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Multivariate analysis of some metric traits in bread wheat (*Triticum aestivum* L.)

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ABSTRACT

Improved yield potential is a basic goal for plant breeders. Progress in yield potential results from the progressive accumulation of genes conferring higher yield or elimination of the unfavorable genes through the breeding process. Analysis of genetic diversity in germplasm collection aids in classification of genotypes and identification of core collections with possible utility for specific breeding goal. The nineteen genotypes were grouped into three clusters on the basis of average linkage. By performing analysis for PCs it was observed that variance for Eigen value was maximum (3.53) in PC-I followed by PC-II (1.97) and least for PC-III (1.16). Total variance percentage was maximum in PC-I (39.17) followed by PC-II and PC-III which was same (21.89) and total variance exerted by three factors was 73.94. Distribution pattern of all the genotypes into three clusters showed the presence of considerable genetics diversity among the genotypes for most of the traits under consideration. The mean values for days to 50% Heading (167), No of tillers per plant (4.74), No of spikelets per spike (15.46), biological yield (148), Grain yield (48.48) and harvest index (32.82) was highest in cluster-I. Cluster-II exhibited the maximum mean value (7.72) for spike length, average values for plant height and 1000 grain weight was higher in cluster-III.

Keywords: Wheat, Genetic variability, Metric traits, Multivariate Analyses.

1. Introduction

Wheat is called the king of cereals. In the world the largest cropped area is devoted to wheat and quantity produced is more than that of any other crop. Bread wheat (*Triticum aestivum*) and durum wheat (*Triticum durum*) are the two principle commercial types of wheat. However, bread wheat covers 90% of world wheat area and makes up about 94% of harvest. Pakistan is an agricultural country and its economy mainly depends on agriculture. The state of Azad Jammu and Kashmir lies in the north-east of Pakistan under the foot hills of Himalayas. Wheat is an important food crop of Azad Jammu and Kashmir and is used as a staple food. Total cultivated area for wheat in Pakistan is 8650 (000ha) with the production of 23473 (000tons) with average yield of 2714 Kgs per hectares ^[1]. Pakistan falls in top ten wheat producing countries of the world and at 9th position in terms area under wheat cultivation.

To ensure food security and to feed the increasing population we need more wheat yields. For yield enhancement maximum variability is a prerequisite. Genetic variability shows that how the genetic material is different between individuals of the same species. The characterization of genetic variability and estimate of the genetic relationship among varieties are essential to any breeding program because artificial crossing among less similar parents allows a large segregation and combination of different favorable alleles ^[2]. The knowledge about germplasm diversity and genetic relationship among breeding material could be an individual aid in crop improvement strategies. Genetic variability is used for detection of genetic diversity in closely related species ^[3].

Hybridization followed by subsequent selection is the important approach for wheat breeding programme. Joshi et al. reported that, for transgressive segregation, genetic variation between parents is necessary ^[4]. In order to maintain, evaluate and utilize germplasm effectively, it is important to investigate the extent of genetic diversity available. Higher the genetic distance between parents, the higher heterosis in progeny can be observed. Morphological traits have been successfully used for estimation of genetic diversity and cultivar development since they provide a simple way of quantifying genetic variation ^[5].

A number of methods are available for analysis of genetic diversity in germplasm accessions, breeding lines and populations. Multivariate analysis methods are also useful tool to access stability and can be used to identify groups with desirable traits for breeding [6]. 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 [7-8]. 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 [9], the principal components are linear transformations of the original variables and could be respective of a particular meaning [10]. 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.

There are substantial differences between the groups, but the individuals within a single group are similar [11]. Cluster analysis identifies and classifies objects individuals or variables on the basis of the similarity of the characteristics they possess. It seeks to minimize within-group variance and maximize between-group variance. It is also helpful for parental selection in the breeding programme and crop modeling [12]. PCA and cluster analysis has been previously used to evaluate the extent of genetic diversity for various morphological and physiological traits in sorghum under rainfed conditions [13-14].

The objective of the present study was to observe the genetic variability among different genotypes of wheat by using cluster analyses so that the genotypes possessing groups of desired traits could be selected for development and improvement of wheat cultivars and germplasm as well.

2. Materials and Methods

A field experiment was conducted at research farms of Plant Breeding and Molecular Genetics Department, University of Azad Jammu & Kashmir, Faculty of Agriculture Rawalakot to evaluate the wheat varieties/lines at Himalayans hills for some metric traits in bread wheat.

Nineteen different varieties/Lines of wheat, i.e Bakhar-2002, Bhrikuti, Blue silver, Buck Buck, C-591, Cartens V, Chakwal-86, Chakwal-97, Chanab-70, Chapio, Darawar-70, Faisalabad-83, Faisalabad-85, Fakhr-e-sarhad, Frontana, GA-2002, Gatcher, Gaurab, Genaro-81, were sown during Rabi season 2009-2010. Each experimental unit was comprised of one line of five meter length. Seed was dibbled in the field with the help of dibbler. Plant to plant and row to row to distance was 15 cm and 30cm respectively. For recording of data ten plants were selected

randomly from each of experimental unit and tagged.

Plant height of the main tiller of each selected plant was measured in centimeters from ground level to the tip of the spike. Number of Tillers/plant was counted from each of the tagged plants at the time of harvesting and their average was calculated. At the time of maturity spike length of main tillers of selected plants was measured in centimeters from base of the awn to its tip and values were averaged. From the main spike of guarded plants the Numbers of spikelets per spike of were counted excluding the basal sterile spikelets and values were averaged. A sample of 1000 grains was taken from randomly selected plants and weight was determined in grams by weighing with the help of electric balance. 50% heading days were counted from the date of sowing in each experimental unit by visual observation of plants. Grain yield was taken from each experimental unit and was converted to kg/ha. Crop biomass recorded by weighing above ground parts of selected plants from each row on complete drying after one week of harvesting, the values were averaged and harvest index was calculated by the following formula.

$$(\text{Grain yield/Biological yield}) \times 100$$

2.1. Statistical Analysis

Simple statistics and numerical taxonomic techniques were analyzed using the procedure of cluster and principal component analysis [15] with the help of computer software 'Statistica' and 'SPSS' 12.0 for Windows. Cluster analysis was conducted on the basis of average distance of k-means and the accessions in each cluster were then analyzed for basic statistics.

3. Results and Discussion

3.1. Principal Component analysis (PCA)

The average data was analyzed by using Principal Component analysis. Principal component analysis reflects the importance of the largest contributor to the total variation at each axis of differentiation. The eigen values are often used to determine how many factors to retain. The sum of the eigen values is usually equal to the number of variables [16]. According to Chahal *et al.* [17] 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. Three principal components showed more than one Eigen value and showed about 73.94% of variability. Table.1 PC-I showed 39.17% PC-II 21.89% and PC-III exhibited 12.89% variability among different traits of the under experiment genotypes. Eigen value and variance associated with each principal component, decreased gradually and stopped at 1.16 and 12.89 respectively.

Table 1: Principal Components (PCs) analysis for metric traits in wheat genotypes

Traits	PC-I	PC-II	PC-III
Eigen value	3.53	1.97	1.16
Total Variance (%)	39.17	21.89	12.89
Cum. Eigen value	3.53	5.50	6.66
Cumulative %	39.17	61.01	73.94

The first PC was related to yield and yield contributing traits i.e. grain yield, biological yield, harvest index, No of spike lets /spike and No of tillers/plant as cleared from the values of Table.2 for PC-I. Poor in 1000 grain weight, Plant height, and Days to 50% heading. The results are agreed with Leilah & Al-Khateeb [18], Saifullah *et al.* [19] who reported the same results for first principal component and reported the maximum variability in the data with respect to succeeding components.

In second principal component exhibited positive effect for

grain yield, Spike length, No of tillers/plant, biological yield and No of spike lets /spike while the values of traits like 1000 grain weight, Days to 50% heading and Plant height remained low (Table.2 PC-II).

In third PC, grain yield, No of tillers/plant, Spike length, No of spike lets /spike and biological yield were the traits of more importance the values for characteristics like Days to 50% heading and Plant height remained lower (Table. 2 PC-III).

Table 2: Communalities for metric traits in wheat genotypes

Characters	PC-I	PC-II	PC-III
Days to 50% Heading	0.29	0.31	0.63
No of tillers/plant	0.38	0.78	0.87
Plant height	0.07	0.38	0.48
Spike length	0.37	0.79	0.81
No of spike lets /spike	0.50	0.73	0.80
1000 grain wt	0.01	0.28	0.76
Biological Yield	0.55	0.78	0.78
Grain yield	0.84	0.91	0.95
Harvest index	0.52	0.53	0.58

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. 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. Accordingly, the first principal component (PC-I) had high positive component loading from grain yield, biological yield, harvest index, No of spike lets/spike, and Spike length and exhibited high negative loading from plant height. In the second principal component (PC-II) high positive component loading was observed

from No of tillers/plant and Plant height while it was high negative from No of spike lets/spike, No of tillers/plant and harvest index. The major contributing characters for the diversity in the third principal component (PC-III) were 1000 grain wt and Days to 50%. Heading exhibited high value for positive loadings and No of tillers/plant, Harvest index, Grain yield and Biological Yield showed the high negative values for morphological traits.

Usually it is customary to choose one variable from these identified groups. Hence, for the first group grain yield is best choice, which had the largest loading from component ones, plant height for the second, 1000 grain wt for the third group.

Table 3: Factor loadings for metric traits in wheat genotypes.

Factors	PC-I	PC-II	PC-III
Days to 50% Heading	0.54	-0.14	0.56
No of tillers/plant	0.61	0.64	-0.30
Plant height	-0.27	0.56	0.31
Spike length	0.61	-0.65	0.15
No of spike lets/spike	0.71	-0.48	0.25
1000 grain wt	0.09	0.52	0.69
Biological Yield	0.74	0.48	-0.05
Grain yield	0.92	0.26	-0.20
Harvest index	0.72	-0.11	-0.22
Expl.Var	3.53	1.99	1.16
Prp.Total	0.39	0.22	0.13

3.2. Cluster mean analysis

The cluster analysis sequestrates genotypes into clusters which exhibit high homogeneity within a cluster and high heterogeneity between clusters [20]. According to Chahal and Gosal [17] 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. All the three clusters were analyzed for mean and standard deviation (Table.4) Distribution pattern of all the genotypes into three clusters showed the presence of considerable genetics diversity among the genotypes for most of the traits under consideration.

Table 5: Grouping genotypes using cluster analysis based on principal component analysis

Clusters	Genotypes
I	Bakhar-2002, Bhrikuti, Chakwal-97, Chapio, Darawar-70, Faisalabad-83, Gaurab, Genaro-81.
II	C-591, Gatcher, Frontana, Blue silver, Buck Buck, Chakwal-86, Faisalabad-85,
III	Cartens V, GA-2002, , Fakhr-e-sarhad, Chanab-70

The characteristic feature of each cluster is discussed here below. The mean values for Days to 50% Heading (167), No of tillers/plant (4.74), No of spikelets/spike (15.46), biological yield (148), Grain yield (48.48) and harvest index (32.82) was highest in

cluster-I. Cluster-II exhibited the maximum mean value (7.72) for spike length. Average values for plant height (115.77) and 1000 grain weight (55.23) was higher in cluster-III (Table, 4).

Table 4: Means, standard deviations and variances for clusters based on morpho- physiological traits.

Characters	Cluster-I		Cluster-II		Cluster-III	
	Mean	SD	Mean	SD	Mean	SD
Days to 50% Heading	167	3.24	165.09	4.64	164.67	2.08
No of tillers/plant	4.74	0.36s	3.57	0.42	4.03	0.55
Plant height	86.66	4.79	85.59	4.26	115.77	13.16
Spike length	7.67	0.64	7.72	1.04	6.23	1.14
No of spikelets /spike	15.46	1.09	14.53	1.54	12.4	2.46
1000 grain wt	52.82	6.51	49.64	8.25	55.23	5.06
Biological Yield	148	10.37	102.73	16.13	110	5.00
Grain yield	48.48	8.34	27.49	4.75	26.8	8.19
Harvest index	32.82	5.78s	27.15	4.88	24.17s	6.32

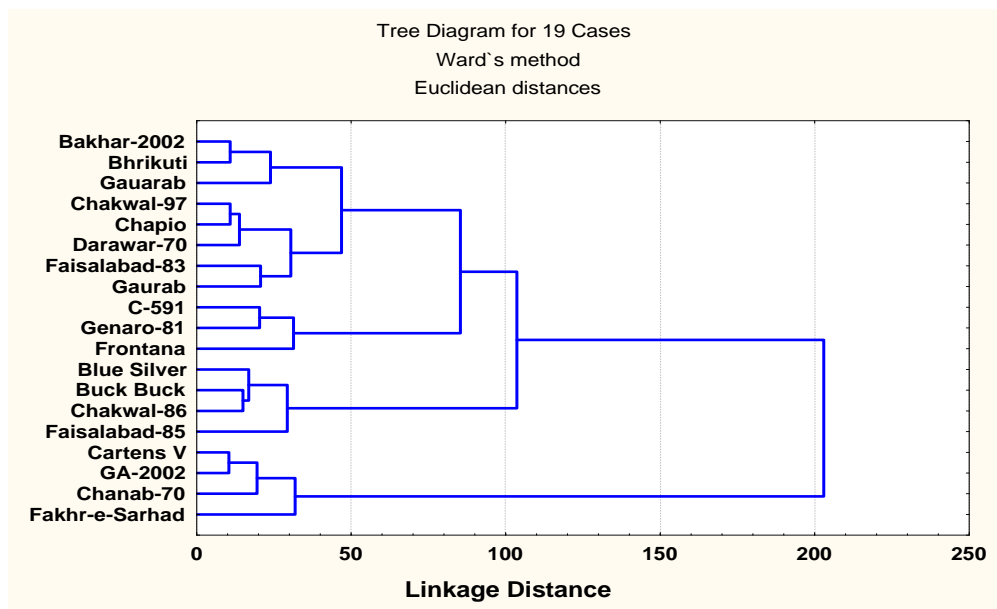


Fig 1: Dendrogram showing relationship among different cultivars of wheat

Showned that Bhakar-2002 has more genetic distance to Fakhr-e-sarhad so the cross between these two genotypes will be helpful to obtain maximum genetic divergence. The results of the genetic distance has shown that there is a room for the genetic improvement of bread wheat varieties and the information generated can be used to plan wide crosses, to exploit genetic diversity and maximize the expression of hetrosis.

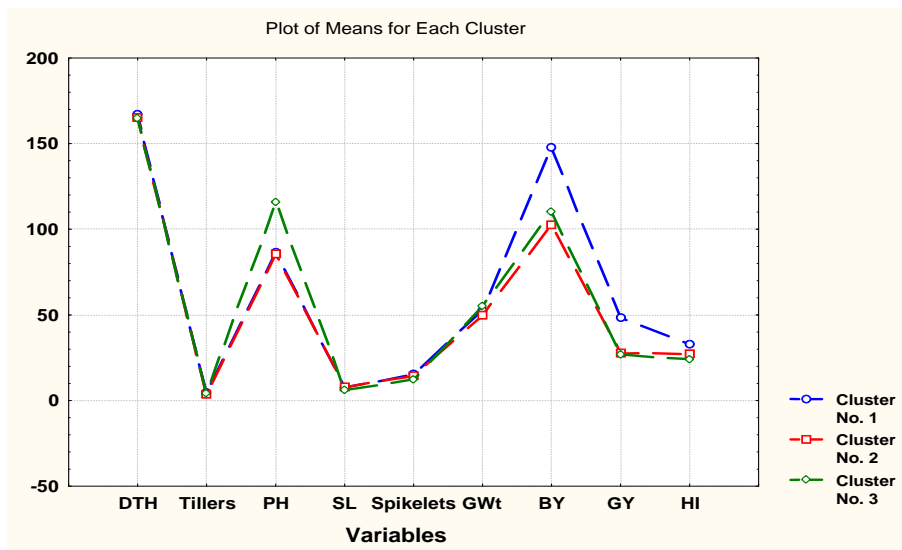


Fig 2: Mean values for metric traits in various clusters of wheat cultivars

Mean values for metric traits in various clusters of wheat cultivars are given in figure 2. Where, DTH = Days to 50% heading, Tillers = Number of tillers per plant, PH = Plant height, SL = Spike length, Spikelets = Number of spikelets per spike, GWt = 1000-grain weight, BY = Biological yield per plant, GY = Grain yield per plant, HI = Harvest index

The present research provided significant information that future may be helpful for genetic improvement of bread wheat. Genotypes grouped into three cluster showed maximum inter cluster diversity. There is significant genetic variability among tested genotypes that shows the presence of excellent opportunity to bring about improvement through wide hybridization by crossing genotypes in different clusters.

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