

GENETIC VARIABILITY ASSESSMENT IN BREAD WHEAT (*TRITICUM AESTIVUM* L.) CULTIVARS UNDER DROUGHT STRESS USING MULTIVARIATE STATISTICAL ANALYSIS

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INTRODUCTION

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). 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 and genetic variability. The higher genetic distance between parents, the higher heterosis in progeny can be observed. 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.

Some appropriate methods, such as cluster analysis and PCA 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. 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.

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

Seeds of 14 winter wheat genotypes (*Triticum aestivum* L.), including, Pishtaz, Arvand, Qods, Sivand, Behrang, Bahar, Sepahan, Roshan, Sardari, Mahdavi, Chamran, Aflak, Kavir, Falat and Triticale were sown in plots of 4 m×1 m with five rows in each plot in a research field, located in the Islamic Azad University, Khorasgan Branch, Isfahan, Iran. The amount of precipitation was 135mm. In spring 2012, measurements for 14 traits Seed yield (g/m²), Plant height (cm), Peduncle length (cm), Days to pollination, Flag leaf lengths (cm), Days to flowering, Days to ripening, No spikelet, Spike weight (g), Spike length (cm), No tiller per meter, 1000seed weight, Harvest index, Number of seed/spikelet and were achieved on 10 normal plants randomly selected from each plot. Eight drought tolerance indices including stress tolerance index (STI), stress susceptibility index (SSI), tolerance index (TOL), geometric mean productivity (GMP), mean productivity (MP), yield index (YI), relative decrease in yield were calculated based on grain yield under drought (Y_s) and irrigated (Y_p) conditions.

Cluster analysis based on ward's method was performed using SPSS and SAS9.2 software for all the morphologic, phenologic, yield and components of yield traits. 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 data were standardized (Mohammadi and Prasanna, 2003). Principal component analysis (PCA) was performed using SAS 9.2 software on tolerant and susceptible indices 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

Cluster analysis divided these 15 cultivars into 5 distinct groups using MANOVA for both control and stress conditions. However under different drought treatments this classification had different result. Under stress condition the first group had been consist of 7 cultivars (“Pishtaz“, “Bahar“, “Sivand“, Arvand“, Begrang“ and “Aflak“ and “Qods.”) and in the second cluster there were 2 cultivars (“Sepahan“, Chamran), furthermore there were 2 cultivars in third cluster (“Sardari“, Triticale) and in fourth and fifth clusters there were 1 (“Roshan“) and 3 (“Kavir“, “Mahdavi“ and “Falat“) cultivars respectively. On the other hand under none-stress condition the first group consisted of 6 cultivars (“Pishtaz“Qods“, “Mahdavi“, Kavir“, Chamran“ and “Sardari“) and in the second cluster there were 3 cultivars (“Arvand“, Bahar“ and “Sepahan“). Additionaly ,there were 2 cultivars in third cluster (“Sivand“,Falat“) and 1 (“Behrang“) and 4 (“Roshan“, “Aflak“, Falat“ and “Triticale) cultivars in the fourth and fifth clusters , respectively. Based on this analysis, the groups number 2 and 4 were the best groups based on grain yield in normal and stress conditions, respectively. The genotypes in these two groups could be cinsider as parental genotypes in breeding programs.

On the other hand, cluster analysis of 8 drought tolerance and susceptible indices (STI, SSI, TOL, MP, GMP, Yp, Ys, Yp and HAM) had been performed which categorized these 15 cultivars in 3 statistically significant clusters. cluster 1 included only two cultivars named “Pishtaz” and “Bahar” while cluster 2 was consist of 7 cultivars (“Arvand“, “Kavir“, “Falat“,Qods“,Sivand“Chamran“, Aflak“,) mean while, other cultivars (“Behrang“, “Roshan“, Sardari“, Sepahan“, Mahdavi“ and “Triticale“) were belonged to cluster 3. Group number 3 was the most tolerant in contrast two other groups.

Two components were extracted from these 8 tolerance indexes using Principal Component Analysis (PCA) which justify 70.36 % and 29.43 % of total variation respectively. According to the estimated coefficient of each index for these two components, the first component implies to the importance of this component on yield related variables while the second component implies to tolerance related variables.

Keywords: genetic variability, principal component analysis, cluster analysis, ward method

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