



Original article

Genetic Distance of New Bulgarian Durum Wheat Varieties and Breeding Lines of FCI-Chirpan, Bulgaria ¹

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Abstract

The durum wheat breeding program in Field crops institute FCI - Chirpan started in 1928. In the last ten years, a number of varieties have been created to meet modern cultural requirements. Genetic distance is of great importance for the success of the combining breeding. In the study are included 13 varieties created over the last 10 years and 8 of the Institute's best advanced durum wheat breeding lines. The field experiment was conducted in experimental field of FCI-Chirpan during 2015-2017 year. A randomized block design in four replicated was used with a trial plot size of 15 m². A standard farming technology for durum wheat in the country was applied. The traits: grain yield, plant height, heading date, test weight, 1000 kernel weight, protein content, wet gluten and vitreousness were observed. The means of three-year trials for all studied traits were calculated and genetic differences between genotypes were found. The coefficients of variation (CV%) obtained for the individual traits show that the heading date and grain yields are the most variable. The correlation analysis determines significant coefficients for 9 out of 28 possible combinations of traits. The multivariate methods for determining the genetic distance between the involved genotypes in the study were used. According to the dendrogram of the cluster analysis, the distances between the four main groups formed are determined. The applied graphical PC analysis shows the interrelations between the traits and the grouping of genotypes in terms of the genetic distance between them. These methods can help for faster breeding progress using the established genetic distance as the basis for deploying the breeding program.

Keywords: Durum wheat, Genetic distance, Breeding, Economic traits.

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INTRODUCTION

In the last ten years more than ten varieties of durum wheat was created in Field crops institute - Chirpan, Bulgaria. The breeding program includes crosses of varieties (parents) from all over the world and a selection in segregating generations. Increasing genetic diversity allows for reliable sources of variation in the future. By determining the genetic distance, a proper selection of the parental forms can be made, to achieve serious progress on the yield potential of the recombinant genotypes (Islam, 2004). The estimation of the genetic distance between genotypes can be based on the phenotypic manifestation of quantitative and qualitative traits (Souza and Sorells, 1991). Most often, genetic distance is measured as a phenotypic distance (Arriel et al., 2007; Gashaw et al., 2007a; Debnath et al., 2008; Kabir et al., 2009). It is assumed that if the genotypes are different phenotypically in many traits they are also genetically distant by their genomes. Some researchers have widely applied cluster analysis and PC analysis methods to determine genetic distance in breeding (Bhatt, 1970; Carves et al., 1987; Mohammadi and Prassana, 2003; Eivazi et al., 2007). The results of cluster analysis and PC analysis may show partial differences between them, furthermore the separation by cluster analysis gives the best estimate of the genetic distance of the genotypes Khodadadi et al. (2011). The PC analysis takes into account the first two components and this results in some distortion of the results Fotokian et al. (2002) and Siahbidi et al. (2013). Fang et al. (1996) applied a cluster analysis of 120 genotypes of durum wheat, defining five clusters based on morphological and economic qualities. Narouee (2006) determines with cluster analysis the genetic distances of local wheat varieties based on their morphological traits. The authors Talebi et al. (2010) tested 24 genotypes of durum wheat to determine their genetic distances by important yield-related traits and using cluster analysis to define three clusters. Hashjin et al. (2014) examine 116 genotypes from several different regions to determine the genetic distance between them. The results show highly significant genetic diversity between genotypes and the participants are divided into three clusters. Authors suggest that the parents from divergent clusters can be used for hybridization to isolate useful recombinants in the segregating generations in breeding programs for improvement of durum wheat.

The aim of our study is to determine the genetic distance between 21 Bulgarian durum wheat varieties and breeding lines created in FCI-Chirpan based on 8 key agronomic traits using multivariate methods.

Material and Methods

In the study are included 13 varieties created over the last 10 years and 8 of the Institute's best advanced durum wheat breeding lines. The field experiment was conducted in experimental field of FCI-Chirpan, Bulgaria during 2015-2017 year. A randomized block design with four replications was used with a trial plot size of 15 m². A standard farming technology for durum wheat in the country was applied. The traits: grain yield - GY (kg/da), plant height - H (cm), heading date - HD (m. may), test

weight – TW (kg/hl), thousand kernel weight – TKW (g), protein content – PR (%), wet gluten content – GL (%) and general vitreousness – VIT (%) were observed. The results were processed through ANOVA (for 3 year results), variation analysis, correlation analysis, cluster analysis and PC analysis over the three year average data. For the statistical treatment of data is using package program Statistica 10 (StatSoft inc). The hierarchical cluster analysis was performed using the Ward’s method by Ward J. (1963).

Results and Discussion

The results of the variation analysis by traits are presented in Table 1. The table shows the mean values (M) with their standard errors ($\pm m$) and the coefficients of variation (CV%). There is evidence of genetic diversity in the studied trait. According to the coefficients of variation the most varying traits are grain yield(GY) (9.94%) and heading date (HD) (10.12%), and the lowest varying - test weight(TW) (2.21%) and vitreousness (1.69%). The other traits occupy an intermediate position. It can be seen that the coefficients of variation are relatively low in the studied traits. Therefore, the breeding process that was led was directed to a particular model of a variety ideal. There is a certain tendency to increase the early maturity of genotypes, which corresponds to the meteorological conditions in the areal of study.

Table 2 presents the two-factor ANOVA by traits and years. The results presented significant differences between genotypes for all traits. The differences in years of cultivation are well significant for all the studied traits and show the significant influence of the conditions of the years on their expression. The genotype-environment interaction indicates that half of the traits: grain yield (GY), heading date (HD), wet gluten (GL) and vitreousness (VIT) are well significant (tab.2). This causes a certain reaction in the conduction of the breeding process. When conducting the breeding process for traits associated with the conditions of the years, observation should prolonged for more years or phenotypic stability of the individual genotypes - to be determined by any of the conventional methods by Kang (1998).

Table 1. Mean values (M), standard error ($\pm m$) and coefficients of variation (CV%) over 3 seasons (2015, 2016, 2017) for 8 traits of 21 genotypes new Bulgarian durum wheats.

Genotype	GY (kg/da)	H (cm)	HD (m. May)	TW (kg/hl)	TKW (g)	PR (%)	GL (%)	VIT (%)
Zvezditsa	372.13	92.0	13.00	73.38	43.16	15.44	33.86	95.40
IPK Deni	411.86	97.3	11.66	74.71	43.10	14.94	29.36	95.60
Deyana	419.03	98.0	11.00	76.06	44.36	15.00	30.23	92.56
Tserera	432.70	92.6	12.66	78.00	45.13	14.30	27.56	94.53
Predel	451.62	91.3	14.00	74.56	42.83	14.44	30.73	95.60
IPK Elbrus	457.16	95.0	14.00	75.17	42.90	14.06	27.26	94.40
Viktoria	462.46	102.0	13.66	75.74	43.60	14.69	30.60	95.46
Trakiets	463.63	100.3	15.33	76.63	43.16	14.59	31.50	96.36

D-7763	479.96	104.0	14.66	79.05	48.73	13.69	25.96	93.40
Kehlibar	482.46	98.3	15.33	77.35	43.96	14.58	28.03	96.53
Raylidur	491.36	95.0	14.00	73.81	73.70	13.77	26.06	95.60
D-8040	500.20	97.3	15.00	78.97	45.03	13.97	25.93	94.40
D-8036	504.86	103.0	13.66	78.03	45.76	13.74	30.46	92.46
Heliks	518.13	99.3	11.66	77.87	52.33	13.69	28.90	95.80
D-8243	518.20	97.0	12.66	75.32	50.56	14.23	31.93	97.06
D-8091	518.60	99.6	16.00	76.77	47.63	13.19	26.33	91.16
Saya	520.63	97.6	15.33	75.72	43.33	14.41	30.76	96.80
D-8031	527.06	98.3	12.33	77.32	51.66	13.97	29.33	94.96
Reyadur	533.36	102.0	15.33	75.99	46.10	14.01	27.13	96.93
D-8148	543.36	107.6	14.66	78.46	48.26	13.68	30.43	93.13
D-8159	559.60	98.0	13.33	78.57	48.90	13.62	29.03	95.33
M	484.20	98.35	13.78	76.54	45.91	14.19	29.11	94.92
±m	10.5	0.87	0.3	0.36	0.66	0.12	0.47	0.35
CV%	9.94	4.08	10.12	2.21	6.66	3.88	7.55	1.69

Table 2. ANOVA of traits by genotypes and years.

No	Trait	Source of variance		
		Genotypes G	Environments E	Interaction GxE
1	Grain yield	**	**	**
2	Heading date	*	**	*
3	Plant height	**	**	n.s.
4	1000 kernel weight	**	**	n.s.
5	Test weight	**	**	n.s.
6	Wet gluten	*	**	**
7	Grain protein content	**	**	n.s.
8	Vitreousness	**	**	**

* - $P \leq 0.05$; ** - $P \leq 0.01$; n.s. – no significant

The established correlation coefficients between the studied traits are presented in Table 3. The table shows significant positive correlations coefficients for grain yield (GY) with: plant height (H) ($r = 0.53$ *), test weight (TW) ($r = 0.52$ *) and thousand kernel weight (TKW) ($r = 0.63$ **). Dogan (2009) and Gashaw et al. (2007) reported same significant and positive correlation between grain yield and thousand kernel weight. The positive correlation between grain yield (GY) and plant height (H) is due to the fact that all genotypes tested are from the group of medium plant height. Authors Nofouzil et al. (2008) also reported significant and positive correlation between grain yield and plant height. On the other hand, there is a very well significant negative correlation ($r = -0.80$ ***) between grain yield (GY) and grain protein (PR). We have established a well significant positive correlation ($r = 0.56$ **) of plant height (H) with the test weight (TW), which once again explains the relationship of plant height with yield. The test weight (TW) is in a positive correlation with the thousand kernel weight (TKW) ($r = 0.53$

*) and negative with grain protein content (PR) ($r = -0.57^{**}$). The thousand kernel weight (TKW) is also found to be negative in relation to grain protein content (PR) ($r = -0.59^{**}$). Expected, very well correlation occurs between protein (PR) and wet gluten (GL) in the grain ($r = 0.61^{**}$). There is no significant correlations with heading date and vitreousness.

Table 3. Correlation coefficients between studied traits

Trait	GY	H	HD	TW	TKW	PR	GL	VIT
GY	1	0.53*	0.39	0.52*	0.63**	-0.80***	-0.29	0.02
H		1	0.29	0.56**	0.37	-0.42	-0.11	-0.30
HD			1	0.17	-0.22	-0.36	-0.32	-0.01
TW				1	0.53*	-0.57**	-0.38	-0.37
TKW					1	-0.59**	-0.11	-0.11
PR						1	0.61**	0.38
GL							1	0.27
VIT								1

* - $P \leq 0.05$; ** - $P \leq 0.01$; *** - $P \leq 0.001$

The results of the hierarchical cluster analysis are presented in Figure 1. The cluster analysis was performed on the average data of the three crop years. The data is standardized in order to align the scale of the traits and obtain a more accurate assessment (Siahbidi et al., 2013). The dendrogram shows two big clusters in the first level of division. The bigger cluster covers exclusively the certified varieties of the institute. In the second level of distance, this group is divided into two subclusters, which include the varieties from the two breeding branches developed at the institute - combining breeding and experimental mutagenesis. In the smaller main cluster are all advanced durum wheat lines included in the experiment. This group also includes the new one variety of the Institute - Heliks (certified 2017) which falls in a subgroup with two of the most promising breeding lines. Therefore, it can be pointed out that the Institute's breeding program leads to the production of relatively diverse genotypes of durum wheat. In conducting the breeding process, we should take into account the genetic distance of the genotypes involved in the combining breeding. To achieve faster success, it is necessary to combine genetically closer parents. In order to achieve greater breeding advances in agronomical traits, it is necessary to cross genetically more remote parents (from different clusters). The authors Khodadadi et al. (2011) reached the same conclusion in the breeding strategy.

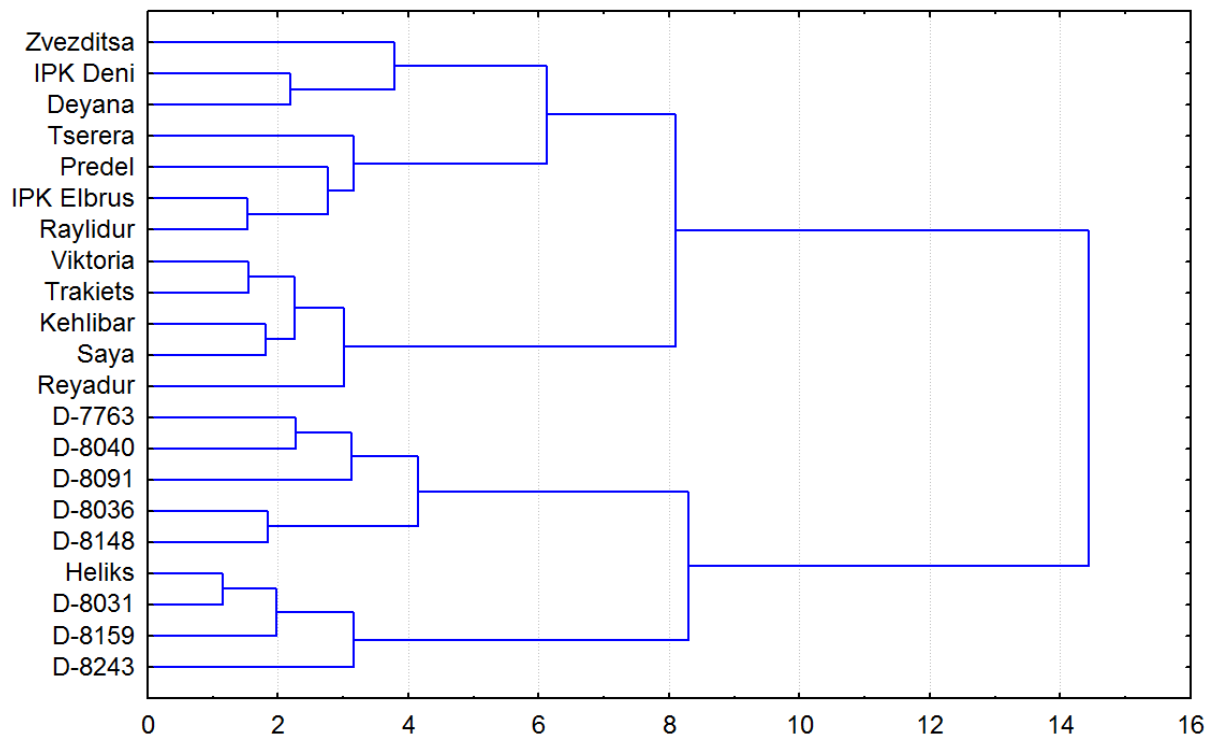


Figure 1. Dendrogram of 21 genotypes of Bulgarian durum wheat by 8 economic traits.

The PC analysis is represented graphically in Figure 2 and Figure 3. The two main components PC-1 and PC-2 account for 62.28% of the total variation for all genotypic traits. This variation is large enough to perform the analysis. Figure 2 shows the points and vectors of the traits investigated in the experiment. From the angles between the vectors of the traits, can be explained the correlation between them. From the magnitude of the angle we can judge the magnitude of the correlation. The smaller the angle, the stronger the correlation between the traits is. At an angle of 90 degrees the correlation is zero. At angles greater than 90 degrees, the correlation is negative, increasing with the increase in the angle. According to the corners of Figure 2, the correlation relationships are close to the correlation coefficients in Table 3. This figure 2 should be viewed in conjunction with Figure 3. Figure 3 shows the distribution of genotype points in the coordinate system the PC-1 to PC-2. According to the quadrant in which the genotyping points and passing vectors of the traits are located, Figure 2 can be judged for the corresponding stronger influence of the particular trait on the genotype. Figure 3 shows a significant similarity between the genotype distribution in the PC analysis (Figure 2) and the data from dendrogram (Figure 1). The authors Golabadi and Arzani (2003) suggest that cluster analysis was similar to factor analysis in grouping the characters. In general, it can be assumed that the separation by cluster analysis gives the best estimate of the genetic distance of the genotypes. Therefore, in studying genetic diversity related to genetic proximity and distance, it is preferable to use cluster analysis (Bhatt, 1970; Carves et al., 1987; Fang et al., 1996; Khodadadi et al., 2011; Siahbidi et al., 2013).

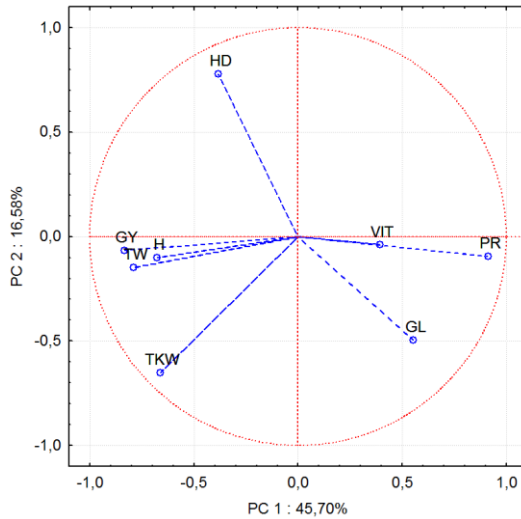


Figure 2. PC - analysis of traits

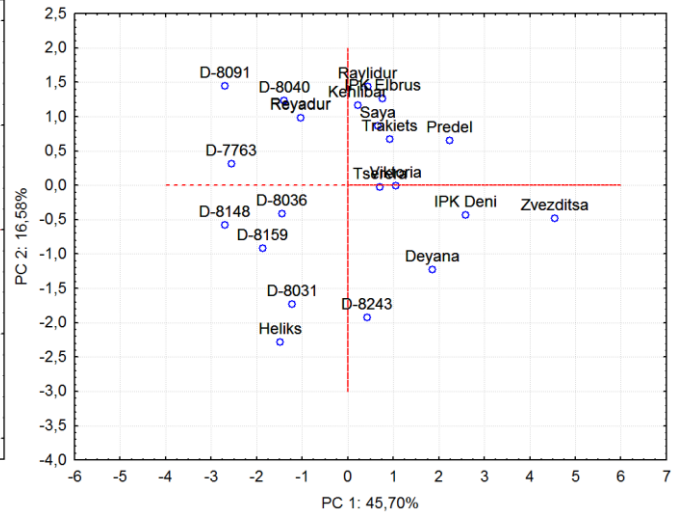


Figure 3. PC – analysis of genotypes

Conclusions

When conducting the breeding process for traits associated with the conditions of the years, observation should be prolonged for more years or the phenotypic stability of the individual genotypes - to be determined by any of the conventional methods.

Established correlation relationships between the studied traits can be successfully used in the breeding of durum wheat.

Using of cluster analysis provides a reliable estimation of the genetic distance of genotypes in our breeding program. The established genetic distance of genotypes allows optimization of the breeding process when choosing its strategy.

Despite the possibility of PC analysis to show clustering of genotypes by genetic proximity and distance, it is preferable to apply cluster analysis for this purpose because its more precision.

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