Genetic variability assessment in bread wheat (*Triticum aestivum* L.) cultivars using multivariate statistical analysis

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**ABSTRACT:** Evaluation of genetic diversity is one of the most important aims in wheat breeding. Breeding science need to genetic variability. On the other hand, wheat (*Triticum aestivum* L.) is the major cereal crop in Iran on which the food security rests. Therefore, in order to evaluate and classify morphological and morpho-physiological traits of bread wheat genotypes, 18 cultivars were sown in randomised complete block design with three replications. Principal component analysis based on the measured traits classified bread wheat cultivars to four distinct groups. Cluster analysis using ward’s method grouped these cultivars in three clusters. Similarity between results of principal component and cluster analysis were observed for classification of genotypes. Overall, crosses among cultivars having maximum genetic distance can be resulted higher transgressive segregation and genetic gain of selection. Increasingly, cross between genotypes 1 and 18 as well as selection among their progeny have the best result.

**Keywords:** Bread wheat, genetic variability, principal component analysis, cluster analysis, ward method

**INTRODUCTION**

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. Genetic diversity of plants determines their potential for improved efficiency and hence their use for breeding, which eventually may result in enhanced food production. 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.

Usually before calculating the genetic distance, the variables are standardized so that all variables are of similar standardization decreases the differences among groups. The results of cluster analysis and PCA may have relative differences with each other. Therefore, before using cluster analysis, the principle components may be avoided. On the other hand, when the two first principal components account for high variation percentage, grouping according to these two components, can certainly be a useful method to find the clusters (Fotokian et al., 2002).

Various algorithms have been used in studying of genetic diversity in cluster analysis of which, UPGMA and Ward’s methods are the most popular approaches. Of the algorithms, UPGMA, Ward’s, SLINK, and CLINK, applied for cluster analysis and exploring genetic diversity and grouping of plant materials in the past, the UPGMA is the most valid method in accordance with the relationship of family based on their genetic material (Mohammadi and Prasanna, 2003). Chaining effect in UPGMA model is considered as the major drawback on application of this
approach in cluster analysis and results in confusions in interpretation of the results (Mohammadi and Prasanna, 2003).

Ward’s approach is similar to UPGMA method but it without having chain effect issues. Results of using PCA showed that this method is limited when the pattern of variation is not based on a 0 and 1 scores. Therefore, combined PCA and other techniques can be appropriately used for grouping (Mohammadi and Prasanna, 2003). The cluster analysis is an appropriate method for determining family relationships. 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 capture the potential genetic diversity between wheat genotypes grown in Iran by using cluster analysis and cluster analysis-PCA-based methods.

**MATERIALS AND METHODS**

In this study, 18 bread wheat cultivars randomly selected from collection were planted at the beginning of November 2011 at the Research field of Jehad and Agriculture research institute of Isfahan, Isfahan, Iran. The plots were 2m long and 0.4m apart with 6 planting rows per plot. Amount of precipitation was 135mm. In spring 2012, measurements for 12 traits; seed yield (g), plant height (cm), No.tiller, days to tillering, days to flowering, days to ripening, No.spike, spike weight (g), spike length, number of seed/spike and spike yield (g) were achieved on 10 normal plants randomly selected from each plot.

The principal component analysis method explained by Harman (1976) was followed in the extraction of the components. The percentage variability explained by each component were determined (Harman, 1976; Sharma, 1996; Tadesse and bekele, 2001). Cluster analysis based on ward’s method was performed using SPSS and SAS. softwares for all the traits of bread wheat cultivars. Clusters generated through both approaches were manually compared by searching for the presence and absence of each genotype in each cluster generated by each model. Because of non-uniformity of measurement scale of traits date were standardized (Mohammadi and prasanna, 2003). Principal component analysis (PCA) was performed using Minitab 14 software and the values of the first five components were selected and analyzed using SPSS and the related clusters were plotted based on the main components.

**RESULTS AND DISCUSSION**

There were significant differences between wheat genotypes for all traits measured. By incision the dendrogram at 0.8 unit distance, the genotypes categorized into four groups. Using discriminant analysis revealed that in this case 10% of the members of the second group were classified into the first Group. Then cutting point was determined at distance 0.7 and four clusters was obtained, in which the members completely belonged to the same group (Fig. 1).

Three components were extracted from the 15 studied traits by PCA analysis. The first three components that explained 98.6% of total variation were used for clustering genotypes. In fact, with this method, 15 variables were reduced to three. Using the discriminant analysis the best incision point was determined at distance 0.7. By incision at distance 0.7, six clusters were formed (Fig. 1).

The most effective traits in the first component were plant yield, height at maturity and number of seed per spike and spikelet, respectively. For the second component days to tillering, days to flowering, days to ripening and for the third component number of seed per spike and height at heading time had the greatest effect. Spike length, number of seed/spike and spike yield had effective influence on the fourth component. Comparing these results with the results of figure2 indicated that the traits with the largest impact on the components showed the highest rate of variation and hence can be used for grouping genotypes, effectively. The degree of similarity between dendrogram (obtained from cluster analysis) and dendrogram obtained from the cluster analysis based on PCA was estimated at 95.3%.

Narouee Rad (2006) determined the genetic diversity of wheat landraces in the west of Iran and by using cluster analysis, six clusters were determined for different areas. Fang et al. (1996) clustered 120 genotypes of durum wheat into five groups based on maturity date, plant height, spike length, number of seed per spike, 1000-seed weight and spike seed yield.

Genetic diversity could be the result of geographical impact through evolution and hence traits could be considered as a function of variety (Benadeki, 1992). 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 (Mohammadi and Prasanna, 2003; Eivazi et al., 2007).

In conclusion, Similarity between results of principal component and cluster analysis were observed for classification of genotypes. Overall, crosses among cultivars having maximum genetic distance can be resulted higher transgressive segregation and genetic gain for selection among their progenies. In present study revealed that cross between genotypes 1 and 18 and selection among their progeny have the best result.

Figure 1. Dendrogram of cluster analysis based on ward’s method on the measured traits in bread wheat cultivars

Figure 2. Two dimensional scatter plot of the bread wheat genotypes based on the measured traits
REFERENCES


