component accounts for maximum variability in the data as compared to each succeeding component. Scatter diagram was plotted to show the variation pattern. Mean value of each variable were standardized prior to cluster and principal component analysis to avoid the effects due to difference in scale.

## Results and discussion

### Correlation studies

Yield is a complex trait and is linked with various yield related traits. Effective selection for improvement could not be made, if the yield affecting traits are not taken to consideration. When selection pressure is applied for the enhancement of any trait, highly related with yield, it concurrently influences the number of other associated traits.

**Table 1.** List of genotypes used in the study.

S. No	Genotypes	S. No	Genotypes
1	108	11	Pirsabak-2013
2	110	12	151
3	119	13	152
4	128	14	158
5	131	15	163
6	139	16	168
7	143	17	171
8	192	18	177
9	NARC-2011	19	184
10	NARC-2009	20	Shahakar-2013

**Table 2.** Correlation among different traits.

	D50%	DM	PH	NGS	TG	Y	STW	100SW
D50%	1.00							
DM	0.52	1.00						
PH	0.25	0.33	1.00					
NGS	-0.11	-0.40	0.08	1.00				
TG	0.59	0.57	0.71	0.11	1.00			
Y	0.68	0.60	0.64	-0.03	0.94	1.00		
STW	0.46	0.52	0.71	0.06	0.68	0.56	1.00	
100SW	-0.22	-0.22	-0.19	0.25	-0.14	-0.22	-0.26	1.00

Where, DH = Days to 50 % heading, DM = days to 50 % maturity, Ph = Plant height (cm), NG = Number of grains spike<sup>-1</sup>, GYP = Grain yield plot<sup>-1</sup>, SYP = Straw yield plot<sup>-1</sup>, GW = 100 grain weight (g), YH = yield hectare<sup>-1</sup>

Therefore, knowledge about association of yield and among themselves provides information to the plant breeder for making betterment through selection.

Simple correlation coefficient was computed by using PAST software. Table No. 02 shows the values of correlation coefficient.

Maximum correlation was found for total grain weight with yield (0.94), followed by plant height and total grain weight (0.71), days to 50% maturity with yield (0.68) (Table 2).

Moderate correlation was noticed among straw weight and yield (0.56) followed by Days to 50% maturity and heading (0.52).

**Table 3.** Three cluster grouping wheat genotypes based on eight quantitative traits.

Cluster	Frequency	Members
1	10	119, 128, 131, 139, 143, 151, 168, 171, NARC-2011, Shahkar-2013
2	5	152, 158, 163, 177, 184
3	5	108, 110, 192, NARC-2009, Pirsabak-2013

**Table 4.** Principal component analysis.

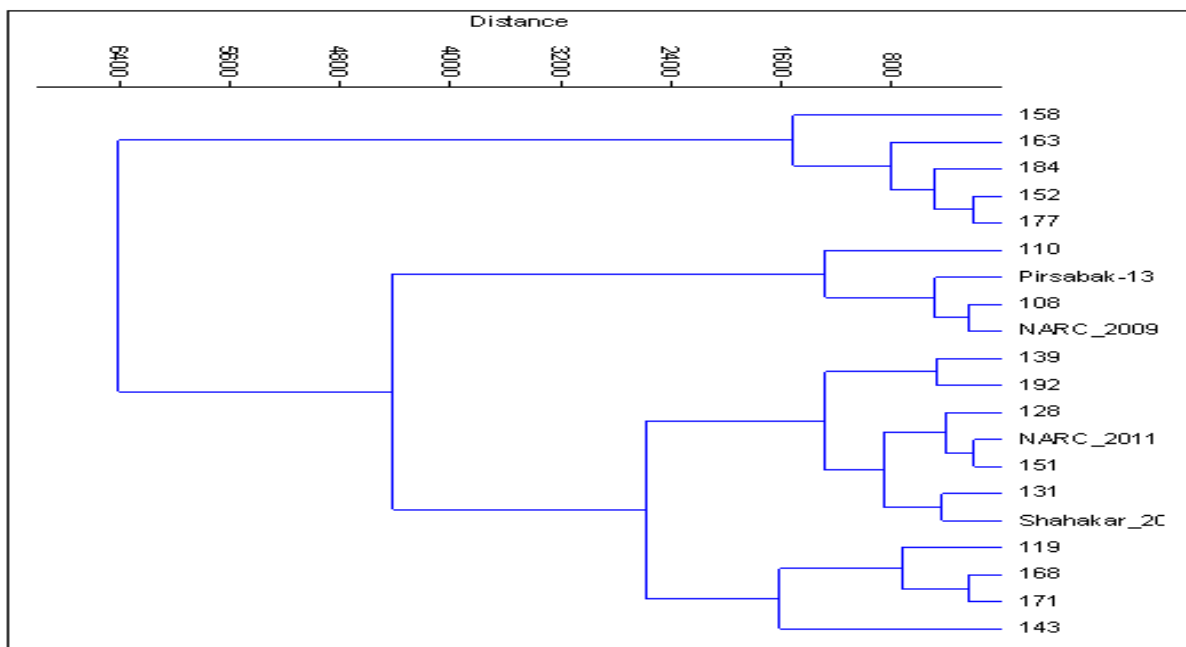
PC	1	2
Eigenvalue	4.1	1.4
% variance	50.7	17.7
Cumulative Variance	50.7	68.4

Negative correlation were noticed for 1000 seed weight with days to 50% heading and maturity (-0.22), 100 seed weight with plant height (-0.19).

#### Cluster analysis

Cluster analysis classified 20 genotypes of wheat into 3 clusters, shared a common node at the linkage distance of near about 4000. Member of each cluster showed in the dendrogram constructed for different wheat genotypes. To estimate the genetic linkage, eight quantitative traits were scored in the present study.

Cluster I was comprised of five genotypes 158, 163, 152, 177 and 184 respectively. 152 and 177 were showing the significant correlation among each other while 158, 163 and 184 were outliers in this sub cluster showing variation from other genotypes. Sub cluster II was consisted of four genotypes. Genotypes 108 and NARC-09 were at same linkage distance showing considerable similarity while 110 and Pirsabak-2013 were outlier for this cluster, showing divergence from other genotypes in the same cluster.

**Fig. 1.** Dendrogram based on average linkage distance for 20 wheat genotypes.

Cluster III was comprised of 11 genotypes. Among them genotype 192 and 139, 151 and NARC-2011, 131 and Shahkar-2013, 168 and 171 were correlated to each other significantly.

While genotypes 128, 119 and 141 were outliers in this cluster. They were showing maximum diversity in this cluster.

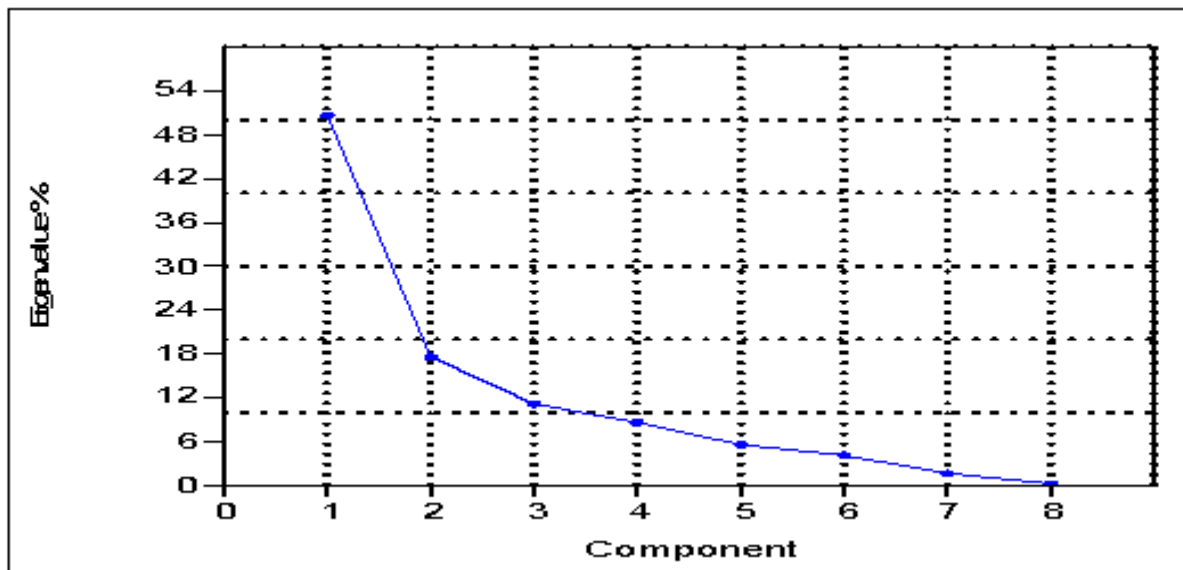


Fig. 2. Scree Plot for Principal component analysis.

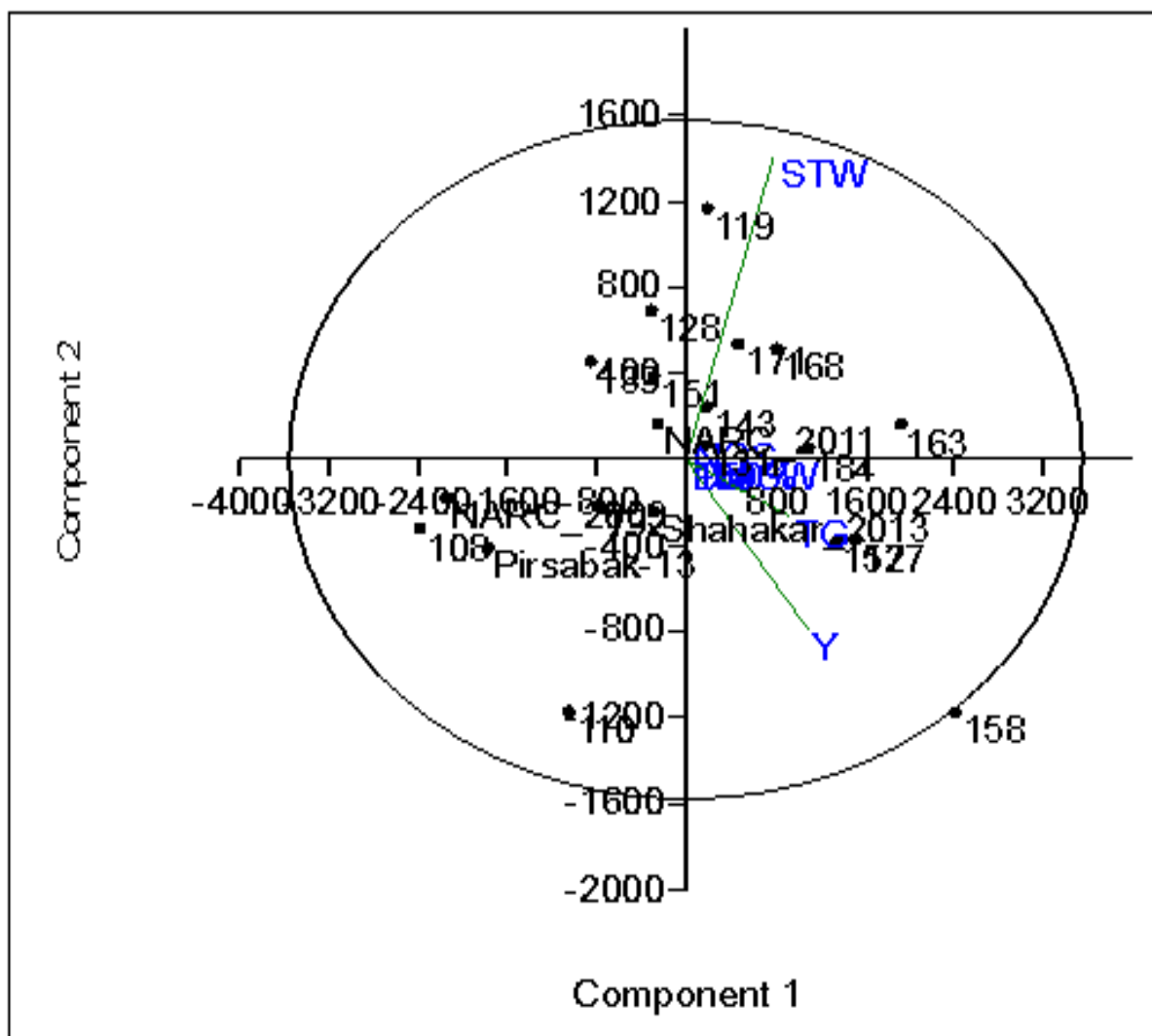


Fig. 3. Scatter diagram of wheat genotypes for first two PCs.

*Principal component analysis*

Principal component analysis simplifies the complex data by changing the number of related variables into smaller number of variables called principal components. The first principal component infers for maximum variation in the data with respect to following components. Table 4 showed the values for principal component analysis. The analysis had grouped the estimated wheat variables into three main components. The first variable with Eigen value > 1 accounted for 68.4 % of total variation for yield. The maximum Eigen value was 4.1 while the minimum was 1.4. Maximum variance was explained by component 01 (50.7) followed by component 2 (17.7).

**Conclusion**

On the basis of multivariate analysis, genotypes 110, 119, 128, 143 and Pirsabak-2013 were showing maximum divergence from other genotypes. From the above discussion it can be concluded that the wheat production can be enhanced by selecting improved high yielding varieties through adaptive trials in the fascinating agro-ecological condition of Gilgit Baltistan. Through cultivation of recommended varieties the yield gap can be minimized at local and national level. This study has shown the existence of considerable genetic variation among the genotypes considered with may help for further selection and breeding.

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