Original article

Multivariate analysis for various quantitative traits in wheat advanced lines

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Abstract

Genetic diversity play key role in the germplasm improvement which is directly correlated with the crop production. Various statistical techniques have been used to study diversity among different genotypes. Among these techniques multivariate is most frequently used one for the genetic association of genotypes. In the present study a total of 64 advance lines included one check cultivar were evaluated under the field conditions of Cereal Crop Research Institute, Pirsabaq Nowshera, Pakistan during September 2017. Data were recorded for nine different parameters. Multivariate analysis divided the total 64 genotypes into four groups. The first five PCs with Eigen values > 1 contributed 86.95% of the variability amongst genotypes. Characters with maximum values in PC1 were Spikelets spike-1 (SPPS) (0.732), spike length (SPL) (0.722) and biological yield (BY) (0.607), PC2 comprised of 100-grain weight (TGW) (0.605), grain yield (GY) (0.482) while days to heading (DH) (0.393), for PC3 major contributors were BY (0.550) and number of tillers meter square-1 (NTPS) (0.289), the contribution of PC4 were flag leaf area (FLA) (0.716) and SPL (0.298) and the maximum values for various traits in PC5 were SPPS (0.732), SPL (0.722) and BY (0.607). From the findings of present study best performing lines can be directly recommended for general cultivation or to be used in future breeding programs.

1. Introduction

Wheat is substantially used cereal crop by majority of the people on all sides of the globe and considerably impart to food security by providing over fifty percent calories to the inhabitants whose staple food is wheat (Gupta et al., 2005). According to Food and Agriculture Organization (FAO), wheat is the integral part of the human food around the globe provides twenty percent of food resources globally (Farzi and Bigloo, 2010).

Wheat is important member of poaceae family and a notable cereal crop in most of countries including Pakistan (Akram et al., 2008). Wheat confers to 36% of world population and 20% of total calories (Khan and Naqvi, 2011). Irrigated and rainfed areas of Pakistan are rearing a wide range of wheat crop.

Since 8000 years, wheat has been main food of most of the communities and is widely cultivated around the globe, covering 17% of cropping area world wide, nutrifying 40% of world population (Gupta et al., 2005; Vinod et al., 2020).

Many food items like bread, chapattis and confectionary items are being made of wheat. It was spread on 9.052 million hectares, with total production of 25.750 million tons of grains with average yield of 2845 kg ha-1 in Pakistan during 2017–18 (PBS, 2017–2018). Burgeoning population demands food security, hence to meet the needs of ever increasing population it is necessary to increase per unit yield by introducing new high yielding wheat genotype having suitable qualities as per society’s need. By breeding these traits to prevailing genotypes can help to accomplish in demand objectives. Germplasm development and genetic diversity are key for the sustainable production of food crops. To efficiently utilize and evaluate the germplasm, measure of extent of available genetic diversity is of great essence (Zubair et al., 2007). Applying various statistical tools is a vital strategy for germplasm categorization and analysis of genetic association among breeding

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material (Mohammadi & Prasanna, 2003). Gathered hard red winter wheats on basis of pedigree, morphological characters, end-use quality traits and molecular markers to get the measure of genetic diversity. Leilah and Al-Khatib (2005) investigated relationship between wheat grain yield and its components. Ahmad et al., (2008) assessed 113 barley accessions by utilizing cluster and principal component analysis. Comparison of seventy wheat genotypes was done for variability including cluster analysis for eight traits by Ali et al., (2008). Aharizad et al., (2012) applied cluster analysis using Wards algorithm and squared Euclidean distances and 94 bread wheat inbred lines were allocated into three groups. Peduncle length had more variation than flag leaf area, number of spikes and grain yield. According to Soleymanifard et al. (2012) 75% variation in grain yield was due to spikes m², 1000 grain weight and plant height. Basic purpose behind the present trial was to explain the extent of genetic variation and relationships among wheat genotypes based on quantitative traits using multivariate analysis and to catalog morpho-agronomic attributes which could be further manipulated in upcoming breeding programs.

2. Material and methods

A total of 64 wheat advance lines along with one check cultivar were assessed under the field conditions of Cereal Crops Research Institute (CCRI), Pirsabak – Nowshera, Pakistan in the during September 2017 (Table 1). Dissemination of the research material was done during November 2017, each plot was comprised of four rows, row spacing was kept 30 cm with a length of two meter. Design used was Randomized Complete Block Design with three replications. Data was recorded on days to heading, plant height (cm), flag leaf area, spike length (cm), number of spikelets spike-1, tillers meter-², 1000 grain weight, grain yield (kg ha-¹) and biological yield. Standard culture practices were applied during the study. After compilation of data it was put through basic simple statistic for the estimation of mean, range, variance, standard error and simple correlation. “Statistica” Version 7.0 and “NYSys 2.1” were used for principal component and cluster analysis. Ward’s method is used in cluster analysis which identifies different variables and then divides into various group and sub groups. To avoid complications in analysis, each value was standardized prior to principal component analysis so that different scaling units could be homogenized (see Table 2).

3. Results

Table 3 showed that substantial amount of variations were recorded for most of the quantitative traits. Biological yield, grain yield, number of spikelets meter square-¹ and flag leaf area showed in consisting values which means they were most variable among all other traits. Contrastingly, least variate traits were plant height, thousand grain weight, days to heading, spike length and seeds spike-¹. Simple correlation coefficients for studied characters were observed and can be seen in Table 6. Results divulged that 1000 grain weight is positively associated with days to heading, grain yield and flag leaf area, on the other hand negative association with plant height, spike length, number of tillers spike-¹ and biological yield, while association with spikelets spike-¹ were significantly positive. Correlation of biological yield with days to heading, grain yield, spikelets spike-¹, number of tillers spike-¹ and flag leaf area is positive, while significant positive association were recorded for spike length. This parameter contributed negatively with plant height. Flag leaf area is positively associated with days to heading, grain yield, spike length and spikelets spike-¹, while on the other hand negative correlation was observed for plant height number of tillers plant-¹. Number of tillers spike-¹ contributed positively with plant height, spike length and spikelets spike-¹ while negative association with days to heading and grain yield. Data recorded for

Table 1

| S.No | Genotypes | Institution | S.No | Genotypes | Institution |
|------|-----------|-------------|------|-----------|-------------|
| 1    | Mpt-1     | CCRI, Pirsabak | 33   | Mpt-33    | CCRI, Pirsabak |
| 2    | Mpt-2     | CCRI, Pirsabak | 34   | Mpt-34    | CCRI, Pirsabak |
| 3    | Mpt-3     | CCRI, Pirsabak | 35   | Mpt-35    | CCRI, Pirsabak |
| 4    | Mpt-4     | CCRI, Pirsabak | 36   | Mpt-36    | CCRI, Pirsabak |
| 5    | Mpt-5     | CCRI, Pirsabak | 37   | Mpt-37    | CCRI, Pirsabak |
| 6    | Mpt-6     | CCRI, Pirsabak | 38   | Mpt-38    | CCRI, Pirsabak |
| 7    | Mpt-7     | CCRI, Pirsabak | 39   | Mpt-39    | CCRI, Pirsabak |
| 8    | Mpt-8     | CCRI, Pirsabak | 40   | Mpt-40    | CCRI, Pirsabak |
| 9    | Mpt-9     | CCRI, Pirsabak | 41   | Mpt-41    | CCRI, Pirsabak |
| 10   | Mpt-10    | CCRI, Pirsabak | 42   | Mpt-42    | CCRI, Pirsabak |
| 11   | Mpt-11    | CCRI, Pirsabak | 43   | Mpt-43    | CCRI, Pirsabak |
| 12   | Mpt-12    | CCRI, Pirsabak | 44   | Mpt-44    | CCRI, Pirsabak |
| 13   | Mpt-13    | CCRI, Pirsabak | 45   | Mpt-45    | CCRI, Pirsabak |
| 14   | Mpt-14    | CCRI, Pirsabak | 46   | Mpt-46    | CCRI, Pirsabak |
| 15   | Mpt-15    | CCRI, Pirsabak | 47   | Mpt-47    | CCRI, Pirsabak |
| 16   | Mpt-16    | CCRI, Pirsabak | 48   | Mpt-48    | CCRI, Pirsabak |
| 17   | Mpt-17    | CCRI, Pirsabak | 49   | Mpt-49    | CCRI, Pirsabak |
| 18   | Mpt-18    | CCRI, Pirsabak | 50   | Mpt-50    | CCRI, Pirsabak |
| 19   | Mpt-19    | CCRI, Pirsabak | 51   | Mpt-51    | CCRI, Pirsabak |
| 20   | Mpt-20    | CCRI, Pirsabak | 52   | Mpt-52    | CCRI, Pirsabak |
| 21   | Mpt-21    | CCRI, Pirsabak | 53   | Mpt-53    | CCRI, Pirsabak |
| 22   | Mpt-22    | CCRI, Pirsabak | 54   | Mpt-54    | CCRI, Pirsabak |
| 23   | Mpt-23    | CCRI, Pirsabak | 55   | Mpt-55    | CCRI, Pirsabak |
| 24   | Mpt-24    | CCRI, Pirsabak | 56   | Mpt-56    | CCRI, Pirsabak |
| 25   | Mpt-25    | CCRI, Pirsabak | 57   | Mpt-57    | CCRI, Pirsabak |
| 26   | Mpt-26    | CCRI, Pirsabak | 58   | Mpt-58    | CCRI, Pirsabak |
| 27   | Mpt-27    | CCRI, Pirsabak | 59   | Mpt-59    | CCRI, Pirsabak |
| 28   | Mpt-28    | CCRI, Pirsabak | 60   | Mpt-60    | CCRI, Pirsabak |
| 29   | Mpt-29    | CCRI, Pirsabak | 61   | Mpt-61    | CCRI, Pirsabak |
| 30   | Mpt-30    | CCRI, Pirsabak | 62   | Mpt-62    | CCRI, Pirsabak |
| 31   | Mpt-31    | CCRI, Pirsabak | 63   | Mpt-63    | CCRI, Pirsabak |
| 32   | Mpt-32    | CCRI, Pirsabak | 64   | Pakhtunkhwa-2015 | CCRI, Pirsabak |
Table 2
Morphological traits recorded in the 64 genotypes of Wheat.

| Trait designation        | Code | Description of the trait                                                                 |
|--------------------------|------|------------------------------------------------------------------------------------------|
| Days to Heading          | GY   | Number of days from seed sowing to the appearance of first open flower                    |
| Grain Yield              | Pht  | Counted total grain in whole spike                                                        |
| Plant Height (cm)        | Pht  | Plant height was measured in centimeters from the ground level to the tip of the plant with the help of a meter rod for each selected plant. |
| Spike length (cm)        | SPL  | Counted the length from spike base to awns                                                |
| Spikelets spike⁻¹        | SPPS | From eight randomly selected spikes, the spikelet per spike was recorded by counting the spikelet in each particular spike and then was averaged. |
| Number of tillers per meter square⁻¹ | NTPS | Counted the tillers in one meter area for each genotype                                   |
| Flag leaf area           | FLA  | Measured from the base to the tip of the flag leaf                                        |
| Biological yield         | BY   | By harvesting and sun drying the whole plant the biological yield was recorded in kilograms (kg) and converted to kg ha⁻¹ from each sub-plot of the replication. |
| Thousand seed weight (g) | TGW  | Weight of 1000 dry seeds                                                                 |

Table 3
Basic statistic data of all the wheat genotypes used in the study.

| Traits   | Mean ± SD       | Minimum value | Maximum value | CV  |
|----------|-----------------|---------------|---------------|-----|
| DH       | 121.50 ± 3.40   | 113.00        | 127.00        | 2.80|
| GY       | 2400.20 ± 333.10| 1403.10       | 3225.50       | 13.90|
| Pht      | 107.80 ± 5.60   | 95.00         | 122.00        | 5.20|
| SPL      | 12.00 ± 1.40    | 8.50          | 16.00         | 12.00|
| SPPS     | 19.90 ± 1.30    | 16.90         | 22.90         | 6.60|
| NTPS     | 274.80 ± 35.90  | 201.60        | 344.90        | 13.10|
| FLA      | 30.80 ± 6.10    | 18.00         | 50.10         | 19.70|
| BY       | 9997.00 ± 1067.10| 7181.30       | 12575.00      | 10.70|
| TGW      | 38.50 ± 3.30    | 31.40         | 46.80         | 9.20|

Table 4
Principal components analysis for morpho-physiological traits in wheat genotypes.

| Traits | PC1    | PC2    | PC3    | PC4    | PC5    |
|--------|--------|--------|--------|--------|--------|
| DH     | 2.01   | 1.50   | 1.24   | 1.07   | 0.92   |
| GY     | 0.395  | 0.482  | 0.277  | 0.468  | 0.358  |
| Pht    | 0.121  | 0.242  | 0.171  | 0.310  | 0.335  |
| SPL    | 0.722  | 0.058  | 0.298  | 0.190  | 0.063  |
| SPPS   | 0.732  | 0.048  | 0.337  | 0.27  | 0.126  |
| NTPS   | 0.176  | 0.289  | 0.036  | 0.200  | 0.181  |
| FLA    | 0.297  | 0.374  | 0.716  | 0.063  | 0.126  |
| BY     | 0.607  | 0.108  | 0.190  | 0.100  | 1.00   |
| TGW    | -0.450 | 0.005  | 0.159  | 0.190  | -0.17  |

Table 5
Correlation studies for various morphological attributes of wheat genotypes used in the study.

| Trait | DH    | GY    | Pht   | SPL   | SPPS  | NTPS  | FLA   | BY    | TGW   |
|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| DH    | 1.00  |       |       |       |       |       |       |       |       |
| GY    | 0.09  | 1.00  |       |       |       |       |       |       |       |
| Pht   | 0.03  | -0.14 | 1.00  |       |       |       |       |       |       |
| SPL   | 0.06  | 0.18  | 0.17  | 1.00  |       |       |       |       |       |
| SPPS  | 0.26  | 0.29  | 0.11  | 0.36  | 1.00  |       |       |       |       |
| NTPS  | -0.13 | -0.16 | 0.01  | 0.02  | 0.03  | 1.00  |       |       |       |
| FLA   | 0.12  | 0.01  | -0.01 | 0.23  | 0.09  | -0.12 | 1.00  |       |       |
| BY    | 0.05  | 0.19  | -0.15 | 0.36  | 0.15  | 0.25  | 0.15  | 1.00  |       |
| TGW   | 0.02  | 0.08  | -0.13 | -0.14 | 0.33  | -0.27 | 0.07  | -0.17 | 1.00  |

Red only: *Significant (0.05); Black & Bold: **Highly Significant (0.01).
spikelets spike\(^{-1}\) showed positive association with days to heading, grain yield and plant height, while positive significant for spike length. Days to heading, grain yield and plant height have positive association with spike length. Number of spikelets per spike showed a positive relation with plant height, spike length and seeds spike\(^{-1}\). Fig. 1 and Fig. 2 showed the behaviour of various genotypes used in the study based on various traits and advances lines. In the present study cluster analysis divided the total 64 genotypes into four main clusters (Fig. 3). Members of each cluster are presented in Table 5. Cluster I consisted of 12 genotypes, cluster II of 23 genotypes, cluster III of 24 genotypes while cluster IV had 05 genotypes. Though cluster analysis grouped genotypes together with greater morphological similarity, the clusters did not necessarily include all genotypes from same origin. Mean values along with standard deviation for each cluster (Table 7) revealed that genotypes in the cluster I showed high yielding, long spikes and bold seed. The genotypes included in cluster II were early heading, moderate plant height and less tillers meter square\(^{-1}\). Cluster III comprised of genotypes having bold seed, tall plants, long spikes, where genotypes of cluster IV had more biological yield and more tillers meter square\(^{-1}\).

The principal component analysis had grouped the estimated wheat variables into three main components. The first three components with eigen values > 1 accounted for 86.95% of the total variation of grain yield. PC1 accounted for about 22.29% of the variation in grain yield; PC2 for 38.99%, PC3 for 52.77%, PC4 for 64.65%.

### Table 6

Mean values and standard deviation (SD) of four clusters based on morphological of wheat genotypes during 2017.

| Trait | Cluster 01 | Cluster 02 | Cluster 03 | Cluster 04 |
|-------|------------|------------|------------|------------|
|       | SD        | CV         | SD        | CV         | SD        | CV         | SD        | CV         |
| DH    | 3.07      | 2.50       | 2.58      | 2.10       | 3.33      | 2.73       | 2.50      | 2.01       |
| GY    | 395.61    | 18.93      | 314.00    | 12.72      | 259.97    | 10.37      | 206.95    | 8.60       |
| Pht   | 3.87      | 3.62       | 4.99      | 4.74       | 5.52      | 5.00       | 8.63      | 7.90       |
| SPL   | 1.18      | 10.30      | 1.37      | 12.10      | 0.90      | 7.28       | 0.60      | 4.00       |
| SPPS  | 0.90      | 4.85       | 1.27      | 6.33       | 1.14      | 5.70       | 0.94      | 4.35       |
| NTPS  | 49.51     | 17.82      | 37.16     | 13.16      | 23.46     | 8.87       | 37.81     | 13.41      |
| FLA   | 5.66      | 20.28      | 4.97      | 17.01      | 5.40      | 16.07      | 10.81     | 20.01      |
| BY    | 745.36    | 7.64       | 1075.36   | 10.44      | 940.80    | 9.84       | 427.42    | 3.56       |
| TGW   | 4.27      | 10.82      | 3.14      | 8.17       | 3.46      | 8.97       | 5.29      | 14.40      |

SD: Standard Deviation.
4. Discussion

The association of plant height is positive with days to heading while negative with grain yield, on the other hand grain yield have positive relation with days to heading. Earlier Samar et al., 2019, Leilah and Al-Khateeb (2005) also reported significant positive relation of 100 grain weight and grain yield. Similarly Singh et al., 2012 and Ali et al., 2008 reported for most of the yield contributing traits. Plant height showed positive association with days to heading and negative with grain yield. Our results were supported by the previous investigations of Ali et al., 2008, who reported significant negative genotypic and phenotypic correlation of plant height with yield plant$^{-1}$. Contrary to these findings Tripathi et al. (2015) and Leilah and Al-Khateeb (2005) reported a significant positive relationship of plant height with grain yield. Various techniques have been used successfully for genetic diversity to create diverse genotypes. Among these techniques the most frequent and successful is the morphological, which is commonly used for estimation of genetic variation in most of the breeding programs (Phougat et al., 2017). The main objective of evaluation of indigenous collected germplasm for various morphological attributes is to classify these genotypes for different breeding programs. Among these techniques cluster and principal component analysis is the most frequently used in the collection and evaluation of genotypes. Cluster analysis divided genotypes into various groups and sub groups based on morphological differences not on geographical affinity (Devesh et al., 2019). Cluster IV and V groups and sub groups based on morphological differences not on geographical affinity (Devesh et al., 2019). Cluster IV and V showed considerable clear separation than cluster I, II and III which might be due to mixture of genotypes with different taxonomic traits grouped in these cluster. Though cluster analysis grouped genotypes together with greater morphological similarity, the clusters did not necessarily include all genotypes from same origin. Our findings are supported by the previous results of Ahmad et al. (2008), who also reported lack of association between morpho-agronomic traits and origin. The process which divided the whole data into various small variables is called principal components analysis. In our findings the major contributing components were the first two principal components, which contributed more than half of the variance, that variance was then plotted to observe relationships between the clusters. Ahmad et al. (2008) also recorded maximum variability in the first principal component with respect to succeeding components which is in line to our findings. Increased yield potential is the ultimate goal of a plant breeder. Progress in yield potential results from the progressive accumulation of genes conferring higher yield or elimination of the unfavorable genes through the breeding process.

![Dendrogram presenting the genetic relationship among different wheat genotypes used in the study.](image)

Table 7

| Cluster | Frequency | Genotypes | Features |
|---------|-----------|-----------|----------|
| I       | 12        | 1,48,44,47,12,29,33,52,36,53,49,50 | High yielding, Long spikes, bold seed |
| II      | 23        | 2,13,60,9,38,11,6,57,64,4,35,39,23,17,19,18,28,62,21,41,40,3,37 | Early heading, moderate plant height, less tillers meter square<sup>1</sup> |
| III     | 24        | 14,15,24,26,56,16,51,30,43,61,45,53,22,20,63,27,42,37,31,25,46,32,34,54,59 | Bold seed, tall plants, long spikes |
| IV      | 5         | 5,8,10,58,59 | More biological yield, more tillers meter square<sup>1</sup> |
5. Conclusion

The present study revealed that 1000 grain weight had strong correlation with number of spikelets per spike and yield, suggesting the need of more emphasis on these components for increasing the grain yield in wheat. Grouping of genotypes by multivariate methods in the study is of practical value for the wheat breeders.

Recommendation

Representative genotypes may be chosen from the particular groups for hybridization programs with other approved cultivars. This will aid in identification, selection and combining genotypes to obtain important traits in one line with a broad genetic base.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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