

Morphological and agronomical comparative study of genetic diversity of common winter wheat cultivars

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Abstract

The aim of this study was to assess the genetic diversity among cultivars with different geographical origin in term of 7 morphological and 7 agronomical traits. Twenty five common winter wheat varieties were included in three growing season evaluation using randomized complete block designs with 3 replications on plots of 10 m². The significant differences among evaluated varieties for plant shape, leaf-flag attitude, spike shape, spike attitude and spike awnedness were recorded as well as the high variation for the most of the agronomical studied traits were found. The first 5 principal components explained a very large proportion of the total variation (73.56%). Spike related characters such as spike length without awn (0.62), spikelets number per spike (0.89), grain number per spike (0.92) and grain weight per spike (0.83) strongly associated with PC1. The clustered heat map based on the Ward method and using the first five PCs grouped the genotypes into five clusters. The clustering of the studied wheat genotypes was not related to their geographical origin but it referred to specific phenotypic characters. The results of the study will be useful for the breeding improvement programs of common winter wheat.

Key words: wheat; PCA; heat map; morphological traits; agronomical traits

INTRODUCTION

Wheat is one of the most important cultivated crop used mainly for human food. The world's total wheat production was estimated at 636,194 thousand tonnes in 2020 (<https://knoema.com/atlas/topics/Agriculture/Crops-Production-Quantity-tonnes/Wheat-production>). Due to importance of wheat in the farming system, many plant breeders are engaged in its improvement throughout the world (Mohammad et al., 2011). Much attention is paid to the selection of high-yielding, high-quality wheat varieties that are resistant to diseases and pests, and adverse environmental factors (Adilova, 2020). Breeders seek to identify crop types that exhibit variation for meaningful breeding work. Knowledge about germplasm diversity and genetic relationship existing in accessions, landraces, lines alien crops, cultivars and varieties is found valuable in improving and in-

creasing genetic variations and developing strategy for conserving and utilization of genetic resources in cropping programmes (Priya et al., 2015).

Genetic diversity play key role in the germplasm improvement which is directly correlated with the crop production. Adilova et al. (2020) noted that investigation of genetic diversity of geographically distant wheat genotypes is a useful approach in wheat breeding providing efficient crop varieties. Morphological and agronomical traits are widely using to determine genetic diversity during breeding processes to produce new cultivars. Increased yield potential is the ultimate goal of a plant breeder. Progress in yield potential results from the progressive accumulation of genes conferring higher yield or elimination of the unfavourable genes through the breeding process (Naushad et al., 2021).

Various statistical techniques have been used to study diversity among different genotypes. Among

these techniques Hierarchical cluster analysis (HCA) and Principal Component Analysis (PCA) are the most frequently used for the genetic association of genotypes. HCA is a statistical technique that identifies groups of samples that behave similarly or show similar characteristics and thus quantify the structural characteristics of the samples or variables (Roessner et al., 2011). Principal component analysis helps researchers to distinguish significant relationship between traits. It is a multivariate analysis method that aims at explaining the correlation between a large set of variables in terms of a small number of underlying independent factors (Priya et al., 2014, 2015). Multivariate statistical tools enable to analyse genotypic stability and creation of groups with distinct traits (Adilova et al., 2020). The use of multivariate statistical algorithms is an important strategy for classification of germplasm and analy-

sis of genetic relationships among breeding material (Mohammadi & Prasanna, 2003).

The aim of this study was to assess the genetic diversity among cultivars with different geographical origin in term of their morphological and agronomical traits by using principal component analysis.

MATERIALS AND METHODS

The study was conducted in three growing seasons (2017/2018, 2018/2019 and 2019/2020) on the experimental field of the Institute of Plant Genetic Resources, Bulgaria. Twenty five common winter wheat varieties were included in this study. The national standard variety Enola was used as control (Table 1). The sowings were carried out in the autumn in optimal terms for the region, in “Dolusene”

Table 1. Twenty five cultivars included in the study in three growing seasons (2017/2018, 2018/2019 and 2019/2020)

Nº	Species	Sub species	Name of cultivar	Origin
1	<i>Triticum aestivum</i> L.	var. <i>erythrosperrum</i> (Koern.) Mansf.	Enola	BGR
2	<i>Triticum aestivum</i> L.	var. <i>lutescens</i> (Alef.) Mansf.	Ines	CZE
3	<i>Triticum aestivum</i> L.	var. <i>lutescens</i> (Alef.) Mansf.	Bohemia	CZE
4	<i>Triticum aestivum</i> L.	var. <i>lutescens</i> (Alef.) Mansf.	Baletka	CZE
5	<i>Triticum aestivum</i> L.	var. <i>lutescens</i> (Alef.) Mansf.	Secese	CZE
6	<i>Triticum aestivum</i> L.	var. <i>lutescens</i> (Alef.) Mansf.	Seladon	CZE
7	<i>Triticum aestivum</i> L.	var. <i>lutescens</i> (Alef.) Mansf.	Silueta	CZE
8	<i>Triticum aestivum</i> L.	var. <i>erythrosperrum</i> (Koern.) Mansf.	Coa	PRT
9	<i>Triticum aestivum</i> L.	var. <i>erythrosperrum</i> (Koern.) Mansf.	Jordao	PRT
10	<i>Triticum aestivum</i> L.	var. <i>lutescens</i> (Alef.) Mansf.	Andalou	FRA
11	<i>Triticum aestivum</i> L.	var. <i>lutescens</i> (Alef.) Mansf.	Muza	POL
12	<i>Triticum aestivum</i> L.	var. <i>lutescens</i> (Alef.) Mansf.	Kobra Plus	POL
13	<i>Triticum aestivum</i> L.	var. <i>erythrosperrum</i> (Koern.) Mansf.	Alcione	ITA
14	<i>Triticum aestivum</i> L.	var. <i>erythrosperrum</i> (Koern.) Mansf.	Bilancia	ITA
15	<i>Triticum aestivum</i> L.	var. <i>erythrosperrum</i> (Koern.) Mansf.	Carisma	ITA
16	<i>Triticum aestivum</i> L.	var. <i>lutescens</i> (Alef.) Mansf.	Delfino	ITA
17	<i>Triticum aestivum</i> L.	var. <i>erythrosperrum</i> (Koern.) Mansf.	Esperia	ITA
18	<i>Triticum aestivum</i> L.	var. <i>lutescens</i> (Alef.) Mansf.	Gemini	ITA
19	<i>Triticum aestivum</i> L.	var. <i>milturum</i> (Alef.) Mansf.	Primoasi	ITA
20	<i>Triticum aestivum</i> L.	var. <i>erythrosperrum</i> (Koern.) Mansf.	Accor	FRA
21	<i>Triticum aestivum</i> L.	var. <i>lutescens</i> (Alef.) Mansf.	Navarro 150	ESP
22	<i>Triticum aestivum</i> L.	var. <i>ferrugineum</i> (Alef.) Mansf.	Albimonte	ESP
23	<i>Triticum aestivum</i> L.	var. <i>erythrosperrum</i> (Koern.) Mansf.	Amarok	FRA
24	<i>Triticum aestivum</i> L.	var. <i>albidum</i> Al.	Geya-1-2010	BGR
25	<i>Triticum aestivum</i> L.	var. <i>lutescens</i> (Alef.) Mansf.	Geya-1	BGR

locality, on soil type meadow-cinnamon resin-like soil, after the predecessor peas. The randomized complete block designs with 3 replications on plots of 10 m² were used. Field management followed local practices.

The morphological traits were scored according to international descriptors lists (Anonymous, 1984). It was evaluated the following characteristics: *plant shape* (scale 1-9, where 1= erect (<25°), 3= semi-erect (25-45°), 5= drooping (46-55°), 7= strongly declined (56-70°), 9=prostrate (>70°)), *leaf-flag-attitude* (scale 1-9, where 1= upright (<15°), 3= semi-upright (15-45°), 5= horizontal (46-90°), 7= drooping (91-135°), 9= very drooping (>135°)), *spike-attitude* (scale 1-9, where 1= erect (<25°), 3= semi-erect (25-45°), 5= horizontal (46-90°), 7= nodding (91-135°), 9= very nodding (>135°)), *spike – shape* (scale 1-9, where 1=pyramidal, 3=cylindrical, 5= clavate, 7= fusiform, 9= other), *spike-colour* (1= white, 4= red), *spike-awnedness* (scale 1-9, where 1= absent, 3= awnless (<21 mm), 5= semi-awned (21-60 mm), 7= awned (61-100 mm), 9= long awned (>100 mm)), *awn-colour* (1= the same as the spike-colour, 9= different from the spike-colour) and *grain colour* (1= white, 4= red).

The agronomical characters included: grain yield (t/ha), plant height (cm), spike length without awn (cm), spikelet number per spike (number), grain number per spike (number), grain weight per spike (g) and 1000 grain weight (g).

The data for plant height (cm), spike length without awn, spikelet number per spike, grain number per spike and grain weight per spike were recorded on a plant basis by randomly chosen 10 plants from each plot. Grain yield and 1000 grain weight were estimated on a plot basis.

Data were analysed by analysis of variance (ANOVA), mean values were compared by the least significant difference (LSD) at 0.05, 0.01 and 0.001 probability levels using the SPSS22.0 software. PCA and clustered heat map were performed on the mean values recorded on 13 phenotypic traits using the JMP trial 15 software.

RESULTS AND DISCUSSION

In the table 2 are presented the scores of the studied morphological traits of the 25 common winter wheat genotypes included in the investiga-

tion. Results indicated the presence of significant differences among evaluated varieties for plant shape, leaf-flag attitude, spike shape, spike attitude and spike awnedness and low variation of spike and grain colours. The cultivars did not differ in terms of the awn-colour morphological trait. Sixteen cultivars were with semi-erect, six with drooping and two with strongly declined plant shapes. The largest numbers of cultivars were characterized with semi-upright leaf-flag-attitude (13 accessions), cylindrical *spike shape* (16 accessions), nodding *spike-attitude* (12 accessions) and awnless *spike-awnedness* (12 accessions). Only Geya-1-2010 had white colour of grains, while Albimonte and Primoasi were with red colour of spikes. The awn colours in the all studied cultivars were the same with these in the spike colours.

The mean values of studied agronomic characters are presented in Table 3-5. The genotypes showed the high variation for all of studied traits except of the number of spikelets per spike. Coefficient of variation was between 9.19% for number of spikelets per spike and 20.06% for grain weight per spike.

Plant height in the studied varieties varied from 85 cm to 115 cm, with a mean value for standard check of 90 cm.. Nine cultivars had significantly higher and eight cultivars significantly lower stems compare to the Enola standard. The tallest plants had Albimonte (115 cm), while the shortest had Amarok (75 cm), following from Gemini (77.50 cm). In the group of the standard variety Enola were 5 cultivars: Jordao, Bilancia, Carisma, Esperia and Geya-1-2010 (Table 3).

Spike length ranged from 6.50 cm to 12.50 cm. Spike length of Bohemia (12.50 cm), Delfino (11 cm) and Geya-1-2010 (11 cm) were the longest than spike length of standard Enola (8.50 cm). Significantly longer spikes had also 9 cultivars. Navarro 150 (6.50 cm) and Accor (7 cm) were with the shortest spike lengths than those of Enola (Table 3).

The analysis of the results showed that the average number of spikelets per spike in the studied 25 varieties was 19.13. All of the studied cultivars had a lower number of spikelets per spike than those of the standard, and in twenty of them the differences were statistically proven at $p \leq 0.001$ and $p \leq 0.05$, respectively (Table 3).

Average number of grain per spike was 56.13. Three accessions had higher values than Enola, but

Table 2. Morphological parameters of plant shape, leaves, spikes, and grains in 25 common winter wheat genotypes

Cultivars	Plant shape	Leaf-flag-attitude	Spike - shape	Spike-attitude	Spike-colour	Spike-awned-ness	Awn-colour	Grain colour
Enola	3	3	1	7	1	7	1	4
Ines	3	5	3	5	1	3	1	4
Bohemia	5	5	3	7	1	3	1	4
Baletka	3	3	3	7	1	3	1	4
Secese	3	1	3	7	1	3	1	4
Seladon	3	3	3	5	1	3	1	4
Silueta	3	3	3	5	1	3	1	4
Coa	3	5	1	7	1	7	1	4
Jordao	3	5	1	7	1	7	1	4
Andalou	5	3	3	5	1	3	1	4
Muza	3	3	3	7	1	3	1	4
Kobra Plus	3	3	3	3	1	3	1	4
Alcione	3	3	3	5	1	7	1	4
Bilancia	5	5	1	7	1	5	1	4
Carisma	7	3	3	3	1	7	1	4
Delfino	3	3	3	5	1	3	1	4
Esperia	3	3	1	5	1	5	1	4
Gemini	3	3	1	3	1	3	1	4
Primoasi	3	3	3	3	4	3	1	4
Accor	7	5	1	7	1	7	1	4
Navarro 150	3	1	7	3	1	3	1	4
Albimonte	3	3	3	5	4	5	1	4
Amarok	5	5	1	7	1	7	1	4
Geya-1-2010	5	3	3	7	1	3	1	1
Geya-1	5	3	3	7	1	3	1	4

differences were statistically proven only for one of them. The highest numbers of grain per spike were recorded for Gemini (88), Alcione (70) and Geya-1-2010 (67.50). Sixteen cultivars were with significantly lower values than Enola. Significantly the lowest number of grain per spike at $p \leq 0.001$ level was noted for Andalou (43) (Table 4).

Genotypes showed the highest variation for grain weight per spike ($CV=20.06\%$). Grain weight per spike ranged from 1.68 g for Bilancia to 3.08 g for Geya-1-2010. None of the studied varieties exceeded the standard on this character, except for the Geya-1-2010 variety, which was at the level of the standard (Table 4).

Thousand grain weight was between 31.66 g and 52.25 g, with mean value for standard Enola of 45.68 g. The highest thousand grain weight had Geya-1 (52.25 g), following from Seladon (49.85 g),

Bohemia (49.30 g) and Kobra Plus (46.77 g). Cultivars with significant lower thousand grain weight than standard check Enola were above half number of studied accessions (15 cultivars). Alcione had the lowest thousand grain weight – 31.66 g (Table 4).

The obtained average yield per hectare was 5.32 t/ha, with an average yield for Enola of 5.75 t/ha. In eight of the varieties, higher yields were obtained than those of the Enola standard. Significantly the highest yields were registered in the varieties Baletka, Carisma, Geya-1 and Delfino, which exceeded the standard by 0.70 t/ha, 0.75 t/ha, 0.83 t/ha and 0.83 t/ha, respectively. Relatively the lowest yield was reported for Coa (58.26%) (Table 5).

The Principal Component Analysis (PCA) clearly indicates the genetic variation of the accessions and measures the important characters with a greater impact to the total variability (Kandel et al., 2018). De-

Table 3. Significance of the differences between the standard variety Enola and the studied 24 varieties of *Triticum aestivum* L. in terms of plant height, spike length without awn, and number of spikelets per spike

Variety	Plant height, cm	Differences to Enola, cm	Spike length without awn, cm	Differences to Enola, cm	Number of spikelets per spike	Differences to Enola, numbers
Enola St.	90.00		8.50		22.00	
Ines	92.50	-2.50	8.00	0.50	18.00	4.00***
Bohemia	107.50	-17.50***	12.50	-4.00***	21.00	1.00
Baletka	97.50	-7.50***	9.50	-1.00*	21.00	1.00
Secese	100.00	-10.00***	10.00	-1.50**	18.00	4.00***
Seladon	100.00	-10.00***	10.00	-1.50**	20.00	2.00*
Silueta	87.50	2.50	9.00	-0.50	17.00	5.00***
Coa	85.00	5.00**	9.50	-1.00*	17.00	5.00***
Jordao	90.00	0.00	8.00	0.50	17.50	4.50***
Andalou	82.50	7.50***	9.00	-0.50	17.00	5.00***
Muza	107.50	-17.50***	10.00	-1.50**	19.00	3.00***
Kobra Plus	95.00	-5.00**	9.00	-0.50	20.00	2.00*
Alcione	85.00	5.00**	9.00	-0.50	21.00	1.00
Bilancia	90.00	0.00	9.00	-0.50	16.00	6.00***
Carisma	90.00	0.00	10.00	-1.50**	20.00	2.00*
Delfino	95.00	-5.00**	11.00	-2.50***	20.00	2.00*
Esperia	90.00	0.00	8.00	0.50	18.00	4.00***
Gemini	77.50	12.50***	10.00	-1.50**	22.00	0.00
Primoasi	82.50	7.50***	9.00	-0.50	19.00	3.00***
Accor	82.50	7.50***	7.00	1.50**	17.00	5.00***
Navarro 150	110.00	-20.00***	6.50	2.00***	19.00	3.00***
Albimonte	115.00	-25.00***	10.00	-1.50**	20.00	2.00*
Amarok	75.00	15.00***	9.00	-0.50	21.00	1.00
Geya-1-2010	90.00	0.00	11.00	-2.50***	20.00	2.00*
Geya-1	85.00	5.00**	9.00	-0.50	17.00	5.00***
Mean	92.31		9.25		19.13	
CV, %	11.02		13.69		9.19	
LSD 5%		3.01		0.98		1.58
LSD 1%		4.01		1.31		2.11
LSD 0.1%		5.24		1.70		2.76

***, **, *= significant at $p \leq 0.001$, $p \leq 0.01$ and $p \leq 0.05$, respectively

CV-variation coefficient, %

gewione & Alamerew (2013) noted that genotypes with wide amount of variations for the phenotypic traits ample opportunities for genetic improvement of bread wheat genotypes through selection directly from bread wheat genotypes and conservation of the germplasm for future utilization.

In our study PCA was carried out on 13 phenotype traits (six quantitative traits and seven of eight

analysing qualitative traits). The eigenvalues, contribution rate, and accumulative contribution rate are given in table 6. A very large proportion of the total variation (73.56%) was explained by the first 5 principal components that confirm a wide amount of variations between cultivars in term of the studied characters. The first principal component alone accounted for 20.49% of the variation followed by

Table 4. Significance of the differences between the standard variety Enola and the studied 24 varieties of *Triticum aestivum* L. in terms of plant height, spike length without awn, and number of spikelets per spike

Variety	Grain number per spike	Differences to Enola, numbers	Grain weight per spike, g	Differences to Enola, g	1000 grain weight, g	Differences to Enola, g
Enola St.	67.00		3.07		45.68	
Ines	59.50	7.50	2.69	0.38	45.31	0.37
Bohemia	59.00	8.00*	2.92	0.15	49.30	-3.62
Baletka	62.00	5.00	2.17	0.90***	35.16	10.52***
Secese	55.00	12.00**	2.18	0.89***	39.55	6.13**
Seladon	60.50	6.50	3.02	0.05	49.85	-4.17*
Silueta	43.00	24.00***	1.78	1.29***	41.45	4.23*
Coa	50.50	16.50***	2.07	1.00***	40.62	5.06*
Jordao	47.50	19.50***	1.73	1.34***	36.37	9.31***
Andalou	43.00	24.00***	1.80	1.27***	41.92	3.76
Muza	49.00	18.00***	2.24	0.83***	45.57	0.11
Kobra Plus	47.50	19.50***	2.23	0.84***	46.77	-1.09
Alcione	70.00	-3.00	2.21	0.86***	31.66	14.02***
Bilancia	47.50	19.50***	1.68	1.39***	35.25	10.43***
Carisma	54.00	13.00**	2.22	0.85***	41.20	4.48*
Delfino	66.50	0.50	2.70	0.36	40.58	5.10*
Esperia	44.50	22.50***	1.71	1.36***	38.05	7.63***
Gemini	88.00	-21.00***	2.86	0.21	32.74	12.94***
Primoasi	51.50	15.50***	2.15	0.92***	41.47	4.21*
Accor	47.50	19.50***	1.69	1.38***	36.15	9.53***
Navarro 150	48.50	18.50***	2.05	1.02***	42.18	3.50
Albimonte	65.50	1.50	2.57	0.50*	39.14	6.54**
Amarok	65.00	2.00	2.55	0.52*	39.15	6.52**
Geya-1-2010	67.50	-0.50	3.08	-0.01	45.50	0.18
Geya-1	53.00	14.00***	2.80	0.27	52.25	-6.58**
Mean	56.13		2.33		41.70	
CV, %	18.96		20.06		12.83	
LSD 5%		7.90		0.41		3.88
LSD 1%		10.53		0.54		5.17
LSD 0.1%		13.75		0.71		6.75

***, **, * = significant at $p \leq 0.001$, $p \leq 0.01$ and $p \leq 0.05$, respectively
CV-variation coefficient, %

the second principal component, which explained 17.13% of the variation. The third and fourth principal component accounted for 15.69% and 11.25% of the variation, respectively. The fifth principal component accounted for 9.01% of the total variation in the experiment. PC1 was strongly associated with spike related characters such as spike length without awn (0.62), spikelets number per spike (0.89), grain number per spike (0.92) and grain weight per spike (0.83). Therefore, selection based on first component is helpful for a good hybridization breeding program (Habibpour et al., 2012). High posi-

tive coefficients for weight of grains/spike, number of spikelets/spike and number of grains/spike also found Priya et al. (2015) and Naushad et al. (2021). In PC2, the eigenvalue was 2.40 and the contribution rate was 17.13% of the total variation among the accessions. These values were mainly explained by 1000 grain weight (0.80), plant height (0.65), and spike shape (0.49). In PC3, the eigenvalue was 2.20 and the morphological traits as leaf-flag-attitude, spike-attitude and spike-awnedness were strongly associated with this component. Plant shape was highly positively loaded in PC4, while spike-colour

Table 5. Average yield per hectare for 25 varieties of common winter wheat

Variety	Grain yield t/ha	Differences to Enola, t/ha	Relative yield, %
Enola	5.75		
Ines	4.68	1.07***	81.39
Bohemia	6.08	-0.33	105.73
Baletka	6.45	-0.70*	112.17
Secese	6.10	-0.35	106.09
Seladon	5.65	0.10	98.26
Silueta	4.73	1.03***	82.26
Coa	3.35	2.40***	58.26
Jordao	4.25	1.50***	73.91
Andalou	5.48	0.28	95.30
Muza	6.00	-0.25	104.35
Kobra Plus	5.33	0.43	92.70
Alcione	5.50	0.25	95.65
Bilancia	5.50	0.25	95.65
Carisma	6.50	-0.75**	113.04
Delfino	6.58	-0.83**	114.43
Esperia	5.35	0.40	93.04
Gemini	3.95	1.80***	68.70
Primoasi	5.23	0.53	90.97
Accor	4.90	0.85**	85.22
Navarro 150	4.13	1.63***	71.83
Albimonte	4.58	1.18***	79.65
Amarok	5.80	-0.05	100.87
Geya-1-2010	4.50	1.25***	78.26
Geya-1	6.58	-0.83**	114.43
Mean	5.32		
CV, %	16.55		
LSD 5%		0.56	
LSD 1%		0.74	
LSD 0.1%		0.97	

***, **, * = significant at $p \leq 0.001$, $p \leq 0.01$ and $p \leq 0.05$, respectively

CV-variation coefficient, %

was highly negative associated with PC4. PC5 was associated with grain colour (0.80) and grain yield (0.69) (Table 6).

The cluster analysis of the 25 accessions based on the Ward method and using the first five PCs led to grouping the accessions into five main clusters (Figure 1). Cluster I included four cultivars of var. *erythrospermum* (Koern.) Mansf. (Enola from Bulgaria, Amarok from France, Carisma from Italy, Alcione from Italy) and one cultivar of var. *lutescens* (Alef.) Mansf. (Gemini from Italy). Cluster II included 8 genotypes- Bohemia (Czech Republic),

Geya 1 (Bulgaria), Baletka (Czech Republic), Secese (Czech Republic), Delfino (Italy), Kobra Plus (Poland), Seladon (Czech Republic), Muza (Poland) belong to var. *lutescens* (Alef.) Mansf. and one belong to var. *ferrugineum* (Alef.) Mansf. – Albimonte (Spain). Cluster III consisted of six cultivars belong to different subspecies (var. *lutescens* (Alef.) Mansf., var. *milturum* (Alef.) Mansf., var. *erythrospermum* (Koern.) Mansf. and geographical origin (Ines from Czech Republic, Primoasi, Esperia from Italy, Andalou from France and Navarro 150 from Spain). The cluster IV composed four geno-

Table 6. The eigenvalues, contribution rate, and accumulative contribution rate of 14 quantitative and qualitative characters

Quantitative and qualitative characters	Component				
	1	2	3	4	5
Plant shape	-0.10	-0.04	0.21	0.75	-0.04
Leaf-flag-attitude	-0.09	-0.21	0.81	0.09	-0.08
Spike – shape	-0.09	0.49	-0.74	-0.10	-0.02
Spike-attitude	-0.04	0.25	0.78	0.20	0.00
Spike-colour	0.05	0.00	-0.06	-0.65	-0.01
Spike-awnedness	-0.06	-0.63	0.46	0.12	0.12
Grain colour	-0.25	-0.24	-0.02	-0.25	0.80
Plant height	-0.01	0.65	-0.16	-0.45	0.20
Spike length without awn,	0.62	0.47	0.21	0.03	0.04
Spikelets number per spike	0.89	-0.08	-0.20	-0.09	0.13
Grain number per spike	0.92	-0.22	-0.03	-0.10	-0.12
Grain weight per spike	0.83	0.35	0.01	0.00	-0.18
1000 grain weight	0.04	0.80	-0.01	0.16	-0.07
Grain yield	0.24	0.36	-0.02	0.45	0.69
Eigenvalues	2.87	2.40	2.20	1.58	1.26
%Variation (Contribution)	20.49	17.13	15.69	11.25	9.01
Cumulative variation %	20.49	37.61	53.30	64.56	73.56

types belonging to the subspecies var. *erythrospermum* (Koern.) Mansf. regardless of their geographical origin (Coa and Jordao from Portugal, Bilancia from Italy and Accor from France). Bulgaria cultivar Geya-1-2010 separated in the last cluster V. and belongs to var. *albidum* Al. Genetically the closest were Delfino with Baletka, following from Kobra plus with Secese and Coa with Jordao, while genetically the most distant were Geya-1-2010 with Albimonte, Carisma and Alcione.

PC-based dendrogram showed that the clustering of the studied wheat genotypes was not related to their geographical origin but it referred to specific phenotypic characters. This is in confirming of Devesh et al. (2019) and Naushad et al. (2021).

A heat map is another way to visualize hierarchical clustering. Heat maps allow us to simultaneously visualize clusters of samples and characters. The clustergrams represent each participant's row of data across each of the columns of variables as a colour block, using stronger intensities of one colour to represent lower levels of the variable, and increasing intensities of a different colour to represent higher levels (Lee et al., 2016).

In our study the heat map of the first five PCs-based dendrogram provides information about the

importance of each PC in the formation of the clusters and their sub clusters, as well as on the arrangement of the genotypes in each cluster (Zimisuhara et al., 2015). According to the clustergram, the varieties grouped in cluster I were with higher values for the quantitative characters related with the spike, while the genotypes in the clusters III and IV had from lower to the lowest values for PC1. The highest genetic variation was recorded between genotypes classified in the cluster II in term of the quantitative and qualitative characters connected with the most of the PCs. Genotypes in cluster IV varied slowly by characters connected with PC1 and PC3. Genotypes (Baletka and Carisma) with the highest values of PC5, noted with red colour in the heat map clustergram belong to two different but adjacent clusters (Fig.1).

The results of using double dendrogram (clustered heat map) in our study confirm that the genetic relationship between studied cultivars cannot only be reflected by the similarity between quantitative and qualitative characters traits, as they affected by environmental conditions and cultural practices. Lack of association between morpho-agronomic traits and geographic origin of cultivars (Li et al., 2010; Wang et al., 2013; Shen et al., 2019; Naushad et al.; 2021).

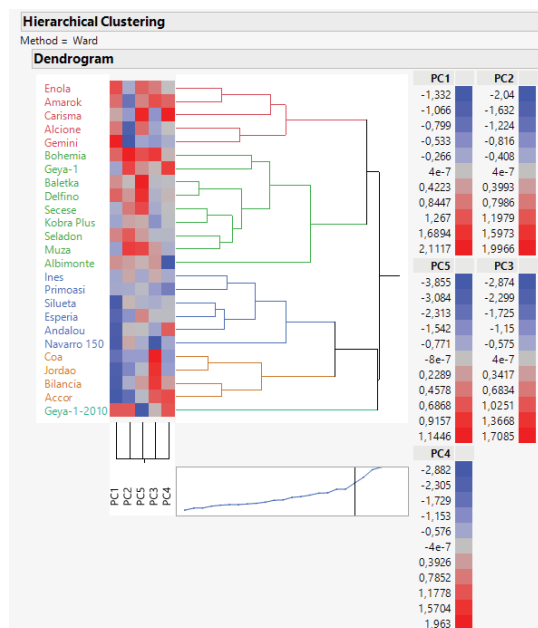


Figure 1. Dendrogram of 25 common winter wheat varieties generated by the Ward clustering method on the basis of the first five PCs with heat map

CONCLUSION

The studied cultivars significantly differed by qualitative traits connected with plant shape, leaf-flag attitude, spike shape, spike attitude and spike awnedness and showed the high variation for the most of the studied agronomical traits. A very large proportion of the total variation was explained by the first 5 principal components. PC1 strongly associated with spike length, spikelets number per spike, grain number per spike and grain weight per spike. PC2 associated with 1000 grain weight, plant height, and spike shape. PC3 strongly associated with leaf-flag-attitude, spike-attitude and spike-awnedness. PC4 associated positively with plant shape and negatively with spike-colour. PC5 associated with grain colour and grain yield. The clustered heat map based on the Ward method and using the first fives PCs grouped the genotypes into five clusters. The clustering of the studied wheat genotypes was not related to their geographical origin but it referred to specific phenotypic characters. A clustered heat map is useful tool for simplified representation of the phenotypic traits distribution in analysing a big set of accessions. The results of the study will be useful in the breeding improvement programs of common winter wheat.

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