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Genetic Variability Assessment in Bread Wheat (Triticum Aestivum L.) Cultivars under Different Drought Stress Treatments using Multivariate Statistical Analysis

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Abstract – **The improvement of tolerance to drought has been a principal goal of the majority of breeding programmes for a long time, as a water deficit in certain stages of wheat growth is common for many wheat growing regions of the world. Determination of genetic diversity is useful for plant breeding and hence production of more efficient plant species under different conditions. 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 and tolerance indices of bread wheat genotypes, 15 cultivars were sown in randomised complete block design with three replications under two moisture treatments. Cluster analysis using ward's method grouped these cultivars in five clusters both in stress and control conditions. Principal Component bi- plot of tolerance indices and cultivars according to PCA suggested a better understanding of each cultivar potential under drought condition. This result suggested that "Sepahan" and "Roshan" are two best cultivars under both control and stress condition. Overall, crosses among cultivars having maximum genetic distance result in higher transgressive segregation and genetic gain of selection.**

Keywords – **Bread Wheat, Cluster Analysis, Genetic Variability, Principal Component Analysis.**

I. 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 [7]. 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 [13]. 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. In order to benefit transgressive segregation, genetic distance between parents is necessary [12]. The higher genetic distance between parents, the higher heterosis in progeny can be observed [11]. Benadeki (1992) investigated the genetic diversity of five local geographical regions across central provinces of Iran for bread wheat. It has been proposed that the differences for studied traits across regions were significantly (P=0.01) different and resulted in nine classes discriminated by geographical regions [1]. 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. Jain et al. (1975) investigated the geographical patterns of phenotypic diversity of durum wheat using the world collection and achieved a developed program for the protection of genetic resources to identify and assess inter variation and intra societies. Genetic diversity could be the result of geographical impact through evolution and hence traits could be considered as a function of variety [1]. 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 [9]. 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 [2;3;4; 16].Usually before calculating the genetic distance, the variables are standardized so that all variables are of similar importance in determining the distance. Unfortunately, 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 [6]. 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 [16]. 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 [16].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 [16]. The cluster analysis is an appropriate method for determining family relationships [14]. The main advantage of using PCA over cluster analysis is that each genotype can be assigned to one group only [15]. One of the issues with breeding projects based on hybridization is to estimate the relationship between parents before initiating the crossing. Euclidean distance can theoretically estimated the genetic distance between parents to maximize the trangressive segregation [8]. Determination of genetic diversity is useful for plant breeding and hence production of more efficient plant species under different conditions. Accordingly, the most common wheat genotypes including 36 winter wheat genotypes cultivated in different parts of Iran were selected, grown and analyzed for their genetic diversity based on the studied traits explained in this paper. 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. The results of present study have been used in selection of appropriate parents for breeding program based at Shahed University.

II. 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 prepared from the Natural Resources and Agriculture Research Center of Isfahan and Seed and Plant Improvement Institute of Karaj, Iran. This experiment was performed in Novamber 2011-2012 in a research field, located in the Islamic Azad University Khorasgan Branch, Isfahan, Iran. The land for the experiment was prepared by deep plowing, two disks and furrowing.

Then, nitrogen, phosphor and potassium fertilizers were added according to results of the soil nutrient test.Seeds were sown in plots of 4 m×1 m with five rows in each plot Amount of precipitation was 135mm. In spring 2012, measurements for 14 traits; Seed yield (g/m2), Plant height (cm), Pedancle 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 (Ys) and irrigated (Yp) conditions. Cluster analysis based on ward's method was performed using SPSS and SAS9.2 soft wares 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, data were standardized [16].

III. RESULTS AND DSCUSSION

Cluster analysis divided these 15 cultivars into 5 distinct groups using Ward's method for both control and stress conditions. However, under different drought treatments this classification had different results. Under stress condition the first group consisted of 7 cultivars ("Pishtaz"," Bahar"," Sivand","Arvand", Begrang", "Aflak" and "Qods") and 2 cultivars ("Sepahan", Chamran)were included in the second cluster .Furthermore, there were 2 cultivars in third cluster ("Sardari", Triticale) and there were 1 ("Roshan") and 3 ("Kavir", "Mahdavi" and "Falat") cultivars in the fourth and fifth clusters, respectively (Fig.1).

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"). Additionally ,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 (Fig.2).Furthermore cluster analysis was performed on the basis of 8 drought tolerance indices (STI, SSI, TOL, MP, GMP, Yp, Ys, Yp and HAM) which categorized these 15 cultivars in 3 statistically different clusters. Cluster I included only two cultivars named "Pishtaz" and "Bahar" while cluster II consist of 7 cultivars ("Arvand", "Kavir", "Falat", "Qods", "Sivand", "Chamran" and Aflak",). Meanwhile, other cultivars ("Behrang", "Roshan",Sardari",Sepahan", Mahdavi" and "Triticale") were belonged to cluster III (Fig.3).

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 the importance of this component on yield related variables while the second component implies tolerance related variables (Table.1). Genetic diversity could be the result of geographical impact through evolution and hence traits could be considered as a function of variety [1]. 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 [9]. Some appropriate methods such as 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 [16; 4]. According to Rahim et al. (2010) who showed that the hybrids of genotypes with maximum distance resulted in high yield, the cross between these genotypes can be used in breeding programs to achieve maximum heterosis.

Table 1: PCA analysis for studied 8 tolerance indices in the 15 winter wheat genotypes

Cumulative variance percent	Variance percent	Eagen value	YP	YS	HAM	YSI	YI	STI	GMP	MP	TOL	SSI	Indices / Principal Component
70/36	70/36	7/34	0/43	0/99	0/98	0/78	990/	950/	0/94	0/86	-0/42	-0/78	Pc1
99/79	29/43	2/94	0/90	-0/13	0/17	-0/63	12-0/	310/	0/33	0/51	0/91	0/62	Pc2

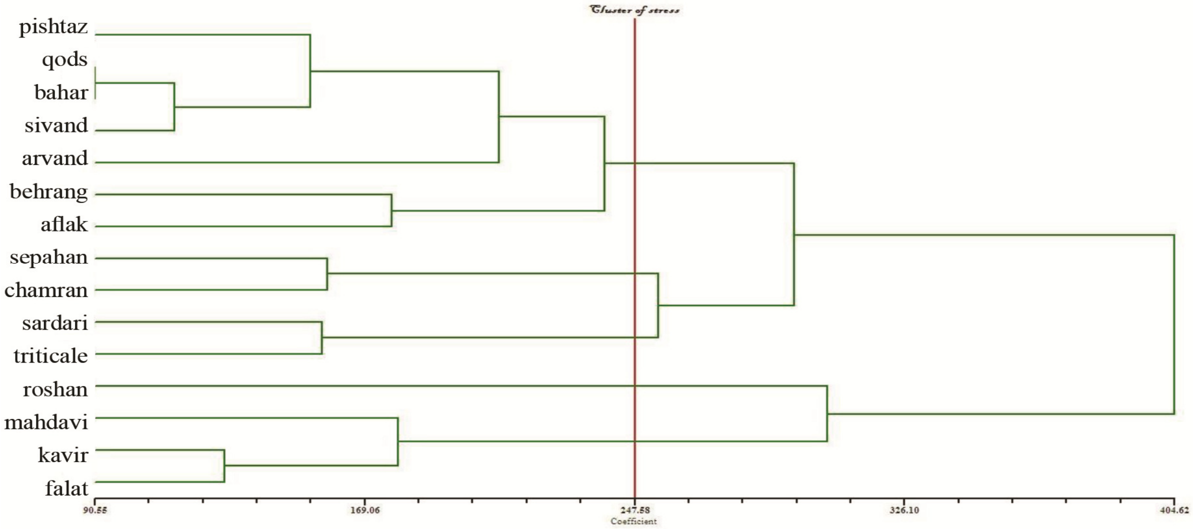

Fig.1. Dendrogram of cluster analysis based on ward's method on the measured traits in bread wheat cultivars

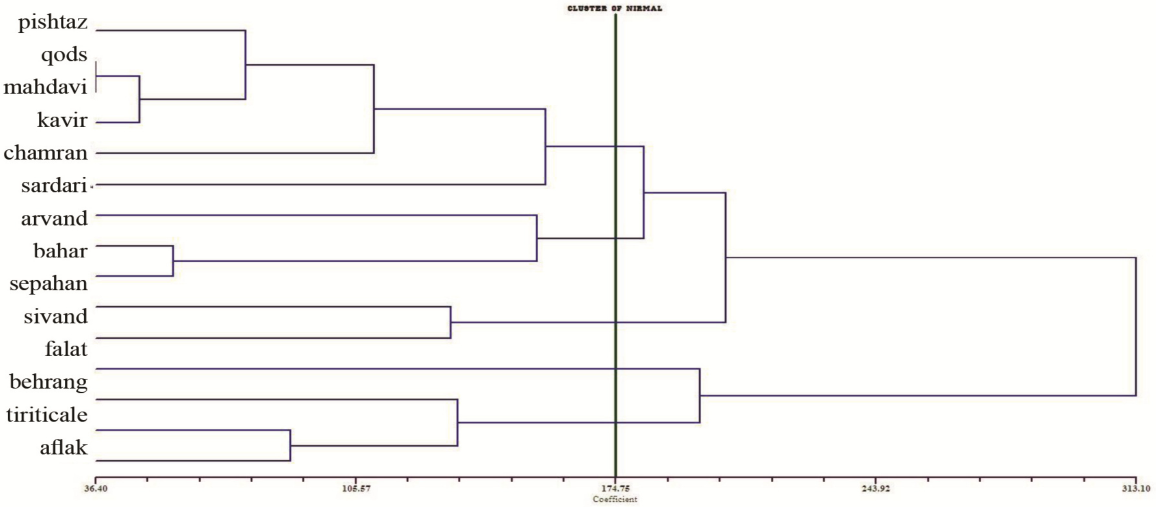

Fig.2. Dendrogram of cluster analysis based on ward's method on the measured traits in bread wheat cultivars

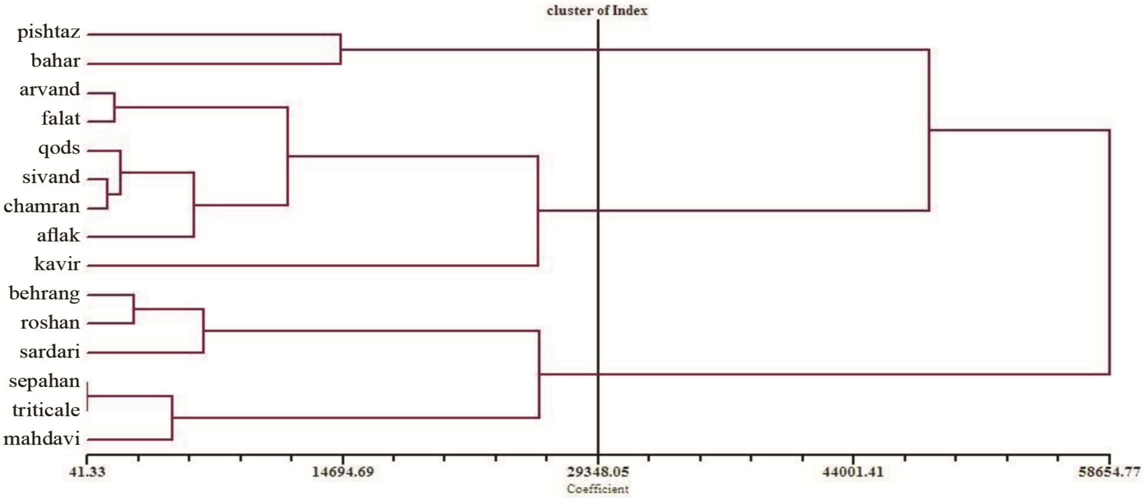

Fig.3. Dendrogram of cluster analysis based on ward's method on 8 drought tolerance indices in bread wheat cultivars

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