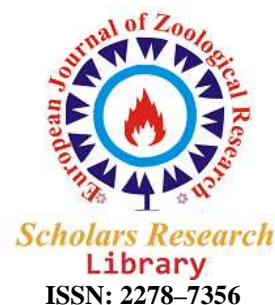




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Assess the genetic diversity in some wheat genotypes through agronomic traits

Farzaneh Pordel-Maragheh

Young Researchers Club, Ardabil Branch, Islamic Azad University, Ardabil, Iran

ABSTRACT

In order to evaluate the genetic diversity in some wheat genotypes through agronomic traits, an experiment was conducted in a randomized complete block design with 9 wheat promising lines and Shahriar cultivar (control) and two replications at Agricultural and Natural Resources Research Station, located 12 km south of Ardabil (Khalkhal road) in 2012. Traits such as, total number of tillers, number of fertile tillers, number of infertile tillers, spike length, grain weight per spike, plant height, biologic yield, peduncle length and weight, seed weight, days to flowering, days to maturity, harvest index and grain yield were measured in this study. Cluster analysis was used based on standardized data and WARD to classify the studied genotypes. cluster analysis were classified into three groups: the second cluster that included genotypes 2 and 3 were high value in terms all evaluated properties excluding peduncle weight, this cluster accounted for the highest average in terms of performance. So to increase the performance, it can be used the clusters genotypes in the hybrids. Estimate the phenotypic and genotypic coefficients for different traits indicated that genotypes had greater genetic diversity in terms traits such as total number of tillers, number of fertile tillers, number of infertile tillers, spike length, peduncle weight, days to flowering and days to maturity than other traits. Therefore, they can be used as selection criteria to improve yield.

Keywords: wheat, genetic diversity, morphological traits, cluster analysis

INTRODUCTION

Wheat with scientific name *Triticum aestivum* is the first cereal and most important crop in the world [1]. High adaptability and diverse uses of this crop in human nutrition has caused that it be considered as the most important crops in the world, especially in developing countries. Wheat constitutes about 22% of the world's food supplies [2]. Regarding the fact that the world population as of the beginning of 21st century is already more than 6 billion people which more than 700 millions of them are struggling with the lack of food and famine and up to 3 billion suffer from malnourishment [3]. With irregular and uncontrolled increase of world population it is predicted that the world it will reach 8 billion people by year 2020, from which 6.7 billion live in developing countries. Therefore, one of the politically, economically and socially important issues, especially in developing countries, is to supply for food requirements of vast human population [4].

Wheat is not an only important commodity but it is as the best weapon in the world that its strategic importance is increasing day by day. Wheat bread has particular importance as the main food in the country. In addition, need for its presence is completely tangible as political economy weapon [2]. The most important wheat consumption is for human nutrition in the world. It is also used in the rearing livestock, making paper and many other industries [5].

Apart from its important commercial aspect in the world, wheat is an increasingly functional tool in political and global relations. Although Iran boasts only around 1% of the world population, it consumes roughly 2.5% of wheat produced in the world. Wheat is a strategic good like energy and is considered one of the important indices of agriculture [6].

Therefore, it is highly important to investigate the genetic variation of the varieties and lines of this plant in breeding programs. Results from an experiment conducted by Heydari et al. [7] in order to examine the genetic variation of various traits in 157 replication haploid lines of bread wheat, suggested that these lines were of more genetic variation in terms of traits such as last internode length, number of fertile spike per unit area, plant height, grain number and grain yield per main spike than other ones including volumetric weight of grain, days number to maturity, days number to heading and anthesis. Golabadi et al. [8] after studying the genetic variation of 300 durum wheat genotypes reported that these genotypes are of significant variation for traits such as grain yield, harvest index and spike number per unit area. Additionally, in their study grain yield had a positively significant correlation with harvest index, biological yield, day's number to maturity, grain number per spike and grain weight per spike.

Geravandi and Kahrizi [9] the genetic diversity of 20 wheat genotypes reported that evaluated genotypes have greater genetic diversity in terms of yield, number of spikes per square meter, number of grains per spike, spike density and length of awn than other traits. Mahfouzi et al. [10] after examining breeding methods to increase wheat yield in cold and arid areas of Iran reported that genetic variation among genotypes may contribute to the grain yield increase in arid areas.

Shahryari et al. [11] in their study to examine the genetic diversity among 18 bread wheat genotypes in terms of phenological and morphological traits, demonstrated that the genotypes were genetically more diverse in terms of traits such as plant height, weight of 1000 grains, grain number per spike, spike length, spike weight, peduncle length, peduncle weight and grain yield than in terms of other traits.

This study were performed to identify the genotype or genotypes with high yield, introduce effective traits in grain yield to the wheat breeding for use in breeding programs and to identify far and near groups of genotypes to use them in appropriate crosses.

MATERIALS AND METHODS

This experiment was conducted at Agricultural and Natural Resources Research Station, located 12 km south of Ardabil (Khalkhal road) in 2012. In the study 9 wheat promising lines and Shahriar cultivar (control) (Table 1) was performed based on randomized complete block design with two replications in 2012. The station has a cold semi-arid climates, the temperature is often below zero in winter. Altitude is 1352 mm, average rainfall 307.1 mm, longitude length and width 48° and 15' of eastern longitude, 38° and 15' northern latitude. The average annual minimum and maximum temperatures is respectively 1.98 and 18.18 and the maximum absolute temperature is 21.8° C. Seed consumption has been 452 seeds per square meter and fertilizer consumption rate based on soil test results has been 92 kg nitrogen and phosphate and 62 kg potassium. Thus, total phosphorus and potash fertilizer was used in the autumn and nitrogen fertilizer was used at three stages tillering and heading. Broadleaf weed control was performed using 2, 4-D herbicide in the tillering stage. During the growth period characteristics such as time to 52% flowering and physiological maturity were recorded. Half-foot three lines were harvested when crop handling and the average of three samples, unfertilized spike dry matter per unit area and harvest index were determined. Plant height and number of grains per Spikes was measured the average of 12 spikes randomly harvested. Yield per unit of harvested crop were measured from each plot. Seed weight was measured after final harvest of the plots. Traits such as, total number of tillers, number of fertile tillers, number of infertile tillers, spike length, grain weight per spike, plant height, biologic yield, peduncle length and weight, seed weight, days to flowering, days to maturity, harvest index and grain yield were measured in this study. Analysis of variance and mean comparison was performed between the traits by Duncan test at 5% level. Environmental, genetic and phenotypic variance and general heritability was also estimated. Mathematical of squares mean was used in variance analysis table to estimate the genetic variance. To estimate the heritability, the following formula was used:

$$h^2_b = \sigma^2_g / (\sigma^2_g + \sigma^2_e / r)$$

In this formula: σ^2_g is the genetic variance; σ^2_e is the environmental variance and r is the number of occurrences. Real genetic variance was calculated due to Mathematical MS from the following formula:

$$\sigma^2_g = \text{MST} - \text{MSE} / r$$

Statistical analysis was used using softwares MSTAT-C and SPSS-18.

Table 1 – List of study genotypes in this investigation

C-86-1	Shahryar
C-86-2	C-80-4
C-86-3	Bloudan/3/Bb/7C*2//Y50E/3*Kal/4/MV 17
C-86-4	Yan 7578. 128/4/Chil/24*Star
C-86-5	Yan 7578. 128/5/Chil/2*Star
C-86-6	Yan 7578. 128/6/Chil/2*Star
C-86-7	ID800994W/Vee//F900K/3/Pony/Opata
C-86-8	Bhr*5/Aga//Sni/3/Trk13/4/Drc
C-86-9	Bilinmiyen 96. 40
C-86-10	LC 909 Mima

RESULTS AND DISCUSSION

Results the variance analysis in the agronomic and morphological traits showed (Table 2) that there are significant differences between 10 wheat genotype in terms traits such as number of fertile tillers, number of spike per square meter, grain weight per spike, peduncle weight, days to flowering, days to maturity, harvest index, grain yield (at 1% level), biological yield and thousand grain weight (at 5% level) that indicates there is variation among the genotypes but there is no significant difference in terms traits such as the number of infertile tillers, plant height and peduncle length. This indicates that the studied genotypes are close to each other in terms these traits.

Coefficients of variation (CV %) except for plant height and number of infertile tillers was below 22% for other traits which indicate a high accuracy measurement or experimental error are low. As can be seen, there was significant difference between genotypes for agronomic and morphological traits at 1% level.

In this study, genotypes were classified using cluster analysis based on standardized data and WARD. Cluster analysis was cut the location of the maximum distance between the groups, based on detection function and 9 promising lines was located with shahriar cultivar (control) into three groups (Figure 1). To determine the incision and classification the equation \sqrt{n} . 2 data and were classified to \sqrt{n} . 2. The discrimination function analysis to determine cutting the dendrogram are shown in table 3 based on all traits. To distinguish the characteristics for each group in terms studied traits, the mean of each cluster and mean deviation in each cluster were calculated out of the total (Table 4). Cluster which has had higher average about trait than total average can be recommended as a parent for crosses. cluster analysis were classified into three groups: the second cluster that included genotypes 2 and 3 were high value in terms all evaluated properties excluding peduncle weight, this cluster accounted for the highest average in terms of yield. So, it can be used the clusters genotypes in the hybrids to increase yield.

Determining an appropriate method for correcting population depends on heritability of traits which is needed to be reformed. Genetic variance among recombinant inbred lines is an addition of the two increasing variances of the main population [12]. Heritability of a trait shows that how much of the varieties among individuals (phenotype) can be associated to genotype of them and how much the environment is effective in this issue. It is obvious that if the heritability of a trait be high then it can be hoped that by selecting individuals with improved quality there will be a better result [13]. Heritability of grain yield was lower than the yield components. Heritability for grain yield was respectively 64.73 (Table 5). This suggests that grain yield has been more influenced by environmental factors compared with its components. This question is also mentioned by Heydari et al [7] and Garavandi and Kahrizi [9]. Farzi and Shecari Mustali Baglu [14] showed that the highest heritability is related to the peduncle length and weight respectively is 87% and 81% and the lowest heritability is related to the plant weight and harvest index.

Although Erskin and Goodrich [15] by studying 23 genotypes which were collected from different countries, have reported the heritability of this trait as 77% and Khdavirdi [16] in his research has reported it as 93% in Kurt unit and 60% in a single plant unit, it seems that in Erskin and Goodrich [15] study the 23 genotypes was little and cannot be considered as a good criterion and in the research developed by Khdavirdi [16] the high genetic variance led to his result.

However, in this study, the heritability in general concept for all the studied traits was estimated between 99.43 – 38.12 percent (Table 5).

Table 2 - Variance analysis of studied traits

S. O. V	df	MS						
		total number of tillers	the number of fertile tiller	the number of infertile tiller	length of spike	grain weight per spike	plant height	Biological yield
Replication	1	56.23	2.1	3.73	1.562	0.112	735.4	1963.3
Genotypes	9	869.98**	905.9**	4.83	487.88**	1.209**	293.9	6236.9*
Error	18	65.41	2.58	0.47	37.114	0.152	695.7	1935.9
CV%		4.05	0.82	35.21	5.88	14.45	28.31	19.33

* and ** Significantly at $p < 0.05$ and < 0.01 , respectively.

Table 2 – Continued

S. O. V	df	MS						
		Peduncle length	Peduncle weight	1000 grain weight	Harvest index	Days to flowering	Days to maturity	Grain yield
Replication	1	54.75	0.001	30.75	3.9	0.001	3.55	3.83
Genotypes	9	31.76	0.009**	132.8*	32.31**	7.46**	118.9**	0.855**
Error	18	14.23	0.01	513.57	0.937	0.667	21.92	0.183
CV%		10.02	13.22	14.34	0.7	0.46	9.18	14.29

* and ** Significantly at $p < 0.05$ and < 0.01 , respectively.

Table 3 - Analysis of detection function to determine the cutting location resulting from cluster analysis based on all traits

Test of Function(s)	Wilks' Lambda	Chi-square	Sig.
1	0.002	25.93	0.026
2	0.103	9.08	0.017

Table 4 – Average, deviation from the total mean in three clusters from cluster analysis for all traits

Cluster	Number	total number of tillers (m ²)	the number of fertile tiller (m ²)	the number of infertile tiller (m ²)	length of spike (m ²)	grain weight per spike (gr)	plant height (cm)	Biological yield
1	6	178.70	172.5	6.34	98.99	2.18	94.99	217.7
2	2	189.10	185.2	3.92	102.7	3.2	99.95	219.2
3	2	168.1	159.3	9	95.41	1.8	88.47	242.2
Total Average		178.6	172.40	6.38	99.01	2.31	94.68	222.9

Table 4 continued

Cluster	Number	Peduncle length (mm)	Peduncle weight (gr)	1000 grain weight (gr)	Harvest index (%)	Days to flowering	Days to maturity	Grain yield (ton/ha)
1	6	36.41	0.26	44.09	46.96	136	175.50	2.67
2	2	37.57	0.26	53.32	54.9	139.3	177	3.09
3	2	33.83	0.3	42.62	42.18	133.6	173.3	1.96
Total Average		36.12	0.28	45.64	47.59	136.2	175.4	2.61

Table 5 - Amounts of genetic and phenotypic and environmental variance and the heritability of evaluated traits

Traits	Mean	σ^2_e	σ^2_g	σ^2_{ph}	heritability
total number of tillers	178.60	65.41	402.28	467.70	86.01
the number of fertile tiller	172.4	2.58	451.66	254.24	99.43
the number of infertile tiller	6.38	0.47	2.18	22.65	82.26
length of spike	99.01	34.114	225.38	262.5	85.86
grain weight per spike	2.31	0.152	0.529	0.681	77.74
plant height	94.68	695.7	-	-	-
Biological yield	222.9	1935.9	2150.5	4086.4	52.62
Peduncle length	36.12	14.23	8.765	22.99	38.12
Peduncle weight	0.28	0.01	0.45	0.46	97.82
1000 grain weight	45.64	51.57	40.62	92.18	44.06
Harvest index	136.20	0.937	15.68	16.62	94.32
Days to flowering	175.40	0.667	3.39	4.06	83.43
Days to maturity	47.59	21.92	48.49	70.41	68.86
Grain yield	2.61	0.183	0.336	0.519	64.73

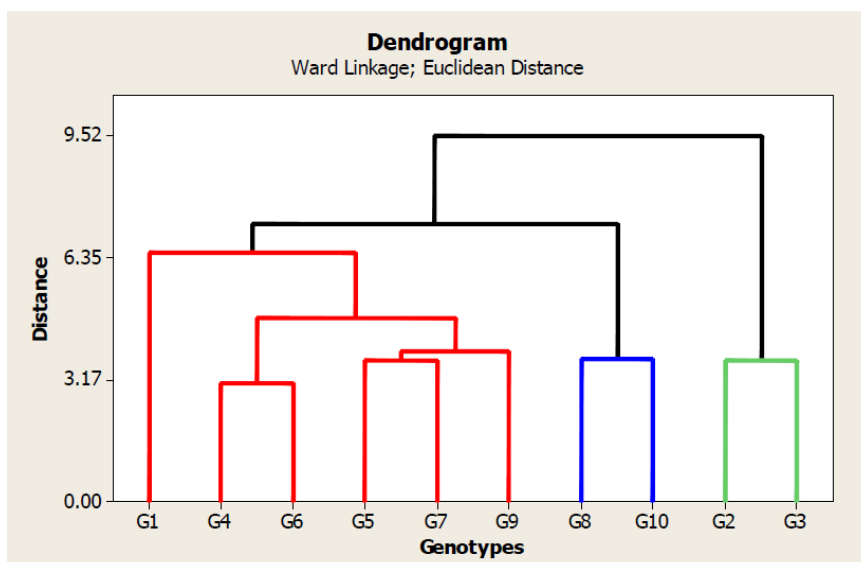


Figure 1 - Dendrogram resulting from the cluster analysis by variance method (Ward) based on all traits

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