

## THE GENETIC DISTANCE OF ADVANCED LINES COMMON WINTER WHEAT BY IMPORTANT ECONOMIC TRAITS

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### Abstract

*The study was conducted in the period 2019-2021 on the experimental field of IRGR "K. Malkov" Sadovo. Twenty advanced breeding lines and four common winter wheat varieties were studied according to important economic traits. Grain yield, plant height, thousand grain weight and test weight were reported. To assess the genetic similarity and distance between the different genotypes, cluster analysis and analysis of the main components were applied. Based on the results of the cluster analysis, the studied genotypes were divided into five large cluster groups. The applied analysis of the main components shows that the components PC 1 and PC 2 explain 67.9% of the total variation of all traits by genotypes. The line MX 270/86 and the Enola variety, located in the most distant parts of the coordinate system, can be mentioned as a source of strong variation and genetic difference.*

**Key words:** common winter wheat, breeding lines, genetic distance, cluster analysis, PC analysis.

### INTRODUCTION

In the modern world, common wheat is of paramount importance to human nutrition and is widespread in almost all latitudes. (Rodomiro et al., 2008). Wheat is the main food cereal crop in Bulgaria. It is of great economic importance for the national economy. Its cultivation is favored by the appropriate soil and climatic conditions in the country. It occupies about 35% of the arable land in the country (between 11.5 and 12.5 million decares). As of the beginning of December 2021, the sown areas with wheat for the harvest of 2022 are by 1.1% more on an annual basis than the reported area for the previous year ([https://www.mzh.government.bg/media/filer\\_public/2021/12/15/operativen\\_analiz\\_2021-12-15.pdf](https://www.mzh.government.bg/media/filer_public/2021/12/15/operativen_analiz_2021-12-15.pdf)).

The wide application and the growing demand on a global scale are a prerequisite for new scientific endeavors and continuous development of selection programs, as it is the subject of large-scale research work (Chamurliski, 2019). By determining the genetic distance for the correct selection of parental forms, significant progress can be made in the potential for recombinant

genotypes (Islam, 2004). The success of any breeding program depends on the use of diverse genetic material (Pevicharova & Todorov, 2001; Todorov & Pevicharova, 2002; Markovic et al., 2002; Strano et al., 2011). Genetic diversity in plants determines their potential for achieving breeding advance, when applying the method of hybridization, according to the available genetic distance of genotypes. The more genetically distant the parental forms, the greater the potential for gene interaction in the form of dominance and epistasis leading to an increase in the potential for heterosis and transgression (Falconer, 1989). Estimation of genetic distance between genotypes can be based on the phenotypic manifestation of quantitative and qualitative traits (Kennedy et al., 1991; Souza & Sorells, 1991; Stoyanova, et al., 2019; Yanev, et al., 2021), molecular markers (Cao et al., 1998) or on the relationship coefficient (Mercado et al., 1996). Most often, genetic distance is measured as phenotypic distance (Anjani, 2005; Bose & Pradhan, 2005; Arriel et al., 2007; Debnath et al., 2008; Gashaw et al., 2007; Kabir et al., 2009; Dragov et al., 2019). The grouping of breeding materials using cluster analysis has been successfully used by various researchers

such as Devesh et al. (2019); Degewione & Alamerew (2013) and Baranwal et al. (2013).

The aim of the present study is to carry out an investigation of advanced breeding lines common winter wheat by important economic traits and determine their genetic distance with a view to their use in the breeding program as sources of starting material for creating new highly productive wheat varieties.

## MATERIALS AND METHODS

The experiment was conducted in the experimental field of IRGR - Sadovo in the period 2019-2021. The common technology for growing common wheat was used. The field varietal experiments were carried out according to a randomized block diagram in three replications, with the size of the experimental plot of 10 m<sup>2</sup>. The studied genotypes were compared with the complex standard for the country variety Sadovo 1. Twenty-four genotypes of common winter wheat were studied according to the following economic indicators: grain yield (kg/da), plant height (cm), 1000 grains weight (g) and test weight (kg/hl). The evaluation of the quality traits was performed in a technological laboratory at the Institute. The degree of variation of the studied traits was determined by calculating a coefficient of variation. It is accepted that variation is considered weak if the coefficient of variation is up to 10%, on average - when it is greater than 10% and less than 20%, strong - when it is above 20% (Dimova & Marinkov, 1999). On the results for mean of genotypes was conducted Duncan's test for multiple comparison between the means at the detected significant differences ( $p < 0.05$ ) (Duncan, 1955) over all studied traits. Statistica 10 software program was used for the two analyzes performed above. Hierarchical cluster analysis by the method of Ward (1963) and Principal Component Analysis (Kim & Mueller, 1978) was used to determine the genetic distance between the individual genotypes, based on the mean values for the study period. Mathematical analysis of the results was performed using the statistical processing programs SPSS 19 and Microsoft EXCEL 10 for Windows.

## RESULTS AND DISCUSSIONS

On the Table 1 are presented the results of the surveyed economic traits for the three-year survey period. According to Duncan's test, it was found that there were significant differences between the genotypes in the studied traits, only for the yield trait the differences are very small and most genotypes are in one group. The data in the table show that the highest average yield was achieved by the lines RU 129/3053 (784.3 kg/da), MX 270/50 (762.6 kg/da) and MX 258/3353 (756.4 kg/da), and low was reported for lines MX 270/86 (639.7 kg/da) and MX 274/717 (625.3 kg/da). Nineteen wheat genotypes fall above the level of the Sadovo 1 standard, nine of which have achieved yields of over 700.0 kg/da.

According to the plant height, the values of the studied samples are in the range from 86.7 cm (Enola) to 110.0 cm (MX 276/3616). In ten breeding lines the reported plant height is less than 100 cm. The lines MX 274/717 (49.5 g), MX 270/3463 (49.3 g) and MX 270/86 (48.8 g) are characterized by a high value in terms of 1000 grains weight, and by line RU 48/2553 (39.6 g) is the lowest. In 54.2% of the total number of studied samples the measured 1000 grains weight is over 45.0 g.

The test weight of the examined materials ranges from 68.2 kg/hl (MX 270/86) to 79.7 kg/hl (MX 286/1759). Exceeding the standard trait was observed in twelve wheat genotypes. On fourteen samples the reported test weight is over 75.0 kg/hl.

The calculated coefficient of variation shows that the variation of the studied traits is assessed as weak ( $CV < 10.0\%$ ), with the lowest variation in the traits test weight ( $CV = 3.3\%$ ) and the highest in the plant height of the rations. Grain yield has a coefficient of variation ( $CV = 6.0\%$ ) (Table 1).

To determine the genetic similarity and distance between the studied breeding materials, a cluster analysis based on the studied economic traits was applied. The study of genotypes through cluster analysis allows breeders to plan and make more effective decisions for the development of their breeding programs. With the help of cluster analysis, the samples can be divided by genotype, depending

on its phenotypic manifestation by a certain trait (based on different environments) or a group of traits. The results of the hierarchical cluster analysis are presented as a dendrogram

on Figure 1. It can be seen from the figure that the studied breeding materials are grouped into five main cluster groups. The first group consists of four wheat genotypes.

Table 1. Results of biometric measurements of economic indicators in genotypes of common winter wheat for the period 2019-2021

№	Genotype	Yield, kg/da	Plant height, cm	1000 grains weight, g grains weight	Test weight, kg/hl
1	Sadovo 1 – st.	656.8ab	98.3abc	47.1abcd	75.8b
2	MX 270/24 (Nany) nnnnbbNany	754.3ab	89.3bde	42.3bcdef	72.0bc
3	MX 270/28	681.0ab	97.3ef	44.2bcdef	72.9bcde
4	MX 270/27	648.9ab	101.3def	44.4efgh	75.1bcd
5	MX 270/50	762.6a	99.0def	46.8h	73.3a
6	MX 270/86	639.7ab	100.3bcde	48.8efgh	68.2bcde
7	MX 268/1008 (Sashez)	725.4ab	97.3fg	47.1defgh	74.6cdef
8	Ayilzla	732.6ab	106.7ef	45.8abc	77.0def
9	Nadita	689.9b	101.3ef	41.6abc	77.3bcdef
10	RU 129/3053	784.3ab	101.7g	41.7fgh	75.9ef
11	MX 276/3616	692.6ab	110.0fg	48.0efgh	78.4bcdef
12	RU 33/3244	712.5ab	106.3a	46.8bcdef	76.2bcde
13	MX 258/3353	756.4ab	88.3ef	44.3efgh	75.0def
14	MX 260/1175	743.9ab	102.0bdef	46.5efgh	77.3bcdef
15	Enola	676.3ab	86.7a	40.6ab	77.7ef
16	MX 265/3430	668.3ab	101.3ef	47.1efgh	76.4bcdef
17	MX 270/3461	675.5ab	97.3bde	48.1fgh	75.9bcdef
18	MX 270/3462	693.0ab	99.3def	48.6gh	74.5bcde
19	MX 270/3463	735.3ab	98.3bdef	49.3h	74.9bcde
20	MX 274/717	625.3a	106.0fg	49.5h	78.8ef
21	MX 286/1759	658.9ab	92.3abcd	44.8cdefg	79.7f
22	MX 286/1777	704.3ab	89.0a	42.5abcd	77.8ef
23	RU 48/2553	681.4ab	90.7abc	39.6a	74.5bcde
24	MX 215/3	691.5ab	88.0a	43.2abcde	72.7bc
	<b>Mean</b>	699.6	97.8	45.4	75.5
	<b>Minimum</b>	625.3	86.7	39.6	68.2
	<b>Maximum</b>	784.3	110.0	49.5	79.7
	<b>Coef. var., %</b>	6.0	6.7	6.4	3.3
	<b>Standard error</b>	8.6	1.3	0.6	0.5

Mean values (in each column), followed by the same letters are not significantly different at  $p < 0.05$  according to Duncan's multiple range test (DMRT).

The lines MX 270/24 (Nany), MX 258/3353 and MX 270/50 form a separate subgroup, to which line RU 129/3053 joins at a higher Euclidean distance. The characteristic of this group is that the high yielding selection materials are united here. The results obtained are confirmed by the studies of Ajmal et al. (2013) who point out that high-yielding genotypes are grouped into a separate cluster, thus facilitating the process of selecting appropriate genotypes.

A second main cluster group is represented by the Ayilzla variety and the lines MX 270/3463, MX 260/1175, MX 268/1008 (Sashez).

Representatives of this group are characterized by relatively high yields and at the same time have achieved the highest value in terms of mass per 1000 grains.

The third cluster includes five breeding materials. The standard Sadovo 1 and the lines MX 286/1759, MX 270/27, MX 270/86 are separated into a separate subgroup to which line MX 274/717 is connected. The genotypes forming this group had the lowest average yield compared to the other cluster groups.

The fourth cluster group includes the variety Enola and the lines RU 48/2553, MX 270/28, MX 270/3461, MX 265/3430. Samples from

this group are characterized as low yields, with a high value of test weight and relatively low plant height.

The fifth cluster group, represented by six samples, is the most numerous. The lines MX 286/1777 and MX 215/3 form an independent subgroup. An independent subgroup is also

observed between the variety Nadita and the lines MX 270/3462 and MX 276/3616. The line RU 33/3244 joins the two subgroups at a higher Euclidean distance. The representatives of this group have achieved the highest value of the traits test weight.

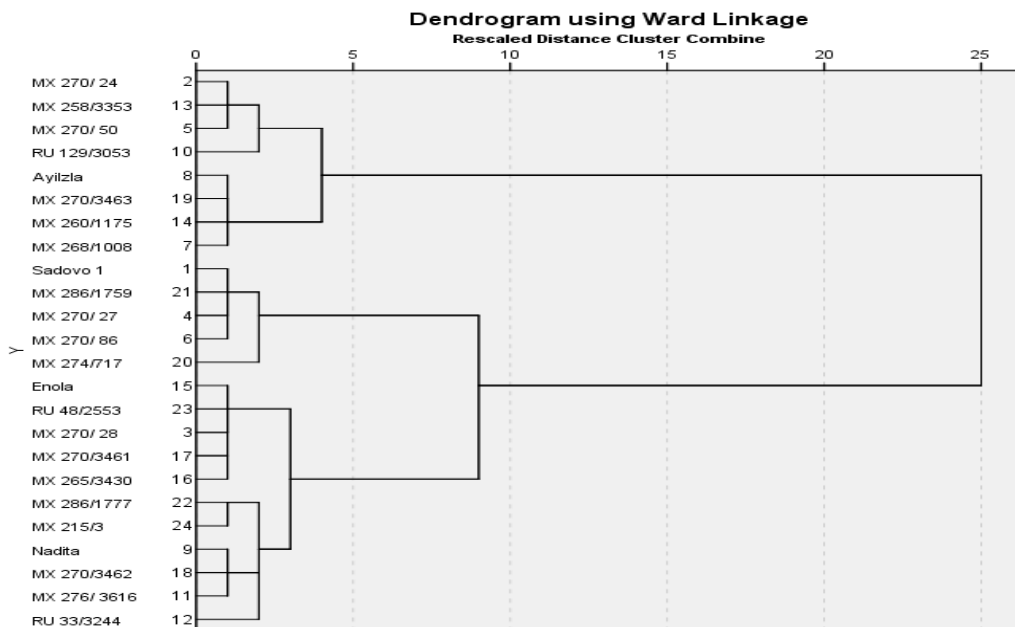


Figure 1. Dendrogram of hierarchical cluster analysis for 24 genotypes of common winter wheat

Dividing breeding materials into groups by using cluster analysis has been successfully applied by various researchers. For example, Devesh et al. (2019) examines sixty wheat lines on agronomically important traits, which are grouped into five cluster groups. Degewione & Alamerew (2013) reported the identification of six cluster groups in the twenty-six wheat genotypes they studied. Baranwal et al. (2013) grouped twenty-four wheat samples into four clusters.

Table 2 presents the genetic proximity and remoteness of the studied breeding materials based on the coefficient at which the individual cluster pairs are formed. The higher the value of the coefficient, the greater the differences between the studied samples. The results of the table show that the line MX 270/24 with line MX 258/3353 (2.145) is characterized by the greatest genetic similarity, followed by the variety Enola with line RU 48/2553 (5.794). In

terms of genetic distance, there are significant differences between the lines RU 129/3053 compared with MX 274/717 (159.276) and MX 270/86 compared with RU 129/3053 (137.615). According to several authors (Fang et al., 1996; Khodadadi et al., 2011; Siahbidi et al., 2013), it can be generally accepted that cluster analysis gives the best assessment of the genetic distance of genotypes and therefore, cluster analysis is preferably used in genetic diversity research. Pooja & Binewal (2018) and Dragov et al. (2019) revealed that results of cluster analysis could be exploited in planning and execution of future breeding improvement program in wheat.

The analysis of the main components is a supplement to the cluster analysis. Principal component analysis (PCA) reflects the importance of the largest contributor to the total variation at each axis of differentiation (Sharma et al., 1998).

Table 2. Genetic similarity between the studied triticale genotypes

№	Genotype	Genotype	Coefficient	Similar/Distant
1	MX 270/24	MX 258/3353	2.145	genetically similar
2	Enola	RU 48/2553	5.794	genetically similar
3	MX 270/28	MX 270/3461	9.484	genetically similar
4	Sadovo 1	MX 286/1759	13.386	genetically similar
5	Nadita	MX 270/3462	17.583	genetically similar
6	MX 258/3353	MX 274/717	132.446	genetically distant
7	MX 270/27	RU 129/3053	135.43	genetically distant
8	MX 270/50	MX 274/717	137.615	genetically distant
9	MX 270/86	RU 129/3053	144.986	genetically distant
10	RU 129/3053	MX 274/717	159.276	genetically distant

The results of the conducted PC analysis (Table 3) show that the two main components PC 1 and PC 2 explain 67.9% of the total variation of the studied traits and genotypes, which is large enough.

Similar results in determining the general variation are mentioned by other authors. Analyzing the genetic diversity of twenty-two bread wheat genotypes, Fouad (2020) reported that three main components accounted for 79.6% of the total variation. Boshev et al. (2016) point out that the overall variation in their study is 71.4% and is due to the three main components.

Table 3. Component analysis of the variance in the studied traits

Component	Total	% of Variance	Cumulative %
1	1.68	42.0	42.0
2	1.04	25.9	67.9
3	0.94	23.6	91.5
4	0.34	8.5	100.0

Table 4 shows the location of the studied economic traits to the two main components. According to Chahal & Gosal (2002) characters with the largest absolute value closer to unity within the first principal component influence the clustering more than those with lower absolute value closer to zero.

In our study, the first component included the traits yield, plant height and 1000 grains weight, with the yield negatively related to PC 1, and the other two traits were positively related to the component. In PC 2 falls the sign hectoliter mass, positively connected component.

Table 4. Explained significant components by indicators by wheat samples

№	Traits	Component	
		1	2
1	Yield	-0.396	-0.228
2	Plant height	0.861	-0.023
3	1000 grains weight	0.847	-0.36
4	Test weight	0.254	0.924

The selected breeding materials relate differently to the two main components (Table 5).

Table 5. Explained significant components by wheat genotypes

№	Genotype	Component	
		1	2
1	Sadovo 1 – st.	0.533	0.293
2	MX 270/24- Nany	-1.304	-1.584
3	MX 270/28	-0.081	-0.737
4	MX 270/27	0.280	0.325
5	MX 270/50	0.243	-1.267
6	MX 270/86	1.454	-2.365
7	MX 268/1008	0.255	-0.610
8	Ayilzla	0.562	0.465
9	Nadita	-0.545	1.012
10	RU 129/3053	-0.786	-0.111
11	MX 276/3616	1.341	1.156
12	RU 33/3244	0.848	0.243
13	MX 258/3353	-1.127	-0.677
14	MX 260/1175	0.291	0.359
15	Enola	-1.819	1.017
16	MX 265/3430	0.688	0.489
17	MX 270/3461	0.584	0.121
18	MX 270/3462	0.836	-0.485
19	MX 270/3463	0.722	-0.687
20	MX 274/717	1.577	1.571
21	MX 286/1759	-0.578	1.691
22	MX 286/1777	-1.373	0.793
23	RU 48/2553	-1.585	-0.013
24	MX 215/3	-1.016	-1.001

The first component is represented by fifteen wheat genotypes, six of which are located in the positive values of PC1, and the remaining samples are located in the negative values. Eight samples fall into component two, four of which are positively related to the component and the other four fall into the negative parts of the component.

On the other hand, genotypes located on the periphery are characterized by a more pronounced specific trait. Those in the middle are more balanced in terms of the studied traits. According to Khodadadi et al. (2011) genetic diversity of plants determines their potential for improved efficiency and hence their use for breeding, which may eventually result in enhanced food production. In this sense, the genotypes MX 270/86, Enola, MX 286/1759 and RU 48/2553, located in the most remote parts of the factorial plane, can be mentioned as sources of variation in order to create a variety

of starting material and enrich the gene pool in common winter wheat. The above mentioned samples can be used as parent pairs in hybridization for selective improvement work in common wheat. They can be expected to produce recombinant ones with higher yields and the creation of new varieties of common wheat is possible.

From the graphical representation of the analysis of the main components by genotypes (Figure 2) we can get a clearer idea of the location of the studied materials in the coordinate system. The more distant location a genotype has in the coordinate system, the more it is genotypically and phenotypically different from other samples.

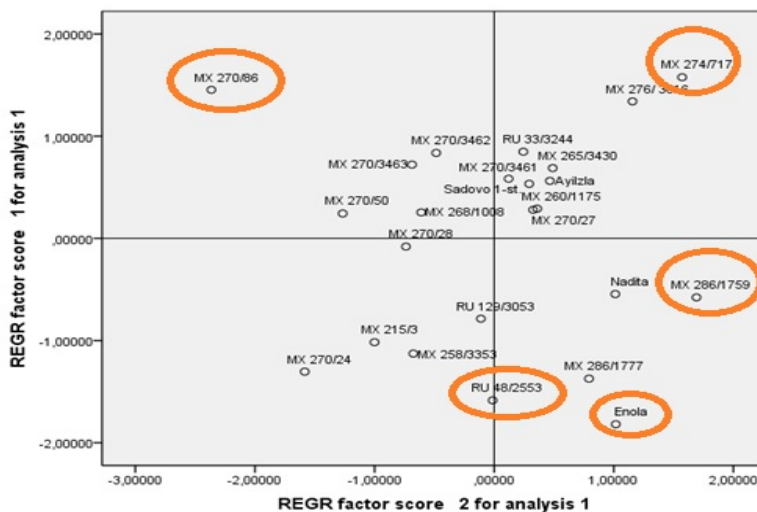


Figure 2. Projection of the studied genotypes by main components

## CONCLUSIONS

Significant differences were found between genotypes on all studied traits.

The studied breeding materials are divided into five main cluster groups, with different degrees of genetic distance. The lines MX 270/24 and MX 258/3353 are characterized by the greatest genetic proximity, and the strongest genetic distance is observed between the lines MX 274/717 and RU 129/3053.

The analysis of the main components shows that the components PC 1 and PC 2 explain 67.9% of the total variation of all traits and genotypes. Component one includes fifteen genotypes, and component two includes nine.

The following genotypes can be determined as sources of variation: MX 270/86, Enola, MX 286/1759 and RU 48/2553

Genetically distant breeding materials falling into different cluster groups and components can be used as sources of starting material to increase genetic diversity in the selection

process and create new lines and varieties of common winter wheat.

## REFERENCES

- Ajmal, S., Minhas, N., Hamdani, A., Shakir, A., Zubair, M., & Ahmad, Z. (2013). Multivariate analysis of genetic divergence in wheat (*Triticum aestivum* L) germplasm. *Pakistan Journal of Botany*, 45(5), 1643–1648.
- Anjani, K. (2005). Purple-coloured castor (*Ricinus communis* L.) - a rare multiple resistant morphotype. *Current Science*, 88(2), 215–216.
- Arriel, N., Mauro, D., Arriel, F., Costa, M., Barbaro, M., & Muniz, F. (2007). Genetic divergence in sesame based on morphological and agronomi traits. *Crop Breeding and Applied Biotechnology*, 7, 253–261.
- Baranwal, D., Mishra, V., & Singh, T. (2013). Genetic Diversity Based on Cluster and Principal Component Analyses for Yield and its Contributing Characters in Wheat (*Triticum aestivum* L.). *Madras Agricultural Journal*, 100(4-6), 320–323.
- Bose, L., & Pradhan, S. (2006). Genetic divergence in deepwater rice genotypes. *Journal of central European agriculture*, 6(4), 635–640.



- Boshev, D., Jankulovska, M., Ivanovska, S., & Jankuloski, L. (2016). Assessment of winter wheat advanced lines by use of multivariate statistical analyses. *Genetika*, 48(3), 991–1001.
- Cao, W., Hucl, P., Scoles, G., & Chibbar, R. (1998). Genetic diversity within spelta and macha wheats based on RAPD analysis. *Euphytica*, 104(3), 181–189.
- Chahal, G., & Gosal, S. (2002). Principles and Procedures of Plant Breeding Biotechnology and Conventional Approaches. *Narosa Publishing House, New Delhi*, 21. 64–89.
- Chamurliski, P. (2019). Historical aspects and achievements of selection in bread wheat (*Triticum aestivum* L.) in southern Dobrogea. *New Knowledge*, 60–70.
- Debnath, N., Rasul, M., Sarker, M., & Rahman, M. (2008). *International Journal of Sustainable Crop Production*, 3(2), 60–68.
- Degewione, A., & Alamerew, S. (2013). Genetic Diversity in Bread Wheat (*Triticum aestivum* L.) Genotypes. *Pakistan Journal of Biological Sciences*, 16. 1330–1335.
- Devesh, P., Moitra, P., Shukla, R., & Pandey, S. (2019). Genetic diversity and principal component analyses for yield, yield components and quality traits of advanced lines of wheat. *Journal of Pharmacognosy and Phytochemistry*, 8(3), 4834–4839.
- Dimova, D., & Marinkov, E. (1999). Experiment and Biometrics. *Academic Publishing House of AU Plovdiv*, 193–205.
- Dragov, R., Dechev, D., & Taneva, K. (2019). Genetic Distance of New Bulgarian Durum Wheat Varieties and Breeding Lines of FCI-Chirpan, Bulgaria. *International Journal of Innovative Approaches in Agricultural Research*, 3(3), 402–410.
- Duncan, D. (1955). Multiple Range and Multiple F-tests. *Biometrics*, 11(1), 1–42.
- Falconer, D. (1989). Introduction to quantitative genetics. 3rd Edition, *Longman Scientific and Technical*, New York.
- Fang, X., Xiong, E., & Zhu, W. (1996). Cluster analysis of elite wheat germplasm. *Jiangsu Agric Sci*, 4. 14–16.
- Fouad, H. (2020). Principal Component and Cluster Analyses to Estimate Genetic Diversity in Bread Wheat (*Triticum aestivum* L.) Genotypes. *Journal of Plant Production*, 11(4), 325–331.
- Gashaw, A., Mohammed, H., & Singh, H. (2007). Genetic divergence in selected durum wheat genotypes of Ethiopian plasm. *African Crop Science Journal*, 15(2), 67–72.
- [https://www.mzh.government.bg/media/filer\\_public/2021/12/15/operativen\\_analiz\\_2021-12-15.pdf](https://www.mzh.government.bg/media/filer_public/2021/12/15/operativen_analiz_2021-12-15.pdf)
- Islam, M. (2004). Genetic diversity in irrigated rice. *Pakistan Journal of Biological Sciences*, 2. 226–229.
- Kabir, M., Khan, A., & Hassain, M. (2009). Genetic divergence in pointed gourd. *Journal of Agriculture & Rural Development*, 87–92.
- Kennedy, H., Anderson, J., Lapitan, V., Sorells, M., & Tanksley, S. (1991). Construction of a restriction fragment length polymorphism map for barley (*Hordeum vulgare* L.). *Genome*, 34. 437–447.
- Khodadadi, M., Fotokian, M., & Miransari, M. (2011). Genetic diversity of wheat (*Triticum aestivum* L.) genotypes based on cluster and principal component analyses for breeding strategies. *Australian Journal of Crop Science*, 5(1), 17–24.
- Kim, J., & Mueller, C. (1978). Factor Analysis: Statistical Methods and Practical Issues. *Beverly Hills and London: Sage Publications*.
- Marcovic, Z., Zdravkovic, J., Mijatovic, M., & Damjanovic, M. (2002). Breeding Potential of Local Tomato Populations for  $\beta$ -Carotene and Vitamin C. Proceedings of the Second Balkan Symposium on Vegetables and Potatoes. *Acta Horticulturae*, 579. 157–162.
- Mercado, L., Souza, E., & Kephart, K. (1996). Origin and diversity of North American hard spring wheat. *Theoretical and Applied Genetics*, 93. 593–599.
- Pevicharova, G., & Todorov, T. (2001). Biochemical and organoleptic evaluation of Bulgarian and foreign (F1) tomato varieties for fresh consumption. *Bulgarian Journal of Agricultural*, 7. 297–301.
- Pooja, D., & Beniwal, R. (2018). Genetic diversity based on cluster and principal component analyses for yield and its contributing characters in RILs of bread wheat (*Triticum aestivum* L.). *International journal of pure and Applied Bioscience*, 6(2), 242–247.
- Rodomirol, O., Braun, J., Crossa, J., Crouch, H., Davenport, G., Dixon, S., Dreisigacker, E., Duveiller, Z., Huerta, A., Joshi, M., Kishii, P., Kosina, Y., Manes, M., Mezzalama, A., Morgounov, J., Murakami, J., Nicol, G., Ferrara, J., Monasterio, T., Payne, R., Penˆa, M., Reynolds, K., Sayre, R., Sharma, R., Singh, J., Wang, M., & Warburton, H. (2008). Wheat genetic resources enhancement by the International Maize and Wheat Improvement Center (CIMMYT). *Genetic Resources and Crop Evolution*, 1095–1140.
- Sharma, P., Gupta, P., & Balyan, H. (1998). Genetic diversity in a large collection of wheats (*Triticum* spp.). *Indian Journal of Genetics and Plant Breeding*, 58. 271–278.
- Siahbidi, M., Aboughadareh, A., Tahmasebi, G., Teymouri, M., & Jasemi, M. (2013). *International journal of Agriculture*, 3(1), 184–194.
- Souza, E., & Sorrells, M. (1991). Relationships among 70 North American oat germplasms: I. Cluster analysis using quantitative characters. *Crop Science*, 31. 599–605.
- Stoyanova, A., Ganchev, G., & Kuneva, V. (2019). Assess the impact of fertilization on wheat protein and energy nutrition. *Scientific Papers. Series A. Agronomy*, 62(1), 443–449.
- Strano, T., Ruberto G., Patanˆe, C., & La Rosa, S. (2011). Qualitative analysis of volatile compounds in local landraces of tomato cultivated in South Italy. *Acta Horticulturae*, 918. 517–523.
- Todorov, T., & Pevicharova, G. (2002). Quality of fruits in different varieties of tomatoes. *Nauchna*

- konferencia s mezhduнародno uchastie "Hrani, zhdrave i dalgoletie", Smolyan, 338–341.*
- Ward, J. (1963). Hierarchical grouping to optimize an objective function. *Journal of the American Statistical Association*, 58. 234–244.
- Yanev, M., Neshev N., Mitkov, A., Nesheva, M., 2021. Control of mixed weed infestation in winter wheat. *Scientific Papers. Series A. Agronomy, LXIV(2)*, 350–357.