GENETIC DISTANCE OF COMMON WINTER WHEAT VARIETIES

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The study was conducted during the period 2017-2019 in the experimental field of IPGR Sadovo. Wheat is the most important agricultural crop worldwide. Bulgarian wheat production in 2019 amounts to 6.162 thousand tons - an increase of 5.7% compared to 2018, due to the relatively favorable climatic conditions in the process of crop development, which led to an increase in average yield (with 6.8%). Twenty nine common winter wheat varieties (*Triticum aestivum L.*) with Belorusian origin and two Bulgarian varieties – Sadovo 1 and Enola were evaluated. The studied materials were sown in 2 rows with the length – 2 m, at the row spacing – 20 cm and the distance in rows – 5 cm. The standard technology adopted in IPGR for cultivation of common winter wheat was used. The aim of this study is to investigate the genetic distance of common winter wheat genotypes with a view to their use in the breeding process as sources of initial material for the formation of new and highly productive wheat varieties. Biometric measurements were made on 20 plants of each genotype and the main productivity indicators were recorded. To evaluate the genetic similarity between the different varieties, cluster analysis and PC analysis were applied. Based on the cluster analysis, the studied genotypes are classified into five large cluster groups. With the most genetic closeness to each other are characterized the varieties Vasilisa and Uzlet, followed by Daria and Rostan. The greatest genetic distance is shown between the Bulgarian varieties Sadovo 1 and Enola to the varieties from Belarus. The greatest genetic difference was found between Sadovo 1 and Rassvet, followed by Enola and Rassvet. Genetically distant varieties belonging to different cluster groups can be used as sources of initial material to achieve genetic diversity in the breeding of common winter wheat.

Key words: breeding, genetic diversity, genetic distance, *Triticum aestivum L.*

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INTRODUCTION

Wheat is the most important agricultural crop worldwide. Bulgarian wheat production in 2019 amounts to 6.162 thousand tons - an increase of 5.7% compared to 2018, due to the relatively favorable climatic conditions in the process of crop development, which led to an increase in average yield (with 6.8%). The areas sown with wheat in 2019 are 1 201 678 ha - 1.3% less on an annual basis, of which 1 198 682 ha are harvested. The relative share of harvested areas with wheat is 62% of the total harvested areas with cereals (ANNUAL REPORT OF MINISTRY OF AGRICULTURE, FOOD AND FORESTRY, 2020).

A prerequisite condition for successfully increasing yield potential through breeding in common winter wheat is the availability of a variety of initial material that have proven to be highly productive (BOYADJIEVA, 1994; MEREZKO, 1998). Genetic diversity among plant species offers prospects for improving the plant characteristics. Its assessment is necessary to help tackle the threats of environmental fluctuations and for the effective exploitation of genetic resources in breeding programmes (KHAN et al., 2015). With achievement of the biological productivity limit of common wheat in recent years, the need of including of new parental forms in the creation of economically effective varieties has increased significantly (GRAYBOSCH and PETERSON, 2010; RACHOVSKA and UHR, 2010; HAILEGIORGIS et al., 2011). Plant breeder's exploitheterosis as an effective genetic strategy to increase yield and stress resistance in wheat (SINGH et al., 2015). Traditionally, we breeders estimated heterosis in wheat by observing progeny traits. These are often influenced by factors such as genetic relation of the parents and environmental conditions. Genetic variation among wheat (*Triticum aestivum L.*) parents is necessary to derive superior progeny from crossing and selection. However, crosses are often performed among elite lines with similar agronomic and end- use characteristics (CHEN et al., 1994). The controlled selection of varieties suitable for the breeder interest to the environment conditions, as well as the study of the relationships between the yield and the components that determine its formation, is a guarantee for the upward development of productivity breeding (STOEVA et al., 2009). Some researchers have successfully implemented 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; DRAGOV and DECHEV, 2015; STAMATOV and DESHEV, 2018; DRAGOV et al., 2019; STAMATOV and VELCHEVA, 2020). The genetic diversity in plants determines their potential for breeding progress by applying the hybridization method according to the available genetic distance of the genotypes. As more as genetically distant are the parental forms, the potential for gene interaction in the form of dominance and epistasis, leading to increased potential for heterosis and transgression, is bigger (FALCONER, 1989). By determining genetic distance, the correct selection of parental forms to increase the extractive potential in recombinant genotypes could be done (ISLAM, 2004). Most commonly, the genetic distance is measured as phenotypical distance (ARRIEL et al., 2007; DEBNATH et al., 2008; KABIR et al., 2009). It is accepted that if the genotypes are different phenotypically in many characteristics they are also genetically distant by their genomes.

The purpose of this study is to investigate the genetic distance of common winter wheat genotypes with a view to their use in the breeding process as sources of initial material for the formation of new and highly productive wheat varieties.

MATERIAL AND METHODS

During the period 2017-2019 the productivity components of twenty nine common winter wheat varieties with Belorusian origin and two Bulgarian varieties (Sadovo 1 and Enola) were evaluated in the experimental field of the Institute of Plant Genetic Resources (IPGR) – Sadovo. The studied materials were sown in 2 rows with the length of 2 m, at the row spacing – 20 cm and the distance in rows – 5 cm. The standard technology adopted in IPGR for cultivation of common winter wheat was used (HRISTOVA and CHERESHAROV, 2007). Biometric measurements were made on 20 plants of each genotype and the following productivity indicators were recorded: PH – plant height (cm), TT - total tillering, PT – productive tillering, SL – central spike length (cm), NSS – number of spikelets per central spike, NGS – number of grains per central spike, WGS – grain weight per central spike (g), NGOS – number of grains per other spikes, WGOS – grain weight per other spikes (g), NGP – number of grains per plant, WGP – grain weight per plant (g). The degree of variation of each of the components of productivity is determined by calculating a coefficient of variation. It is accepted that variation is considered weak if the coefficient of variation is lower than 10%, on average - when it is greater than 10% and less than 20%, strongly - when it is above 20% (DESHMUKH *et al.,* 1986; DIMOVA and MARINKOV, 1999). To determine the genetic distance between the different genotypes cluster analysis and PC analysis based on averages in the study period were used. The mathematical processing of the results was performed using the statistical programs SPSS 19 and STATISTICA 10 for Windows.

RESULTS AND DISCUSSION

The results of biometric measurements of the productivity components of the studied wheat varieties are presented in Table 1, with the mean values, minimum, maximum, standard deviation, variation coefficient and error of the arithmetic mean. For the trait plant height, the values vary from 71.3 to 108.5 cm. The lowest are the plants of the Kapela variety, and the highest are Sadovo 1, Harmony, Suzore and Arina (up 100 cm). The average value of the trait is 89.7 cm. There are seven varieties close to the mean value. The variation on this trait is weak. The Kapela variety is characterized by the highest total tillering, followed by Augustina, Uzrim and Suita. The varieties Sadovo 1 and Enola have the lowest total tillering. The data obtained for the productive tillering trait is similar to those for the total tillering. In 22 samples the spike lenght is larger than the average value this trait. Oda, Arina and Augustina have the largest number of spikles number per central spike. Rassvet and Toma have the largest number of grains number per central spike. Twenty samples are with a weight of grains per the central spike over 2 g. The trait number of grains per the other spikes is in the range from 36.0 to 118.9. The grain weight per the other spikes is in the range of 1.8 to 4.2 g, and mean value is 2.9 g. The number of grains per plant is the greatest in Rassvet, Beloruskaya and Augustina. The weight of grains per plant is the highest of Rassvet and Pogiuk. By analyzing the results by obtained traits, it can be concluded that the variety Rassvet shows the best results by six traits. Our results show a rich genetic diversity in Belarusian varieties.

Table 1. Results of biometric measurements of the structural components of productivity

№	Variety	PH	TT	PT	SL	NSS	NGS	WGS	NGOS	WGOS	NGP	WGP
1	Laska	85.80	4.00	3.60	11.25	21.20	45.90	1.56	76.20	2.46	122.10	4.02
2	Sonata	98.00	3.90	3.80	9.87	21.40	47.90	1.84	85.00	3.07	132.90	4.91
3	Kapell a	71.30	4.50	3.70	11.70	22.60	49.60	1.42	96.70	2.82	146.30	4.24
4	Daria	96.60	4.00	3.70	12.35	23.30	51.90	1.72	95.70	3.10	147.60	4.82
5	Arina	101.80	3.60	3.50	12.32	24.30	50.40	2.23	85.70	3.64	136.10	5.87
6	Pogiuk	83.90	3.50	3.30	11.09	21.90	49.70	2.27	86.10	4.16	111.59	6.43
7	Augustina	76.40	4.40	3.90	12.50	24.30	54.10	1.81	105.30	3.38	159.40	5.19
8	Suita	77.60	4.40	3.90	11.95	21.80	39.70	1.51	74.80	2.73	114.50	4.24
9	Corona	93.80	4.00	3.80	9.86	21.50	53.80	1.90	93.80	3.22	147.60	5.12
10	Uzrim	78.20	4.30	4.00	10.60	21.70	54.00	1.98	87.40	3.25	141.40	5.23
11	Vasilisa	85.60	4.00	3.80	11.47	23.20	51.30	2.00	82.40	3.15	133.70	5.16
12	Suzore	103.00	3.60	3.30	13.35	23.30	44.40	1.82	64.60	2.58	109.00	4.40
13	Visa	89.90	3.60	3.40	9.78	20.70	47.90	1.94	70.10	2.76	118.00	4.70
14	Sofia	93.10	3.30	3.20	10.34	22.20	55.60	1.78	85.60	2.97	141.20	4.75
15	Credo	81.80	3.40	3.30	11.27	23.20	51.30	2.02	65.80	2.75	117.10	4.78
16	Harmony	103.70	3.40	3.10	13.96	22.70	55.30	1.94	85.70	2.43	141.00	4.37
17	Avangardnaya	92.30	3.80	3.60	11.17	24.10	51.30	1.84	91.60	2.89	142.90	4.73
18	Rassvet	96.30	4.00	3.60	12.27	22.30	60.00	2.18	118.90	3.89	178.90	6.06
19	Uzlet	86.20	3.70	3.60	12.04	23.90	53.40	2.22	80.40	2.96	133.80	5.19
20	Beloruskaya	98.20	4.30	3.80	11.10	23.30	58.40	2.00	102.00	2.58	160.40	4.58
21	Rostan	97.20	4.00	3.60	11.35	22.50	52.80	1.99	92.50	3.00	145.30	4.98
22	Anuta	94.10	3.50	3.20	12.76	22.30	52.30	2.10	68.90	2.27	121.20	4.37
23	Lyubava	88.10	4.30	3.90	12.45	22.40	50.90	2.22	93.40	3.48	144.30	5.70
24	Sudarinya	93.90	3.60	3.30	11.10	23.80	52.60	1.97	84.10	2.43	136.70	4.39
25	Sakret	83.30	4.00	3.60	11.62	23.00	52.50	2.19	100.00	3.74	152.50	5.94
26	Oda	83.50	3.90	3.50	12.95	25.30	57.70	2.28	86.90	2.80	144.60	5.08
27	Canveer	80.50	3.30	3.20	12.22	24.50	49.90	2.00	70.20	2.38	120.10	4.38
28	Toma	89.00	3.50	3.30	10.27	22.90	62.30	2.17	83.90	2.57	146.20	4.73
29	Elegya	80.80	4.10	3.80	11.03	21.90	47.43	1.79	109.23	3.30	156.65	5.09
30	Sadovo 1	108.50	2.37	2.03	9.26	20.00	39.10	2.12	36.00	1.95	74.20	4.07
31	Enola	89.08	2.85	2.06	10.89	22.1	47.3	2.069	42.4	1.781	89.8	3.85
	Mean	89.7	3.8	3.5	11.5	22.7	51.3	2.0	83.9	2.9	134.4	4.9
	Minimum	71.3	2.4	2.0	9.3	20.0	39.1	1.4	36.0	1.8	74.2	3.9
	Maximum	108.5	4.5	4.0	14.0	25.3	62.3	2.3	118.9	4.2	178.9	6.4
	Std. deviation	9.0	0.5	0.5	1.1	1.2	5.1	0.2	17.4	0.5	21.3	0.6
	Coef. var., %	10.0	12.4	13.1	9.6	5.2	9.9	11.2	20.7	18.5	15.8	12.8
	Standard error	1.61	0.08	0.08	0.20	0.21	0.91	0.04	3.12	0.10	3.82	0.11

Mean - Average value, Minimum - Minimum value, Maximum - Maximum value, Std. deviation - Standard deviation, Coef. var. % - Variation coefficient, Standard error - Error of arithmetic mean

The data shows that there is a proven genetic diversity by the components of productivity in the studied genotypes. The coefficient of variation indicates that lowest variability is observed in the traits number of spikelets per central spike, length of central spike and number of grains per central spike. High variation is observed for the number of grains per other spikes. The other traits are characterized with average variation.

Cluster analysis can be used to identify variables which can be classified into main groups and subgroups based on similarity and dissimilarity. This technique is useful for parental selection in breeding programs (EL-DEEB and MOHAMED, 1999; LEILAH and KHATEEB, 2005) and crop modeling (JAYNES *et al.,* 2003). Cluster analysis is a method for classification and hierarchy, in which the studied population is divided into a number of groups called clusters.
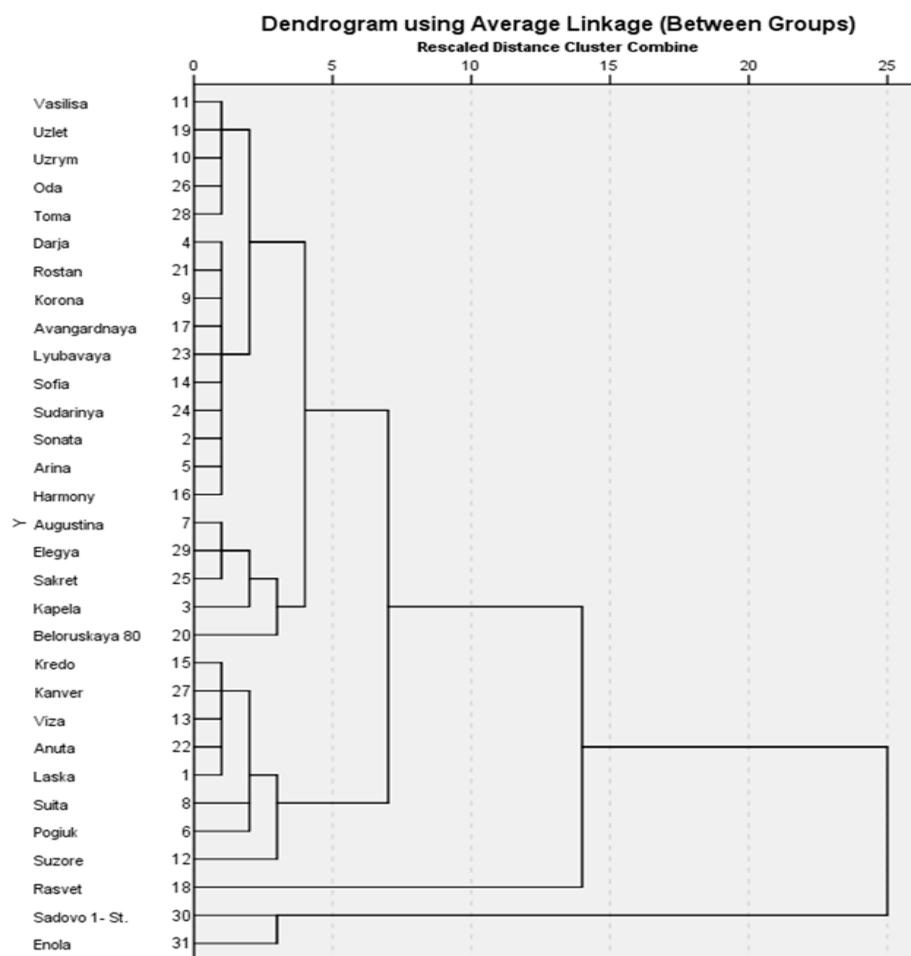
Fig. 1. Dendrogram of cluster analysis

The study of breeding materials through cluster analysis allows breeders to plan and make more effective decisions for the development of their improvement programs. Using clustering, the samples can be separated by genotype, depending on its phenotypic expression by a particular trait or group of traits. The results of clustering are presented in the dendrogram (Fig. 1). The dashed horizontal line of the dendrogram shows the scalar distance at which clusters are formed. From the data presented in Fig. 1 it can be seen that the studied breeding materials are grouped into five main cluster groups. The first cluster group includes the varieties Vasilisa, Uzlet, Uzrim, Oda and Toma. The second cluster group is the most numerous and includes ten genotypes of common wheat - Daria, Rostan, Corona, Avangardnaya, Lyubava, Sofia, Sudarinya, Sonata, Arina and Harmony. The third cluster group consists of two sub groups. The clusters of Augustina, Elegya and Sakret (first sub group) form an independent cluster in this group, to which the varieties Kapela and Beloruskaya (second sub group) join at a higher rescaled distance. The fourth cluster group consists of nine wheat genotypes. A separate cluster in this group is observed between the varieties Credo, Canveer, Visa, Anuta and Laska. A separate cluster also forms the Suita and Pogiuk, to which the varieties Suzore and Rassvet are connected. The fifth cluster group is the smallest and is represented by the Bulgarian varieties Sadovo 1 and Enola.

Table 2. Genetic similarity between the studied wheat genotypes

№	Genotype	Genotype	Coefficient
1	Vasilisa	Uzlet	9.810
2	Daria	Rostan	18.458
3	Daria	Corona	23.762
4	Avangardnaya	Lyubava	29.302
5	Credo	Canveer	34.920
6	Sadovo 1	Beloruskaya 80	12286.825
7	Sadovo 1	Elegya	13013.155
8	Sadovo 1	Augustina	13356.941
9	Enola	Rassvet	14019.461
10	Sadovo 1	Rassvet	18447.349

Table 2 shows the genetic similarities between the different wheat genotypes based on the coefficient at which the individual cluster pairs are formed between the studied samples. The results show that the most genetically closeness to each other is characterized by the varieties of Vasilisa with Uzlet (9.810), followed by Daria with Rostan (18.458). In terms of genetic distance, we can summarize that the Bulgarian varieties Sadovo 1 and Enola are genetically furthest from the Belarusian varieties, with the greatest difference observed between Sadovo 1 and Rassvet (18447.349), followed by Enola and Rassvet (14019.461). The varieties Sadovo 1 and Enola, which were created under soil and climate conditions of Bulgaria, drastically differ from the Belarusian breeding in a number of agronomic traits. This is the reason that they are genetically distant. For example, Bulgarian varieties are characterized by relatively lower values of the following traits: TT, PT, NGS, NGOS, WOGS, NGP and WGP.

The performed PC analysis presented graphically in Fig. 2 and Fig. 3. Fig. 2 shows the points and vectors of the studied productivity indicators. The two main components PC 1 and PC 2 explain 63.8% of the total variation of all traits of the genotypes, which is enough large for the propose.
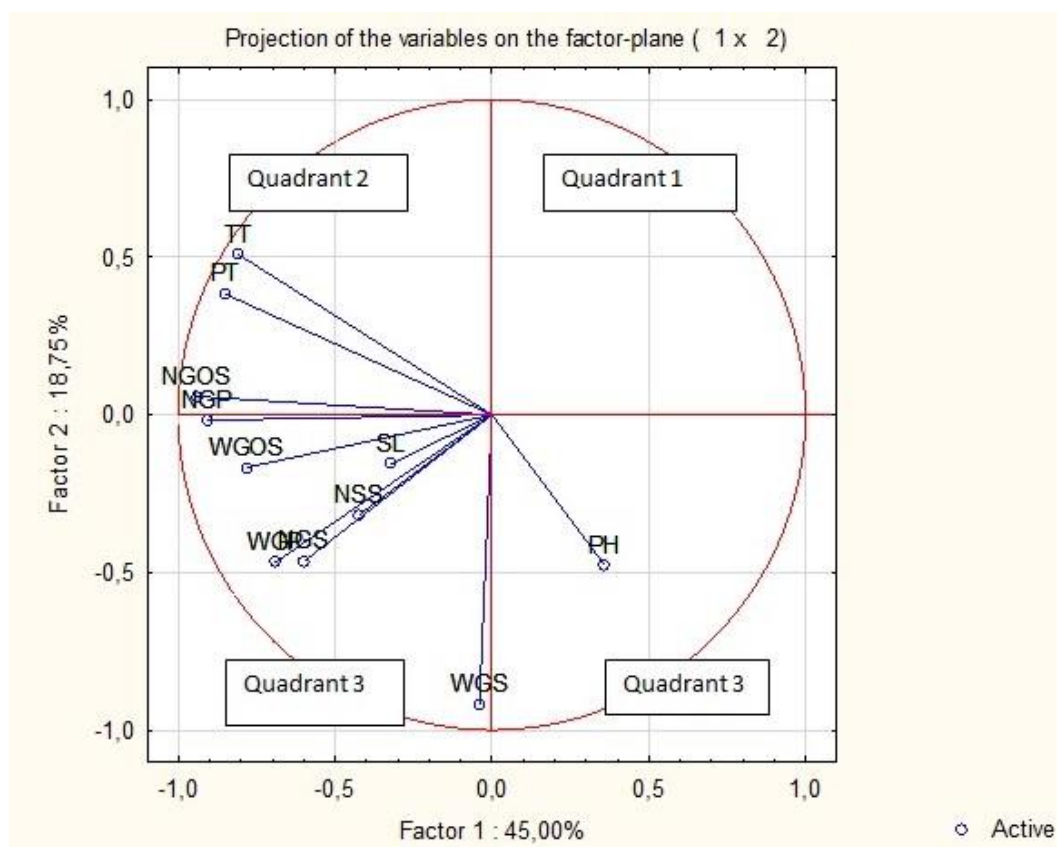

Fig. 2. Results of PC-analysis of the studied traits

PH – plant height (cm), ОБ = TT - total tillering, PT – productive tillering, SL – central spike length (cm), NSS – number of spikelets per central spike, NGS – number of grains per central spike, WGS – grain weight per central spike (g), NGOS – number of grains per other spikes, WGOS – grain weight per other spikes (g), NGP – number of grains per plant, WGP – grain weight per plant (g)
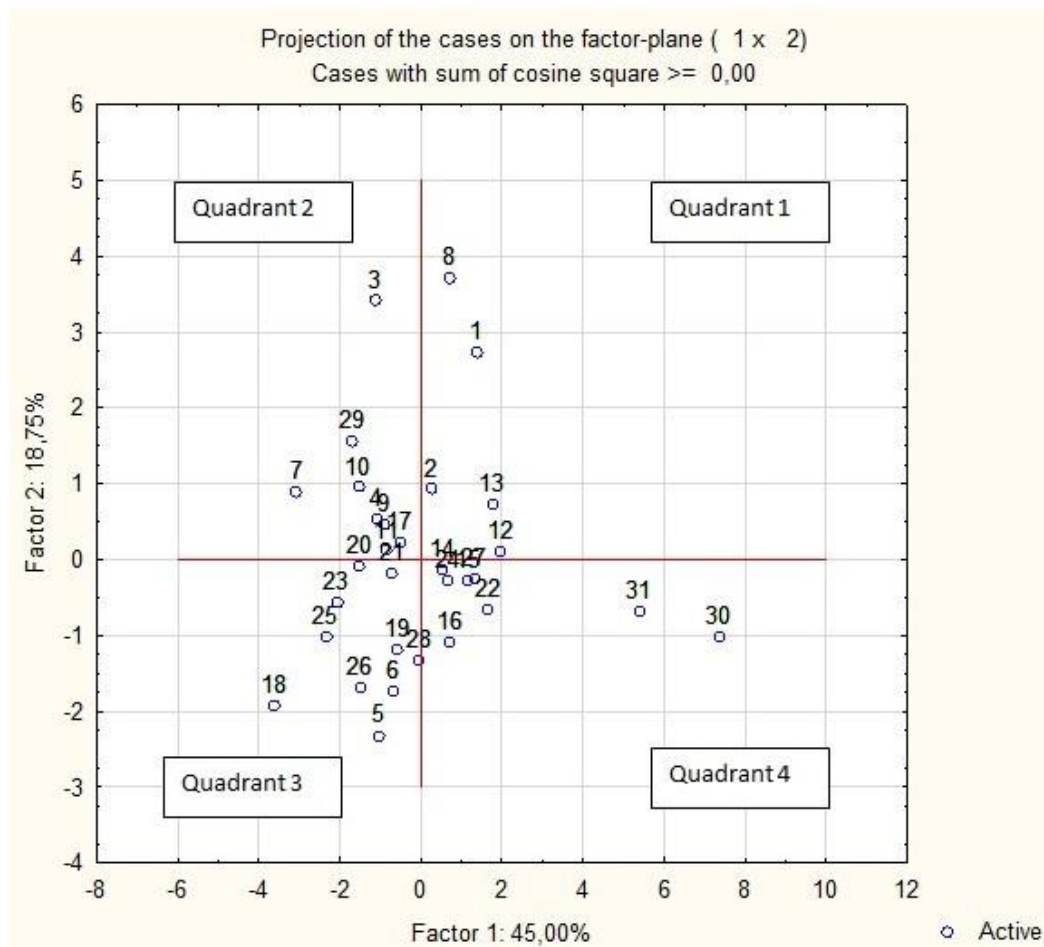
Fig. 3. Results of PC-analysis of the studied varieties

1-Laska, 2-Sonata, 3-Capella, 4-Daria, 5-Arina, 6-Pogiuk, 7-Augustina, 8-Suita, 9-Corona, 10-Uzrim, 11-Vasilisa, 12-Suzore , 13-Visa, 14-Sofia, 15-Credo, 16-Harmony, 17-Avangardnaya, 18-Rassvet, 19-Uzlet, 20- Beloruskaya 8 80, 21-Rostan, 22-Anuta, 23-Lyubava, 24-Sudarinya, 25-Sacret, 26-Oda, 27-Canveer, 28-Toma, 29-Elegya, 30-Sadovo 1, 31-Enola.

According to the angles between the feature vectors could show the correlations between them. As much as the angle is sharper, the correlation is stronger and more positive. At right angles, the correlation is zero and the dull angle defines a negative correlation (DRAGOV and DECHEV, 2016). The results obtained in Fig. 2 show that the plant height is negatively correlated with all components of productivity except the grain weight per central spike. The key factor for improving the wheat productivity in historical terms is lowering the plant height and increasing feeding efficiency (NONAKA, 1983; BOROJEVIC and BOROJEVIC, 2005). Such results are also

reported by DENCIC and KOBILJSKI (2010), who consider the main factors affecting wheat productivity are low plant height and early ripeness, which lead to increased efficiency of assimilates transfer from leaves and stem to the grain.

The strongest, positive and proven correlation is observed between the number of grains per plant with number of grains per other spikes, grain weight per central spike with grain weight per other spikes, and total tillering with productive tillering. A strong correlation between the number of grains and grain weight per spike was also found by STOYANOV (2013). Although grain weight per spike is a direct component of the yield and correlates highly with it (RACHOVSKA and UHR, 2010; STOYANOV, 2013) gives preference to the grain weight per spike as a more valuable breeding trait, which will be sufficient reliable in the breeding process. At the same time, ZHANG *et al.* (2012) reported that a higher number of grains per spike do not always determine a higher yield. As the grain weight per spike is directly related to the yield as its component, it is important to determine the presence or absence of correlation between the other characteristics of the spike with this trait. This would allow new lines to be evaluated at an early stage in their breeding process. SLAFER *et al.* (2014) reported that differences in grain yield are due to the number of grains per unit area, which is most influenced by the number of grains per spike. They consider that the increasing in grain yield is named by a compromise combination between the number of grains per spike with their size and productive tillering.

According to the quadrant in which the points of the varieties are located (Fig. 3) and the trajectory vectors of the traits - Fig. 2, can be found the most relevant influence of the particular trait on a variety. There is also a significant similarity between the distribution of varieties in the factorial plane (Fig. 3) and the results obtained from the dendrogram of the cluster analysis. For example, the figure clearly shows the distance of the Bulgarian varieties Sadovo 1 (№ 30) and Enola (№ 31) to the Belarusian samples. The Sofia variety (№ 14), Sudarinya (№ 24) and Harmony (№ 16), falling into the second cluster group, are also located relatively close to each other in the PC coordinate system. Observing the quadrants in which the individual genotypes are located, we can summarize that the smallest number of genotypes are located in quadrant 1 - 5, and the most of the samples are in quadrant 3 - 10. The positive values of PC1 include 13 genotypes of which the Bulgarian varieties Sadovo 1 and Enola, while 18 are located in the negative values of the factor. According to a number of authors (FANG *et al.,* 1996; KHODADADI *et al.,* 2011; SIAHBIDI *et al.,* 2013), it can be generally accepted that cluster analysis gives the best estimate for the genetic distance of genotypes and therefore, cluster analysis is preferably used in genetic diversity research.

CONCLUSION

The use of multivariate methods, such as cluster analysis and PC analysis, is a reliable way to group genotypes by their genetic distance.

The studied wheat genotypes are grouped into four large cluster groups, with varying degrees of genetic distance. The closest relation is found between the varieties of Vasilisa with Uzlet, and the greatest genetic distance was shown between the two Bulgarian varieties Sadovo 1 and Enola in comparison with the Belarusian genotypes.

Genetically distant varieties belonging to different cluster groups can be used as sources of initial material to achieve genetic diversity in the breeding of common winter wheat.

REFERENCES

ANNUAL REPORT OF MINISTRY OF AGRICULTURE, FOOD AND FORESTRY, (2020): https://www.mzh.government.bg/bg/politiki-i-programi/otcheti-i-dokladi/agraren-doklad/

ARRIEL, N., A., MAURO, E., ARRIEL, M., COSTA, I., BARBARO, F., MUNIZ (2007): Genetic divergence in sesame based on morphological and agronomic traits. Crop Breed Appl Biotechnol, *7*: 253-261.

BHATT, J.M. (1970): Multivariate analysis approach to selection of parents for hybridization aiming at yield components in self-pollination crops. Aust. J. Agric. Rec., *21*: 1-7.

BOROJEVIC, K.A., K.S., BOROJEVIC (2005): The Transfer and History of "Reduced Height Genes" (Rht) in Wheat from Japan to Europe". J. Heredity, *96* (4): 455–459.

BOYADJIEVA, D. (1994): The result of different germplasm using in the wheat breeding program in Bulgarian dry conditions. Evaluation and Exploitation of Genetic Resources Pre-Breeding Meeting of Eucarpia, 15-18 March,1994. Clermon-Ferrant, France.

CHEN, H.B., J.M., MARTIN, M., LAVIN, L.E., TALBERT (1994): Genetic diversity in hard red spring wheat based on sequence tagged site PCR markers. Crop Sci., *34*: 1629–1634.

DEBNATH, N., M., RASUL, M., SARKER, M., RAHMAN (2008): Genetic divergence in buckwheat. Int. J. Sustain. Crop, *3*(2): 60-68.

DENCIC, S., B., KOBILJSKI (2010): Current Status and Trends in NS Wheat Breeding Program. UK-Eastern and Southern Europe wheat Workshop, 15-17 June, Novi Sad, Serbia.

DESHMUKH, S.N., M.S., BASU, P.S., REDDY (1986): Genetic variability, character association and path coefficients of quantitative traits in Virginia bunch varieties of ground nut. Indian J. Res. Agric. Sci., *56*: 515-518.

DIMOVA, D., E., MARINKOV (1999): Experiment and Biometrics. Academic Publishing House of AU. Plovdiv: 193-205.

DRAGOV, R., D., DECHEV (2015): Phenotypic stability of yield on varieties and lines of durum wheat (*Triticum durum* Desf.). Agric. Sci. Tech., *7* (2): 204-207.

DRAGOV, R., D., DECHEV, KR., TANEVA (2019): Genetic Distance of New Bulgarian Durum Wheat Varieties and Breeding Lines of FCI- Chirpan. Bulgaria Int. J. Inn. App. Agric. Res., *3* (3): 402-410.

DRAGOV, R., D., DECHEV (2016): Genetic distance by important economic traits between Bulgarian and foreign durum wheat varieties. Science & Technologies, Volume (6), Number 6: Agrobiological Science: 41-47.

EIVAZI, A. R., M.R., NAGHATI, M., HAJHEIDARI, S.M., PIRSEYEDI, M.R., GHAFFARI, S.A., MOHHAMADI, I., MAJIDI, G.H., SALEKDEH, M., MARDI (2007): Assesing wheat (Triticum aestivum L.) genetic diversity using quality traits, Amplified fragment length polymorphisms, simple sequence repeats and proteome analysis. Ann. Appl. Biol., *152*: 81-91.

EL-DEEB, A.A., N.A., MOHAMED (1999): Factor and cluster analysis for some quantitative characters in sesame (*Sesamum indicum* L.). The Annual Conference ISSR, Cairo University, 4–6 December,Vol. 34, Part (II).

FALKONER, D.S. (1989): Introduction to Quantitative Genetics, Ed. 3. Longmans Green/John Wiley & Sons, Harlow, Essex, UK/New York.

FANG, X., E., XIONG, W., ZHU (1996): Cluster analysis of elite wheat germplasm. Jiangsu Agric. Sci., *4*: 14-16.

GRAYBOSCH, R.A., C.,PETERSON (2010): Genetic improvement in winter wheat yields in the Great Plains of North America, 1959-2008. Crop Sci., *50*(5): 1882-1890.

HAILEGIORGIS, D., M., MESFIN, T., GENET (2011): Genetic Divergence Analysis on some Bread Wheat Genotypes Grown in Ethiopia, J. Central Eur. Agric., *12*(2): 344-352.

HRISTOVA, D., K., CHERESHAROV (2002): 12 technologies for growing cereals and fodder crops. Land - a source of income: 5-10.

ISLAM, M.R. (2004): Genetic diversity in irrigated rice. Pak. J. Biol. Sci., *2*: 226-229.

JAYNES, D.B., T.C., KASPAR, T.S., COLVIN, D.E., JAMES (2003): Cluster analysis of spatio temporal corn yield pattern in an Iowa field. Agronomy J., *95* (3): 574-586.

KABIR, M., A., KHAN, M., HASSAIN (2009): Genetic divergence in pointed gourd. J. Agric. Rural Dev., *7* (1&2): 87-92.

KHAN, M., A., PANDEY, G., THOMAS, M., AKKAYA, S., KAYIS, Y., OZSENSOY, M., HAMURCU, S., GEZGIN, A., TOPAL, E., HAKKI (2015): Genetic diversity and population structure of wheat in India and Turkey. *AoB PLANTS*, Volume 7: 1-17.

KHODADADI, M., M., FOTOKIAN, M., MIRANSARI (2011): Genetic diversity of wheat (Triticum aestivum L.) genotypes based on cluster and principal component analyses for breeding strategies. Aust. J. Crop Sci., *5*(1): 17-24.

LEILAHS, A.A., S.A., AL-KHATEEB (2005): Statistical analysis of wheat yield under drought conditions. J. Arid Environ., Vol. *61*, (3):483-496.

MEREZKO, A. (1998): Impact of plant genetic resources on wheat breeding. In: Wheat: Prospects for Global Improvement (H. J. Brown, F. Altay, W. E. Kronstad and Beniwal eds.). Kluwer Academic Publishers, The Netherlands.

MOHAMMADI, S.A., B.M., PRASSANA (2003): Analysis of genetic diversity in crop plants: salient statical tools and considerations. Crop Sci., *43*: 1235-1248.

NONAKA, S. (1983): History of Wheat breeding in japan. Proc. 6th International Wheat Genetic Symposium, Kioto, Japan: 593.

RACHOVSKA, G., Z., UHR (2010): Inheritance, heterosis and variability of quantitative traits related to productivity in F1 hybrids of common winter wheat. Field Crop Studies, *6* (3): 361-367.

SIAHBIDI, M., A., ABOUGHADAREH, G., TAHMASEBI, M., TEYMOORI, M., JASEMI (2013): Int. J. Agric.: Research and Review, *3* (1): 184-194.

SINGH, S., R., SRIVASTAVA, J., KUMAR (2015): Male sterility systems in wheat and opportunities for hybrid wheat development. Acta. Physiol. Plant., *37*: 1713.

SLAFER, G., A. R., SAVIN, V., SANDRAS (2014): Coarse and fine regulation of wheat yield components in response to genotype and environment. Field Crops Res., *157*: 71-83.

STAMATOV, S., M., DESHEV (2018): Review of the Methods for Breeding of Sesame (Sesamum indicum L.) in Bulgaria. Bulgarian J. Agric. Sci., *3*: 411-416.

STAMATOV, S., N., VELCHEVA (2020): Assessment of genetic diversity in sesame germplasm as an initial materi-al for Bulgarian breeding programs. Bulgarian J. Agric. Sci., *26* (5): 1047–1052.

STOEVA, I., P., CHAMURLIYSKI, N., TSENOV (2009): Study of Bulgarian and foreign varieties and lines of common winter wheat in relation to their use in the breeding of productivity and quality. Field Crops Studies, *5* (2): 253-260.

STOYANOV, H. (2013): Correlation between Spike Characteristics of Common Winter Wheat (*Triticum aesitvim L.*) Varieties. Breeding and genetic studies in field crops: 95-100.

ZHANG, W., A., LI, J., TIAN, L., ZHAO (2012): Development of Near Isogenic Lines of Wheat Carrying Different Spike Branching Genes and Their Agronomic and Spike Characters. J. Agric. Sci., *4-8*: 215-221.

GENETIČKA DISTANCA SORTI OZIME PŠENICE

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Izvod

Studija je sprovedena tokom perioda 2017-2019 na eksperimentalnom polju IPGR Sadovo. Pšenica je najvažnija poljoprivredna kultura u svetu. Proizvodnja pšenice u Bugarskoj u 2019. godini iznosila je 6,162 hiljade tona - rast od 5,7% u odnosu na 2018. godinu, zbog relativno povoljnih klimatskih uslova u toku vegetacije, što je dovelo do povećanja prosečnog prinosa (sa 6,8%). Ocenjeno je 29 sorti ozime pšenice (*Triticum aestivum* L.) beloruskog porekla i dve bugarske sorte - Sadovo 1 i Enola. Proučavane sorte posejane su u 2 reda dužine - 2 m, sa razmakom između redova - 20 cm i rastojanju u redovima - 5 cm. Korišćena je standardna tehnologija usvojena u IPGR za gajenje ozime pšenice. Cilj ove studije je da istraži genetičku distancu genotipova ozime pšenice u cilju njihove upotrebe u oplemenjivačkom procesu kao izvora početnog materijala za formiranje novih i visoko produktivnih sorti pšenice. Biometrijska merenja su izvršena na 20 biljaka svakog genotipa i zabeleženi su glavni pokazatelji produktivnosti. Da bi se procenila genetička sličnost između različitih sorti, primenjena je klaster analiza i PC analiza. Na osnovu klaster analize, proučeni genotipovi su grupisani u pet velikih klastera. Sa najviše genetičke bliskosti karakterišu se sorte Vasilisa i Uzlet, zatim Darija i Rostan. Najveća genetiška distanca prikazana je između bugarskih sorti Sadovo 1 i Enola i sorti iz Belorusije. Najveća genetska razlika utvrđena je između Sadova 1 i Rassveta, zatim Enole i Rassveta. Genetski udaljene sorte koje pripadaju različitim grupama klastera mogu se koristiti kao izvori početnog materijala za ostvarivanje genetičkog diverziteta u oplemenjivanju ozime pšenice.