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GROUPING AGRICULTURAL TRAITS OF WHEAT GENOTYPES WITH CLUSTER ANALYSIS

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ABSTRACT

To group wheat genotypes based on some agricultural traits, an experiment was conducted as randomized complete blocks design with three replications in agricultural year of 2012-2013 in Garmi County. In this research, traits of plant height, number of panicle, number of grain in panicle, panicle length, Thousand Kernel Weight and grain yield were evaluated and random samples mean was used. After standardizing data, cluster analysis was done with WARD method and Square Euclidean distance coefficient and genotypes were included in 2 groups. Cluster analysis results with minimum variance method included the studied genotypes in 2 groups so that the first group with 2 genotypes included Mihan and C-89-6 genotypes were the ones which were more valuable in terms of traits of the number of panicle and grain yield. Therefore, this group can be introduced as the best group in terms of yield. The second group with 3 genotypes including genotypes C-89-19, C-89-7 and genotypes were farmers who plant height, Spike length, number of grains per Spike and 1000 grain weight had the highest average genotypes feet tall are considered. One way ANOVA results show uneven clustering validity studied genotypes.

Keyword: Wheat, Cluster Analysis, ANOVA

INTRODUCTION

Wheat (*Triticumaestivum*) is the most important crop in the world. Broad compatibility of this plant and the varied use of corn for human nutrition made it to be the most important corn in the world especially in developing countries and accounts for 20% of world's food supply (Karimi, 1993). Wheat is the main crop and today it is grown all over the world and it originates from west of Iran and east of Iraq (KazemiArbat, 1992). World food supply stated that world population will reach over than 8 million by 2030 that supplying food for this population requires more attention in science and agriculture. Despite remarkable progress in the past three decades, the annual consumption of food has only increased by about 20%. According to the estimates in 2030, the value of food production in developing countries should be 70% more than current production to be able to progress along with population growth and meet their needs (quoted by Asghari, 2011).

Among several multi-variant analysis methods, principal components analysis, cluster analysis and principal coordinate analysis are the main methods (Muhammadi and prasana, 2003). Breeding specialist is going to classify different varieties and cultivates to find their genetic distance and use their diversity in breeding program. Cluster analysis methods use mathematical formulas to classify (Farshadfar, 2000 and Brayan and Manly, 2004).

Since the numbers in each group have a less genetic distance thanthe numbers in different groups, vessel can be done based on numbers of different groups and mean values of character for each group for more efficiency of some phenomena such as Heterosis and transgressed segregation. A research on 36genotypes of winter bread wheat for morphologic divides the cluster analysis of genotypes into 7 groups (Khodadadi *et al.,* 2011). The purpose of this research grouping of some agronomic traits in bread wheat genotypes using cluster analysis and the detection.

MATERIALS AND METHODS

Specifications of Location and Plant Material:

This study was conducted to investigate yield and some agricultural traits of 5 wheat genotypes (Table 1) as randomized complete blocks design with three replications in Garmi County, one of the cold highland

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regions of Ardabil Province with latitude of 29.10 and longitude of 48.20 and height of 759 m above sea level. It is necessary to note that Mihan Cultivar along with c-89-19 and c-89-7 lines was cultivated in a farmland in Darin Kabood Village, one of the dependent regions of Moran Garmi but Zare cultivar and c-89 – 6 lines were cultivated in 2 other regions of Garmi County.

Table 1: Names of studied genotypes

Number	Genotype
1	C-89-6
2	Zare
3	C-89-7
4	C-89-19
5	Mihan

Agricultural Operations
Land preparation operations were performed according to custom of the region in September 2012 and total fertilizer of ammonium phosphate and 1.4 of urea fertilizer were spread in the farmland considering result of soil degradation and mixed with soil. The remaining fertilizer was consumed in three stages of tillering, shooting and heading. The seeds were disinfected with Vitavax fungicide before cultivation to control Ustilago tritici. The rate of seed was determined based on Thousand Kernel Weight and density of 250 grains per m2. In the first half of Farvardin (March), Granstar and Topic herbicides were used to control grass and broadleaf weeds. At time of physiological ripening, 5 plots each with area of 1 m2 were taken from each line or cultivar and marked with etiquettes and some indices relating to yield components such as plant height, number of panicle, number of grain in panicle, panicle length, Thousand Kernel Weight and grain yield were measured.

Statistical Analysis
To determine the genetic affinity of studied hybrids and group them, cluster analysis was performed using the squared Euclidean and WARD method (Hoque and Rahman, 2006). Average standardized date was used for cluster analysis and diagnosis function was used to determine where to cut the dendrogram. Statistical calculations were used using SPSS and Minitab software.

RESULTS AND DISCUSSION
In this research to cluster studied hybrids we used cluster analysis based on standardized data and WARD method. In a breeding program, the more parents are genetically far from each other, their offspring will be more aggressive, the main objective of cluster analysis is to determine the extent of genetic affinity or distance of hybrids from each other so the researcher could get an ideal genotype by accident rather append energy and time to a host of hybridization, he first cluster studied genotypes based on cluster analysis and then selects limited blocks of hybrid by choosing a hybrid of the best from far cluster considering desirable traits. So by hybrid between two a part genotypes which have been chosen from far cluster, the possibility of getting favorable results increases. The resulting dendrogram was fitted from the maximum distance among the groups based on Discriminant function and 5 wheat genotypes were included in two groups (Figure 1). Discriminant function analysis is given in Table 2 for location of dendrogram cut resulting from cluster analysis based on all traits. Results of cluster analysis with the minimum variance method was included in the studied genotypes in 2 groups so that the first group had 2 genotypes including Mihan and C-89-6 genotypes which had higher value in terms of the number of panicle and grain yield. Therefore, the group can be introduced as the best group in terms of yield. The second group with 3 genotypes included C-89-19, C-89-7 and Zare genotypes which had the highest mean in terms of plant height, Spike length, number of grain in Spike and 1000 Kernel Weight and grain yield and were regarded as tall genotypes (Table 2 and Figure 1). To ensure truth of dendrogram cutting point and compare mean of groups in terms of the measured traits for all possible groups, Multivariate Analysis of Variance was performed based on Completely Randomized design. Results of this analysis indicated the highest significant difference among groups in terms of the studied traits (Tables 1). The most ideal

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result of cluster analysis is obtained when variance within groups is minimum and variable between groups is maximum (Johnson and Wichern, 1988).

Table 2: Average and number of genotypes divided in studied groups

Mean traits

Grain yield	1000 grain weight	Number of Spike	The number of grains per panicle	Spike length	Plant height	Genotype	Cluster
3.19	33.7	36.33	65	7.85	54.15	2	1
2.61	37	26.44	70.56	8.95	60.37	3	2
2.84	35.68	30.4	68.33	8.51	57.87	Mean	
**	*	*	**	*	**	F test	
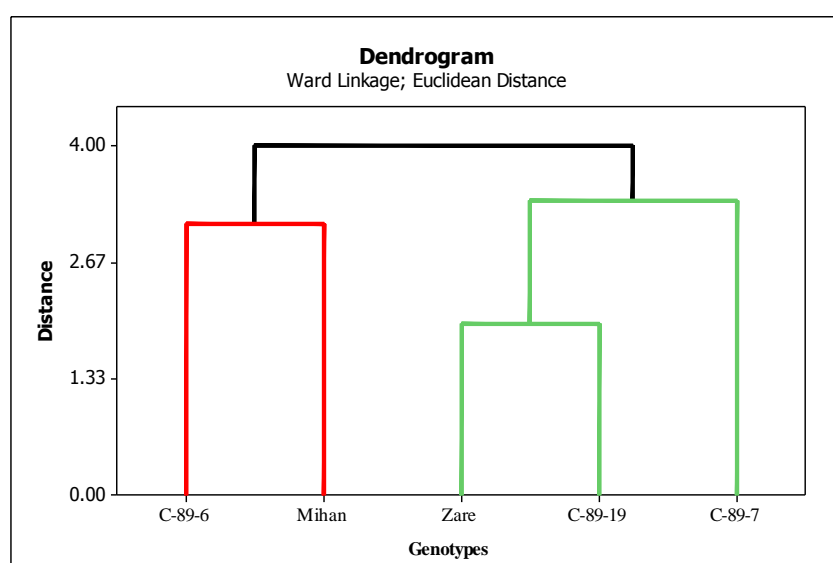
Figure 1: Genotypes divided in resulted groups from cluster analysis

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