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Genetic variation of several bread wheat (*Triticum aestivum* L.) genotypes based on some morphological traits

Zróżnicowanie genetyczne kilku genotypów pszenicy zwyczajnej (*Triticum aestivum* L.) na podstawie niektórych cech morfologicznych

Summary. The genetic diversity among 56 bread wheat (*Triticum aestivum* L.) genotypes was evaluated by 18 agronomical traits in the experimental field at Maragheh, Iran. Significant differences among bread wheat genotypes in all of the measured traits i.e. stem diameter, plant height, leaf number, leaf length, leaf width, tiller number, internode length, peduncle length, spike length, floret number, spikelet number, grain number, length of awn, grain diameter, grain length, the number of days to flowering, thousand seed weight and grain yield. The coefficient of variation (CV) was high for grain yield (25.61%), number of tillers per plant (22.06%) and number of grains per spike (21.45). The other remaining traits recorded moderate to low CV estimates from 14.30% in grain number per spike to 4.81% in days to flowering. The largest thousand seed weight was 45.93 g, the lowest thousand seed weight was 26.16 g and the mean thousand seed weight was 37.85 g. The mean performance of grain yield was 5031.2 kg ha^{-1}, the minimum grain yield was 2835.0 kg ha^{-1} and the maximum grain yield was 7125.3 kg ha^{-1}. Ward's minimum variance cluster analysis based on squared Euclidian distance on the raw data of 18 agronomic traits clearly separated five clusters. In general, cluster analysis of the 56 genotypes based on the selected agronomic traits was consistent with known information. Our plant materials could be important germplasm resources for enriching the genetic background of commercial cultivars. Such genetic differences of bread wheat traits studied in this investigation can be applied as a new source of variation in other breeding programs and crossing nurseries in breeding program.

Key words: agronomic traits, bread wheat, cluster analysis, genetic diversity

INTRODUCTION

Bread wheat is an important cereal crop of Iran, and based on area and production it ranks first in cereals, which is provides more nourishment for the people of the world than any crop, and provides the nutrition for the greater part of the world population. Statistics of Iran show that in 2012 winter wheat was grown on a total area of 7.000.000 ha with total production of 13.800 thousand tones and average yield 2 t ha^{-1}, according to the data of FAOSTAT [2012]. During the last decades, good progress has been made in increasing the unit area yield of wheat, but by comparing the mean wheat yield in Iran with the mean yield of wheat in the advanced countries, we are still outlying at the rear. The important objective of plant breeding is the development of genotypes combining high yielding with good quality and a great success of developing favorable wheat genotypes has been made through genetic improvement [Knezevic *et al*. 2008; Sonmezoglu *et al*. 2012]. Breeders associated the progress in plant improvement with the presence of diverse plant material with new germplasm [Mangova and Rachovska 2004].

Grain yield is the complex trait which is result of yield components (number of plant per area, number of grain per spike, grain weight) as well as other related traits such as plant height, number of spikelets per spike and other traits and also it is influenced by genotype and agro ecological conditions [Drezner *et al.* 2007; Atkinson *et al*. 2008]. Several morphological traits have been identified to influence on grain yield by many researches [Goral *et al*. 2005; Knezevic *et al*. 2008; Aliu and Fetahu 2010]. The global climatic changes and the increasing population lead to stronger emphasis on high yielding genotypes as well as on the high quality property of the new wheat genotypes. Many breeders improve new genotypes, in order to achieve higher production, and demands of the population [Mangova and Rachovska 2004; Sonmezoglu *et al*. 2012]. Bread wheat is produced under a wide range of climactic environments and due to its high adaptability with various environments; its distribution range is more than any other crop. Morphological traits can be used to characterize genetic diversity and in plant breeding programs, it is desirable to have large genetic diversity for the creation of new genotypes. The aim is to measure the genetic similarity and genetic distance among genotypes, which can be used to estimate the expected genetic variation in different combinations of progeny [Gegas *et al.* 2010; Sonmezoglu *et al*. 2012]. In general, the investigation of genetic diversity has two major targets (i) analysis of the levels of polymorphism among individuals and (ii) research of the distribution of polymorphism. Genetic diversity can be assessed form pedigree analysis, morphological traits or molecular markers and it is the material basis for crop improvement [Knezevic *et al*. 2008; Habash *et al*. 2009].

It is important to investigate the genetic variation of the wheat genotypes in breeding programs. According to Mollasadeghi *et al.* [2012], last internode length, number of spike per unit area, plant height and grain number showed more genetic variation. Selection for grain yield could be useful if sufficient genetic variability is present in the genetic material and genotypic association is important in determining the degree to which various yield contributing traits are associated with grain yield. There are several different genetic resources for wheat improvement that commercial cultivars have been the preferred ones due to their ease of crossing. They are genetically homozygous but usually heterogeneous because of non-intense selections by farmers. The characterization of commercial cultivars is crucial for exploiting the genetic variability for various traits.

Genetic diversity in resources can be identified by several methods such as morphological screening and morphological traits of wheat have been used for the identification of genetic diversity and selection criteria in breeding programs [Salem *et al.* 2008; Akcura 2011]. The objective of this paper was to determine variations among examined bread wheat genotypes using morphological data and grain yield waht this information will be useful to improve the developing wheat cultivars.

MATERIALS AND METHODS

In this study, 56 bread wheat genotypes as cultivars or breeding lines from Iran origin were characterized by using morphological characters (Tab. 1). The bread wheat genotypes were kindly provided by the Gene Bank, Seed and Plant Investigation Institute, Iran. The wheat genotypes were subjected to morphological observations. Seeds were cultivated in an experimental and distributed randomly to minimize the environmental effects. The wheat genotypes were sown in a randomized complete block design layout with three replications. The fertilizer application was performed before sowing, 60 kg ha^{-1}of N, 30 kg ha^{-1} of P and 20 kg ha^{-1} of K were broadcast on the surface and tilled into the soil and the weeds were controlled chemically. Normal agronomic and cultural practices were applied to the experiment through out the growing season according to local practices.

Table 1. The name and type (cultivar or line) of 56 wheat genotypes which were from Iran origin
Tabela 1. Nazwa i typ (odmiana lub linia) 56 genotypów pszenicy poochodzących z Iranu

Code Kod	Name Nazwa	Type Typ	Code Kod	Name Nazwa	Type Typ	Code Kod	Name Nazwa	Type Typ
G1	Niknezhad	cv.	G20	C-85-9	ln.	G39	Chanab	cv.
G2	Alvand-1	cv.	G21	Arvand	cv.	G40	Sorkhtokhm	cv.
G3	Shahpasand	cv.	G22	Hirmand	cv.	G41	C-84-5502	ln.
G4	Pishtaz	cv.	G23	Zagros	cv.	G42	Omid	cv.
G5	Marvdasht	cv.	G24	Shiroodi-1	cv.	G43	Akbari	cv.
G6	Golestan	cv.	G25	Zarin	cv.	G44	Tabasi	cv.
G7	MS-81-14	ln.	G26	Azar-2	cv.	G45	Shiraz	cv.
G8	C-85-11	ln.	G27	C-85-13	ln.	G46	Ln. A	cv.
G9	Sepahan	cv.	G28	Alvand-2	cv.	G47	Mahdavi-1	ln.
G10	C-84-55-B	ln.	G29	Verinak	cv.	G48	Mahdavi-2	ln.
G11	Chamran	cv.	G30	C-85-5512	ln.	G49	B-Roshan	cv.
G12	Norstar	cv.	G31	Roshan-2	cv.	G50	Shahriar	cv.
G13	Karaj-3	cv.	G32	Ghods	cv.	G51	Bahar	cv.
G14	Sabalan	cv.	G33	Cross-Shahi	cv.	G52	Kavir	cv.
G15	Arta	cv.	G34	Tous	cv.	G53	Shiroodi-2	ln.
G16	Alborz	cv.	G35	Moghan-1	cv.	G54	Falaat-2	cv.
G17	Bayat	cv.	G36	CDC-Ospray	cv.	G55	Sistan	cv.
G18	C-85-8	ln.	G37	Falat-1	cv.	G56	Saison	cv.
G19	Roshan-1	cv.	G38	Tajan	cv.			

cv. – cultivar – odmiana
ln. – line – linia

Data were recorded for 15 morphological characters of ten randomly selected plants, as follows: stem diameter (SD), plant height (PH), leaf number (LN), leaf length (LL, in cm; Leaf length was defined as the distance from the tip of the leaf to the connecting point of the main stem), leaf width (LW, in cm; Leaf width was measured as the widest region across the lamina perpendicular to the length), tiller number (TN), internode length (NL, in cm, length of five internodes from the genotypes), peduncle length (PL, in cm, uppermost internode), spike length (SL), floret number (FN), spikelet number (SN), grain number (GN), length of awn (AL), grain diameter (GD, in mm), and grain length (GL, in mm). The numbers of days from sowing to flowering, (Zadoks Scale = 60; generally, flowering in wheat begins within three or four days after head emergence) (DF), thousand seed weight (TS) and grain yield (GY, kg ha^{-1}) of each plot traits were measured. Normality test using Shapiro-Wilk method was performed and the means of 18 agronomic traits were used for clustering analyses. Pair-wise distances between the genotypes based on squared Euclidian distance on the raw data of measured agronomic traits were calculated. Ward's minimum variance cluster analysis [Ward 1963] was used to group the tested accessions in the experiment using the statistical software SPSS (version 14, SPSS Inc 2004).

RESULTS

ANOVA indicated significant difference for all of the measured traits of 56 wheat genotypes (results are not shown) and these findings could be a result of large variation among wheat genotypes. Large genetic variation reflects genetic differences and such considerable range of phenotypic variations provided a good opportunity for grain yield improvement of wheat. Days to flowering ranged from 80 to 90 days and its mean for the wheat genotypes was 85.24 days, thus it is possible to use this plant materials for selection of early flowering in wheat (Tab. 2). The mean stem diameter was 3.19 mm and varied from 1.90 to 4.50 mm. The tallest wheat genotype was 114.12 cm, while the shortest one was 47.06 cm and the mean plant height was 83.57 cm. It seems that there is good genetic variation for plant height in measured wheat genotypes and could be used for developing new dwarf cultivars. Mahmood *et al.* [2006] obtained different results for wheat plant height from 62 cm to 110 cm, while Aliu and Fetahu [2010] realized range 71 to 79 cm for plant height in different bread wheat genotypes.

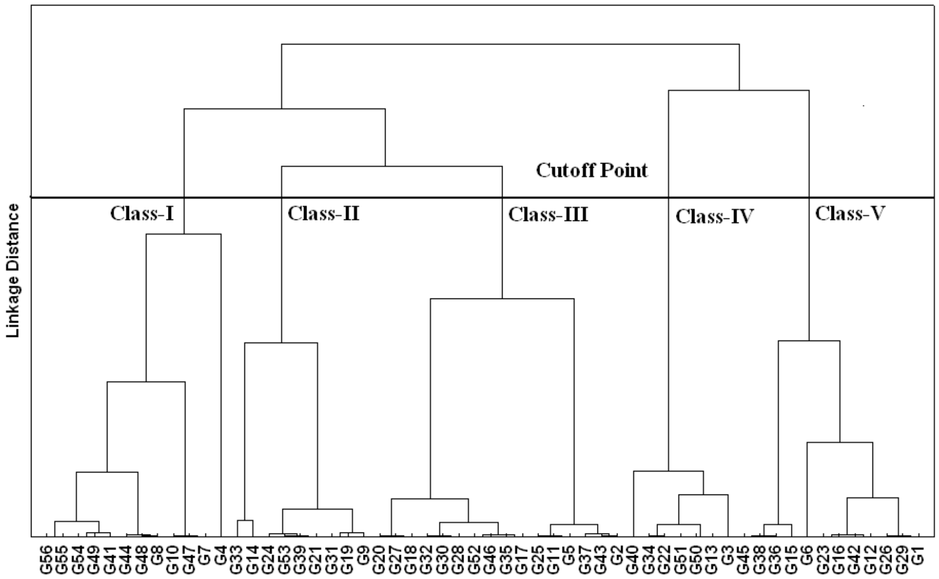
The minimum number of leaves at flowering time was 4, the maximum number of leaves at flowering time was 8, and the mean leaf number was 5.57 (Tab. 2). The leaf length ranged from 7.84 to 24.51 cm and its mean was 14.81 cm while, the leaf width ranged from 4.00 to 12.10 cm and its mean was 8.75 cm. The lowest tiller number was 1 and the highest tiller number was 6, while the mean tiller number was 2.32 (Tab. 2). The estimate coefficient of variation (CV) was high for number of tillers per plant (22.06%). Similar large CV amount was reported for tiller number of wheat by Mollasadeghi *et al.* [2012]. The longest last internode length was 21.05 cm and the shortest one was 10.53 cm while the mean of last internode length was 15.05 cm. According to Austin and Jones [1975], most magnitudes of the wheat plant height variations are attributable to differences in internode length rather than internode number.

Table 2. Descriptive statistics of the measured traits in 56 wheat genotypes
Tabela 2. Statystyka opisowa badanych cech u 56 genotypów pszenicy

Traits – Cechy	Code Kod	Mean Średnia	Minimum	Maximum Maksimum	Range Zakres	CV
Days from sowing to flowering Dni od siewu do kwitnienia	DF	85.24	80.00	90.00	10.00	22.60
Stem diameter Średnica łodygi	SD	3.19	1.90	4.50	2.60	19.01
Plant height – Wysokość roślin	PH	83.57	47.06	114.12	67.06	18.91
Leaf number – Liczba liści	LN	5.57	4.00	8.00	4.00	21.83
Leaf length – Długość liści	LL	14.81	7.84	24.51	16.67	18.15
Leaf width – Szerokość liści	LW	8.75	4.00	12.10	8.10	19.78
Tiller number – Liczba źdźbeł	TN	2.32	1.00	6.00	5.00	25.46
Internode length Długość międzywęźli	NL	15.05	10.53	21.05	10.52	24.59
Peduncle length – Długość dokłosia	PL	28.11	18.83	37.25	18.42	20.62
Spike length – Długość kłosów	SL	7.10	4.53	9.66	5.13	19.89
Floret number – Liczba kwiatów	FN	13.05	7.00	19.00	12.00	18.54
Spikelet number – Liczba kłosków	SN	35.13	24.00	57.00	33.00	17.60
Grain number – Liczba ziaren	GN	2.77	2.00	4.00	2.00	25.06
Length of awn – Długość ości	AL	3.99	0.73	6.89	6.16	18.41
Grain diameter – Średnica ziaren	GD	2.96	2.18	3.61	1.43	19.29
Grain length – Długość ziaren	GL	6.49	5.14	7.84	2.70	18.45
Thousand seed weight Masa tysiąca ziaren	TS	37.85	26.16	45.93	19.77	21.06
Grain yield – Plon ziaren	GY	5031.2	2835.0	7125.3	4290.3	25.47

The mean peduncle length was 28.11 mm, the minimum peduncle length was 18.83 mm and the maximum one was 37.25 mm. The longest spike length was 9.66 cm, the shortest one was 4.53 cm and the mean spike length was 7.10 cm. The mean floret number was 13.05, the minimum one was 7 and the maximum floret number was 19. The higher number of spikelet was 57, while the minimum one was 24. Also, the mean numbers of spikelet was recorded as 35.13 in the 56 wheat genotypes. The mean grain number was 2.77, whereas the minimum one was 2 and the maximum grain number was 4. The estimate coefficient of variation (CV) was high for number of grains per spike (21.45%). Large CV value was reported for grain number of wheat by Drezner *et al.* [2007] and Sonmezoglu *et al.* [2012]. The development of different morphological traits of wheat are highly coordinated processes and so for effective breeding program, it is necessary to considering all of the important traits which influencing on grain yield performance.

The longest awn length was 6.89 mm, the shortest one was 0.73 mm and the mean was 3.99 mm. The mean grain diameter was 2.96 mm, the maximum one was 3.61 mm and the minimum are was 2.18 mm. The mean grain length was 6.49 mm, the maximum grain length was 7.84 mm and the minimum grain length was 5.14 mm. The highest thousand seed weight was 45.93 g, while the lowest one was 26.16 g and the mean thousand seed weight was 37.85 g. The mean performance of grain yield was 5031.2 kg ha^{-1}, the minimum grain yield was 2835.0 kg ha^{-1} and the maximum grain yield was 7125.3 kg ha^{-1}. The estimate coefficient variation (CV) was high for grain yield (25.61%). The other remaining traits recorded moderate to low CV estimates from 14.30% in grain number per spike to 4.81% in days to flowering (Tab. 2).



Linkage distance – Odległośc sprzężeń
Class – Klasa
Cutoff point – Punkt odcięcia

Fig. 1. Dendrogram produced using ward's minimum variance cluster analysis based on distance matrix of 56 bread wheat genotypes
Ryc. 1. Dendrogram opracowany przy użyciu analizy minimalnej wariancji skupień według Warda w oparciu o matrycę odległości 56 genotypów pszenicy zwyczajnej

Table 3. Statistics of different multivariate ANOVA for cutoff point
Tabela 3. Statystyka wieloczynnikowej analizy wariancji dla punktu odcięcia

Statistics Statystyka	Value Wartość	*F*	Hypothesis *df* Hipoteza *df*	Error Błąd
Pillai's Trace Ślad Pillaia	2.19	2.47	72	148.0
Wilks' Lambda Lambda Wilksa	0.00	5.77	72	136.1
Hotelling's Trace Ślad Hotellinga	49.06	22.15	72	130.0
Roy's Largest Root Największy pierwiastek Roya	46.71	96.02	18	37.0

Table 4. The mean comparison of clusters regarding measured traits
Tabela 4. Porównanie analizy skupień badanych cech

Class Klasa	DF	SD	PH	LN	LL
I	85.19 BA	3.35 A	81.54 A	5.45 AB	15.253 A
II	83.67 B	3.30 A	86.42 A	6.00 A	14.071 A
II	85.46 BA	3.10 AB	85.49 A	5.35 B	14.431 A
IV	86.52 A	3.09 B	81.12 A	5.48 AB	15.221 A
V	85.44 BA	3.04 B	82.32 A	5.70 A	15.163 A

Class Klasa	LW	TN	NL	PL	SL
I	8.80 AB	2.83 A	15.44 A	28.53 B	7.40 BA
II	7.98 B	2.67 A	14.72 B	31.41 A	6.58 C
II	9.57 AB	2.25 AB	14.89 AB	27.78 B	7.67 A
IV	8.02 B	1.81 B	15.31 A	26.01 B	6.50 C
V	8.61 AB	1.94 B	14.99 AB	26.89 B	6.79 BC

Class Klasa	FN	SN	GN	AL	GD
I	13.97 A	36.44 BA	2.89 A	4.37 A	3.09 A
II	13.11 AB	35.19 BAC	2.70 A	3.28 B	3.07 A
II	13.46 A	37.94 A	2.79 A	4.38 A	2.97 BA
IV	11.95 AB	33.00 BC	2.76 A	3.41 BA	2.87 BC
V	12.19 B	31.28 C	2.67 A	3.94 BA	2.80 C

Class Klasa	GL	TS	GY
I	6.74 A	39.96 A	6259.4 A
II	6.55 BA	39.97 A	5126.1 C
II	6.50 BA	38.67 BA	5688.4 B
IV	6.34 B	35.92 BC	4173.0 D
V	6.26 B	34.18 C	3356.0 E

SD – stem diameter – średnica łodygi, PH – plant height – wysokość roślin, LN – leaf number – liczba liści, LL – leaf length – długość liścia, LW – leaf width – szerokość liścia, TN – tiller number – liczba źdźbeł, NL – internode length – długość międzywęźli, PL – peduncle length – długość dokłosia, SL – spike length – długość kłosów, FN – floret number – liczba kwiatów, SN – spikelet number – liczba kłosków, GN – grain number – liczba ziaren, AL – length of awn – długość ości, GD – grain diameter – średnica ziaren, GL – grain length – długość ziaren, DF – number of days to flowering – liczba dni do kwitnienia (DF), TS – thousand seed weight – masa tysiąca ziaren, GY – grain yield – plon ziaren.

Regarding the dendrogram, the 56 wheat genotypes are categorized into five groups. Then cutting point was determined using multivariate analysis of variance, in which the members completely belonged to the same group (Fig. 1). Four statistics as Pillai’s trace, Wilks’ lambda, Hotelling's trace and Roy’s largest root were calculated (Tab. 3). According to most of these statistics, the cutoff point of dendrogram is determined correctly.

Twelve genotypes as Saison (G56), Sistan (G55), Falaat-2 (G54), B-Roshan (G49), C-84-5502 (G41), Tabasi (G44), Mahdavi-2 (G48), C-85-11 (G8), C-84-55-B (G10), Mahdavi-1 (G47), MS-81-14 (G7) and Pishtaz (G4) were classified in the first cluster (Class-I) including 21.4% of total genotypes (Fig. 1). Nine genotypes as Cross-Shahi (G33), Sabalan (G14), Shiroodi-1 (G24), Shiroodi-2 (G53), Chanab (G39), Arvand (G21), Roshan-2 (G31), Roshan-1 (G19) and Sepahan (G9) were classified in the second cluster (Class-II) including 16.1% of total genotypes. Sixteen genotypes as C-85-9 (G20), C-85-13 (G27), C-85-8 (G18), Ghods (G32), C-85-5512 (G30), Alvand-2 (G28), Kavir (G52), Line A (G46), Moghan-1 (G35), Bayat (G17), Zarin (G25), Chamran (G11), Marvdasht (G5), Falat-1 (G37), Akbari (G43) and Alvand-1 (G2) were classified in the third cluster (Class-III) including 28.6% of total genotypes. Seven genotypes as Sorkhtokhm (G40), Tous (G34), Hirmand (G22), Bahar (G51), Shahriar (G50), Karaj-3 (G13) and Shahpasand (G3), were classified in the forth cluster (Class-IV) including 12.5% of total genotypes. Twelve genotypes as Shiraz (G45), Tajan (G38), CDC-Ospray (G36), Arta (G15), Golestan (G6), Zagros (G23), Alborz (G16), Omid (G42), Norstar (G12), Azar-2 (G26), Verinak (G29) and Niknezhad (G1) were classified in the fifth cluster (Class-V) including 21.4% of total genotypes (Fig. 1).

The average values of each cluster for measured traits are given in Table 4. The early flowering cluster was Class-II while the late flowering cluster was Class-IV. The large stem diameter was in clusters Class-I and Class-II while the maximum leaf number was in clusters Class-II and Class-V (Tab. 4). The largest leaf width was in clusters Class-I, Class-III and Class-V but, the most tiller number was in clusters Class-I and Class-II. The maximum internode length was in clusters Class-I and Class-IV while the longest peduncle length was clusters Class-II. Class-IV while the longest peduncle length was clusters Class-II. The largest spike length was in cluster Class-III and the maximum of floret number was in clusters Class-I and Class-III (Tab. 4). The maximum of spikelet number was in cluster Class-III and the maximum length of awn was in clusters Class-I and Class-III. The long grain diameter and grain length was seen in Class-I, Class-III and Class-I, respectively. The most thousand seed weight was in clusters Class-I and Class-II while the maximum grain yield was in cluster Class-I (Tab. 4).

DISCUSSION

In our study, the cluster analysis based on 18 agronomic traits separated the genotypes into five main groups, which were in accordance with their properties and characteristics. The result also corresponded well with the clustering result [Mollasadeghi *et al*. 2012] and indicated that, when the suitable cluster algorithm is used, the clustering result based on agronomic characters is comparable to the other studies. However, the results we obtained are not fully consistent with the results of Mangova and Rachovska [2004], Knezevic *et al*. [2008] and Sonmezoglu *et al*. [2012]. Such diverse genotypes might be useful in breeding program to maintain and wide genetic variation. So far, Iran is one of the important production areas of wheat in the world. Many studies indicated there was large genetic variation among Iranian accessions, and the other accessions were distinguishable from Iranian groups by different markers [Moghadam *et al*. 1997; Talebi *et al*. 2012]. Our results also indicated that there existed a considerable genetic variation among Iranian accessions in most agronomic characters.

Knowledge of the trait variability not only facilitates breeding programs but also helps to define the needs for future collections of germplasm. The principal aim of this research was to provide information which is suitable for the examination of genetic diversity and to assess relationships in the complex of 56 bread wheat genotypes. Our findings indicated existence of high genetic diversity in Iranian wheat genotypes. The magnitude and structure of genetic variation detected in this study could be useful for germplasm management and use in breeding programs [Tanya *et al*. 2011; Koutis *et al.* 2012]. The exploitation of crosses between genetically distant genotypes may produce higher variation, better genetic recombination and segregation in their progenies, and result in varieties with a broad genetic base [Altintas *et al*. 2008]. Finally, cluster analyses of the 56 wheat genotypes based on the agronomic traits was generally consistent with their properties and they could be important genetic resources for enriching the genetic background of wheat, and vice versa.

The genotypes of Class-I (G56, G55, G54, G49, G41, G44, G48, G8, G10, G47, G7 and G4) are good candidates for genetic improving of grain yield due to high potential for grain yield, most of yield components traits and other characters which are associated with grain yield. In our experiment, eighteen agronomical traits of a collection of 56 genotypes were evaluated. Significant differences were observed in all measured traits, i.e. stem diameter, plant height, leaf number, leaf length, leaf width, tiller number, internode length, peduncle length, spike length, floret number, spikelet number, grain number, length of awn, grain diameter, grain length, the number of days to flowering, thousand seed weight and grain yield for the 56 wheat genotypes. The traits' difference among different genetic materials is possibly caused by artificial selection in the breeding program to make the introduced materials adapt to local environmental conditions. In the typical, wheat growing areas in Iran, environmental conditions are vary with each other.

The selection of genotypes in this investigation was based on different origin [Pagnotta *et al.* 2005]. Therefore, we believe that there is a requirement for molecular marker investigation to complement study of morphological characters in the field which it would reduce the amount of material for study as well as the costs of experiments. It is expected that when diverse genotypes are used in genetic improvement programs, as a result of recombination, there are better chances for the appearance of transgressive segregation with useful characters that could be used to extract high yielding genotypes with desirable characters [Fatehi *et al*. 2011]. Further, large genetic variation exists between wheat genotypes, which can be used efficiently for genome mapping, such as high yield, stresses resistance, into the commercial cultivars. The large diversity of studied wheat genotypes has not been exploited effectively in wheat breeding due to the large numbers of genotypes, which makes it difficult and time consuming to evaluate material for target traits [Altintas *et al.* 2008]. Development of core collection could facilitate utilization of the large diversity stored in gene-bank of Iran.

Results of the present investigation indicate that extent of large genetic variability in the Iranian bread wheat seems to have remained quite constant. This constancy should be considered of qualitative relevance, as it shows that the genotypes has been enriched by material different from the local adapted cultivars, which resulted in broadening of the genetic background in different regions from Iran. Therefore, the classification obtained for these Iranian wheat genotypes, based on morphological traits will be a useful tool for wheat breeders to plan crosses for positive agronomic traits by choosing genotypes with appropriate diversity. The current study confirmed the importance of morphological traits, to determine genetic variation among genotypes with the aim to select diverse parents in new crossing programs.

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Streszczenie. Zróżnicowanie genetyczne wśród 56 genotypów pszenicy zwyczajnej (*Triticum aestivum* L.) oceniono na podstawie 18 cech agronomicznych na polu doświadczalnym w Maragheh w Iranie. Stwierdzono istotne różnice pomiędzy badanymi genotypami pszenicy w odniesieniu do wszystkich mierzonych cech, tzn. średnicy źdźbła, wysokości roślin, liczby liści, długości liścia, szerokości liścia, liczby źdźbeł, długości międzywęźli, długości dokłosia, długości kłosów, liczby kwiatów, liczby kłosków, liczby ziaren, długości ości, średnicy ziaren, długości ziaren, liczby dni do kwitnienia, masy tysiąca nasion oraz plonu ziaren. Współczynnik zmienności (CV) był wysoki dla plonu ziaren (25,61%), liczby źdźbeł przypadającej na roślinę (22,06%) oraz dla liczby ziaren w kłosie (21,45). Pozostałe cechy charakteryzowały się wartościami CV od umiarkowanych do niskich: 14,30% dla liczby ziaren w kłosie do 4,81% w odniesieniu do liczby dni do kwitnienia. Najwyższa wartość masy tysiąca ziaren wynosiła 45,93 g, najniższa 26,16 g, natomiast średnia 37,85 g. Średni plon ziaren wynosił 5031,2 kg ha^{-1}, minimalny – 2835,0 kg ha^{-1}, a maksymalny 7125.3 kg ha^{-1}. Analiza minimalnej wariancji skupień według Warda w oparciu o odległość euklidesową obliczona na podstawie surowych danych z 18 cech agronomicznych wyróżniła pięć skupień. Analiza skupień 56 genotypów w oparciu o wybrane cechy agronomiczne była zgodna z danymi z literatury. Nasze materiały roślinne mogłyby być ważnym źródłem materiału genetycznego służącego do wzbogacenia genetycznego tła odmian handlowych. Stwierdzone w niniejszych doświadczeniach zróżnicowanie genetyczne badanych cech pszenicy może być wykorzystane bowiem jako nowe źródło zmienności w programach hodowlanych i krzyżowaniach.

Słowa kluczowe: cechy agronomiczne, pszenica zwyczajna, analiza skupień, zróżnicowanie genetyczne