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Research Article

GROUPING OF PROMISING AGRONOMIC TRAITS OF GENOTYPES AND LINES OF BREAD WHEAT USING CLUSTER ANALYSIS AND DETECTION FUNCTION

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ABSTRACT
In order to group 57 promising lines of bread wheat based on agronomic traits, an experiment was conducted in random block design with three replications every year at the research agriculture station and Natural Resources of Ardabil in 2013. In this study, traits of day to flowering, day to maturity, plant height and yield were evaluated. We used the mean of random samples to analyze data. After data standardization and cluster analysis was performed by Ward's method, distance coefficient by squared Euclidean distance, the promising genotypes and lines were divided into 5 groups. Detect function Dendrogram was selected as the best place to cut. First group containing 21 genotypes were less valued for all measured traits. Second group with 12 genotypes including 39, 10, 11, 34, 31, 4, 50, 49, 16, 13, 2, and the genotypes were earliest flowering in a day. Third group with 9 genotypes including 56, 15, 55, 40, 5, 5, 57, 3, 47 were early flowering and dwarf; the characteristics studied for these genotypes were of lower percent value. The fourth group with 10 genotypes including 52, 7, 42, 41, 28, 25, 27, 20, 6 and 53 were tall with other traits showing moderate value. The fifth group included genotypes such as 32, 33, 30, 12 and 48 which were tall and high yielding. Thus, the fifth could be regarded as the best one in yield. Results of one way unbalanced ANOVA and discrimination function analysis show the cluster validity of the studied genotypes.

Keywords: *Bread Wheat, Cluster Analysis, Discrimination*

INTRODUCTION
Wheat (*Triticum aestivum*) is the most important edible crop in the world. Broad compatibility of this plant and the varied use of corn for human nutrition made it the most important crop in the world especially in developing countries and accounts for 20% of world's food supply (Karimi, 1993). *Triticum* species within 3ploid is composed of diploid (2n=2x=14), Tetraploid (2n=4x=28) and Hexaploid (2n=6x=42). At the moment 11 diploid species, 11 to 12 tetraploid species and 6 species hexaploid *triticum* were recognized. Only two *Triticum* species are important commercially including Hexaploid (*T. aestivum*) bread wheat and wheat is business and tetraploid (*T. durum*) which is used for making macaroni (Qasemi, 2013).

Most human societies, especially the low- income communities, wheat is the main food supply (Institute of Business studies and Research, 1992). 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 (Arbat, 1992). Age of wheat remains, which were obtained from the excavation of Zharmo near Sulaimaniya in Iraq was traced by radioactive carbon dating 10,000- year life (Karimi, 1993). According to FAO statistics, wheat planted area (dry-farming and acqua-culture) in 2011, around 704 million tons hectare, namely it makes 16% make 16% of the worldwide total cultivated lands and it is produced for 601.5 million tons. During this year major wheat-producing countries range in order of value importance including china (120 million tons), India (68.7 million Tons), U.S.A (68.2 million tons), Russia (42 million tons). Hectare yield of wheat worldwide in 1669-1998 is 223776000 tons which around 16% of total lands are arable. Wheat planted area in Iran in crop years 75-76 was around 2.27 million hectors, that is, it is produced 10 million tons, in which 7.1 million tons is related to acqua farming and 2.9 million tons are related to dry-culture. During the

mentioned crop year, wheat yield averaged 1595 kg ha (aqua and dry farming) which represents 60% of the average world production (FAO, 2011).

World population will reach over than 8 million by 2030. Despite remarkable progress in the past three decades, the annual production of food has increased by 20%. According to an estimate, by 2030, the food production in developing countries should be 70% more than current production to be able to meet the demand of the people (Asghari, 2011).

Knowing the physiological traits affecting yield limiting factors and their inheritance for designing more exact plans and for improving yield potential genetically is really necessary (Haul, 2001). 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; Brayan and Manly, 2004).

Since the numbers in each group have a less genetic distance than the numbers in different groups, breeding can be done based on numbers of different groups. A research on 36 genotypes of winter bread wheat for various morphological traits was carried out and they were divided using cluster analysis of genotypes into 7 groups (Khodadadi *et al.*, 2011). In a study to measure the genetic diversity of tetraploid wheat in Ethiopia, cluster method and principal components analysis were used; the results from these two methods were the same (Hailu *et al.*, 2006). The study aims at classifying some of agronomic traits of promising 57 promising genotypes and lines of bread wheat using cluster analysis and diagnosis function.

MATERIALS AND METHODS

We received 65 seed varieties and promising lines of bread wheat from research center for Agriculture and Natural resources of Ardabil. During 2012-2013 in random block designs with three replications, seeds were planted in station of Agriculture Research and Natural Resources of Ardabil. The sowing was done in second half of Mehr and each plot consisted of 5 rows with a planting density of 300 plants square meter. Since 8 genotypes couldn't grow due to damage by storage pests therefore 8 genotypes were removed and the experiment was performed with 57 genotypes. Phonological traits, day to flowering and day to mature during growing period were recorded with regards to 50% flowering plants. Plant height was also measured in an average, 5 plants selected randomly. After plants matured, two lateral bush rows were considered as margins, and seed yield was obtained from 3 middle rows and the area of half a square meter. To determine the genetic affinity of studied hybrids and to 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, more the parents are genetically far from each other, more will be the aggressiveness among the offspring. The main objective of cluster analysis is to determine the extent of genetic affinity or distance of hybrids fromeach 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 hybridby choosing a hybrid of the best from far cluster considering desirable traits. So by hybrid between two apart genotypes which have been chosen from far cluster, the possibility of getting favorable results increases? The resulted dendrogram was cut from the location of the maximum distance between groups on the basis ofdiagnosis function and 57 promising varieties and lines of bread wheat were placed in 5 groups (figure 1).

The diagnosis function analysis for determining cut site of dendrogram from cluster analysis based on all traits is given in table 2. The results from cluster analysis was placed in 5 groups of studied genotypes

based on minimum variance method, so that the first group with 21 genotypes including 46, 45, 1, 29, 44, 23, 36, 37, 22, 14, 19, 54, 18, 8, 38, 24, 17, 51, 26, 9, and 43 which their traits measured and were less

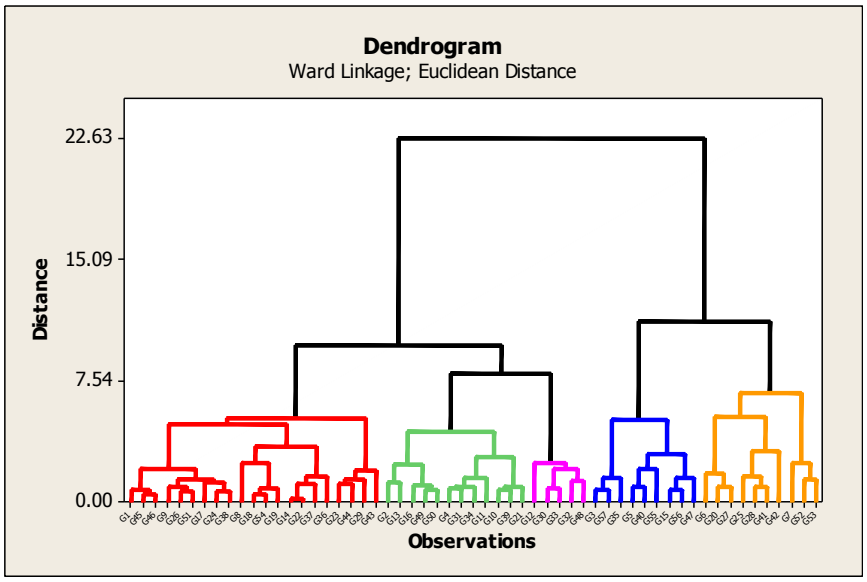

Figure1: Genotypes divided in resulted groups from cluster analysis

valued. The second group with 12 genotypes includes 39, 10, 11, 34, 31, 4, 50, 49, 16, 13, 2 and 21 which were the latest group in day to flowering. The third group with 9 genotypes including 47, 56, 15, 55, 40, 5, 35, 57, 3, which were dwarf and early flowering and were less valued regarding other characters. The fourth group with 10 genotypes including 52, 7, 42, 41, 28, 25, 27, 20, 6 and 53 which tall- feet and were moderate considering other properties. The fifth group with genotypes including 32, 33, 30, 12 and 48 which more high- feet and high yield so this group can be regarded as the best one considering yield (table 1 and figure1).

To ensure more accurate cut off of dendrograph and in order to compare group average in measured traits for all groups, multi-variant of variance analysis was performed based on random unbalanced design. Results from this analysis indicated the greatest significant difference among groups in studied traits, as well as it showed the analysis of diagnosis function of classification and accuracy of the studied genotypes (Tables 1 and 2). The most desired result from cluster analysis is obtained if the variance within the groups is the least one and the variance among groups is the most one (Johnson and Wichern, 1988).

Table 1: Average and number of genotypes divided in studied groups

Cluster	Number of genotypes	Average Traits			
		Days to flowering	Days to maturity	Plant height	Yield
1	21	124.947	175.88	1.12	4710.5
2	12	127.53	175.13	1.17	4903.8
3	9	122.211	174.84	1.03	4629.9
4	10	123.39	173.86	1.19	4018.9
5	5	126.52	177.72	1.19	5276.1
Average total		124.99	175.36	1.13	4666.8
F test		**	**	**	**

Table 2: Results from analysis of diagnosis function based on groups from cluster analysis

Functions	Wilks' Lambda	Chi-square	df	Prob.
1 to 4	0.042	163.4	16	0.000
2 to 4	0.242	73.02	9	0.000
3 to 4	0.755	14.46	4	0.006
4	0.984	0.805	1	0.37

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