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CLUSTER ANALYSIS OF *TRITICUM L.* SAMPLES OF DIFFERENT ECOLOGICAL AND GEOGRAPHICAL ORIGIN

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Abstract. This research paper is devoted to the application of cluster analysis for evaluating samples of soft spring wheat by elements of crop structure. The purpose of the study is to analyse the intraspecific and interspecific variability of morphological features of samples of spring wheat of various ecological and geographical origin according to 8 morphological features. Observations were carried out in 2018-2020 in the training and experimental production centre "Doslidne pole" of the Kharkiv National Agrarian University named after V.V. Dokuchaev. The cluster analysis of the collection of spring wheat samples, which included 76 samples of various ecological and geographical origin, allowed the study to assess the following features: the presence of awns, the colour of awns, the colour of ear scales, the pubescence of leaves, the pubescence of the subcrown internode, the pubescence of the ear internode, the colour of caryopsis, the colour of straw. The results of analysis of the phylogeny of various types of spring wheat by cluster analysis using morphological markers to determine homogeneous groups are presented, and the affected tree of systematic formation of clustering groups is established. Based on the cluster analysis, two separate groups of soft spring wheat samples were identified according to the complex of plant productivity elements. Samples are grouped into each cluster depending on the quantitative characteristics of the crop structure and their interaction with each other. In general, all samples over the years of study showed good results, namely based on "colour of awns", of particular note are the samples of the *Tr. persicum* species. According to the results obtained, all samples have good indicators, and cluster analysis of soft spring wheat samples allowed identifying groups of plants that exceed the parent forms in the optimal set of economically valuable traits, which would allow for a more purposeful selection of valuable forms based on certain traits

Keywords: model, clustering, cluster, dendrogram, evaluation, spring wheat



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INTRODUCTION

Morphological aspects of spring wheat productivity are very important in scientific research, in particular, how exactly morphological features affect the food qualities of the investigated crop. It is the value of morphological features that allows establishing varieties of spring wheat. According to morphological features, wheat species are grouped into two groups: common wheat and spelt. Ecological polymorphism of spring wheat samples can serve as a source of variations for use in breeding, causing the formation of updated forms of economically valuable wheat plants with improved properties. Imperfect genetic information about hereditary material can reduce the effectiveness of breeding activities, since it is not possible to create seed material that is more resistant to adverse factors. Therefore, the conservation of genetic resources and the assessment of their diversity is very important in further studies [1; 2].

To obtain reliable results, when choosing a specific method of cluster analysis, classification was chosen to get more detailed information about the morphological features of the studied samples. Cluster analysis is the only method for organising objects that have the same characteristics. It is used when studying the structure of aggregates of socio-economic indicators or objects: enterprises, regions, sociological questionnaires, collectives. The main purpose of cluster analysis is to divide the set of objects and features under consideration into homogeneous groups or clusters. Cluster analysis is widely used in marketing research. If it is necessary to classify a set of certain information into groups for further processing, cluster analysis is very effective. An achievement of cluster analysis is the ability to split objects not by one parameter, but by a number of features. Also, cluster analysis, unlike most mathematical and statistical methods, does not impose any restrictions on the type of objects under consideration, and allows studying a set of data of arbitrary nature [3; 4].

The analysed literature data on grain production in the world for the period 1965-2019 [5] indicate that the area of grain crops almost does not change, but their yield during this period increased from 1.49 to

3.29 t/ha, or 2.2 times. It was the highest in the EU countries – 5.60 t/ha, the lowest – in the CIS countries – 1.95 t/ha [6]. According to some researchers, the contribution of breeding to yield growth reaches 50% [7; 8], and the study of morphological indicators by cluster analysis of genotypes is a very relevant issue. A very important world-class task is to search for highly productive genotypes for arid conditions, especially cereals. A negative trend is recognised as a drop in yields in South-Eastern Europe [9; 10].

The purpose of the study is to investigate the intraspecific and interspecific variability of the collection of spring wheat samples of various ecological and geographical origin in the conditions of the eastern forest-steppe of Ukraine by 8 morphological features. For the furtherance of this goal, the following *tasks* were set: to assess the genetic divergence of the investigated plant material; based on the results obtained, to draw a conclusion about the phylogenetic relationships between the spring wheat species involved in this study.

MATERIALS AND METHODS

The source material was represented by 76 samples of *Triticum aestivum* (10 pcs.) and *Triticum durum* (10 pcs.); sparsely distributed: (*Monococcum* (8 pcs.), *boeoticum* (1 pc.), *sinskajae* (1 pc.), *timopheevii* (1 pc.), *militinae* (1 pc.), *dicoccum* (9 pcs.), *ispahanicum* (1 pc.), *persicum* (2 pcs.), *turgidum* (3 pcs.), *aethiopicum* (1 pc.), *spelta* (9 pcs.), *compactum* (4 pcs.) and *amphidiploid samples* (15 pcs.). The source material was obtained from the National Centre for Plant Genetic Resources of Ukraine (NCPGRU) and has a number of economically valuable features. Samples were introduced from different ecological and geographical areas (Table 1-3), differ not only in economically valuable characteristics (weight of 1000 seeds, duration of the growing season, plant height, etc.), but also is characterised by different gradations of morphological features (presence or absence of awns, colour of awns, colour of caryopsis, colour of straw, pubescence of leaves, pubescence of the ear internode, pubescence of the subcrown internode).

Table 1. Characteristics of the studied samples *Triticum aestivum* and *Triticum durum*

No.	National catalogue number	Institution registration number	Sample name	Variety	Country of origin*
<i>Triticum aestivum</i>					
1	UA0100098	IR 08517S	Sunnan	<i>var. lutescens</i>	SWE
2	UA0101113	IR 11742S	Prokhorovka	<i>var. lutescens</i>	RUS
3	UA0104110	IR 12602S	Kharkivska 30	<i>var. lutescens</i>	UKR
4	UA0106145	IR 13173S	L 501	<i>var. lutescens</i>	RUS
5	UA0110938	IR 15164S	Simkodamironivska	<i>var. lutescens</i>	UKR
6	UA0111008	IR 15206S	Yrym	<i>var. erythrosperrum</i>	KAZ

Table 1, Continued

No.	National catalogue number	Institution registration number	Sample name	Variety	Country of origin*
<i>Triticum aestivum</i>					
7	UA0105661	IR 12049S	CIGM.250-	<i>var. erythrosperrum</i>	MEX
8	UA0110937	IR 14892S	Fito14/08	<i>var. erythrosperrum</i>	UKR
9	UA0110936	IR 14891S	Fito33/08	<i>var. erythrosperrum</i>	UKR
10	UA0111123	IR 15595S	L 685-12	<i>var. lutescens</i>	UKR
<i>Triticum durum Desf</i>					
11	UA0201229	IR 12313S	Zolotko	<i>var. muticohorde-iforme</i>	UKR
12	UA0201199	IR 13580S	Orenburgskaya 21	<i>var hordeiforme</i>	RUS
13	UA0201431	IR 14943S	Nurly	<i>var. hordeiforme</i>	KAZ
14	UA0201201	IR 14045S	Slavuta	<i>var. leucomelan</i>	UKR
15	UA0200923	IR 12773S	Bukuria	<i>var. melanopus</i>	UKR
16	UA0201428	IR 14941S	Altyn Shygys	<i>var. hordeiforme</i>	KAZ
17	UA0201386	IR 14438S	Metiska	<i>var. melanopus</i>	UKR
18	UA0201452	IR 15566S	Novatsia	<i>var hordeiforme</i>	UKR
19	UA0201453	IR 15548S	Diana	<i>var. hordeiforme</i>	UKR
20	UA0201426	IR 14937S	Kustanayskaya 80	<i>var. hordeiforme</i>	KAZ

Note: *SWE – Sweden; RUS – Russia; UKR – Ukraine; KAZ – Kazakhstan; MEX – Mexico

Table 2. Characteristics of the studied samples of the genus *Triticum L.*

No.	National catalogue number	Species	Variety	Country of origin*
21	UA0300104	<i>monococcum</i>	<i>var. vulgare</i>	BGR
22	UA0300221	<i>monococcum</i>	<i>var. monococcum</i>	AZE
23	UA0300223	<i>monococcum</i>	<i>var. vulgare</i>	ALB
24	UA0300254	<i>monococcum</i>	<i>var. monococcum</i>	ARM
25	UA0300282	<i>monococcum</i>	<i>var. monococcum</i>	HUN
26	UA0300310	<i>monococcum</i>	<i>var. hohensteinii</i>	GEO
27	UA0300311	<i>monococcum</i>	<i>var. nigricultum</i>	SYR
28	UA0300313	<i>monococcum</i>	–	HUN
29	UA0300008	<i>dicoccum</i>	<i>var. aeruginosum</i>	RUS
30	UA0300327	<i>dicoccum</i>	<i>var. aeruginosum</i>	RUS
31	UA0300407	<i>dicoccum</i>	<i>var. nudidicoccum</i>	UKR
32	UA0300406	<i>dicoccum</i>	<i>var. nudirufum</i>	UKR
33	UA0300199	<i>dicoccum</i>	<i>var.pseudogunbadi</i>	IRN
34	UA0300009	<i>dicoccum</i>	<i>var.serbicum</i>	RUS
35	UA0300183	<i>dicoccum</i>	<i>var.serbicum</i>	RUS
36	UA0300021	<i>dicoccum</i>	<i>var. volgense</i>	KAZ
37	IU070615	<i>dicoccum</i>	<i>var.submajus</i>	BGR
38	UA0300238	<i>spelta</i>	<i>var.subbaktiaricum</i>	UZB
39	UA0300304	<i>spelta</i>	<i>var.album</i>	AUS

Table 2, Continued

No.	National catalogue number	Species	Variety	Country of origin*
40	UA0300387	<i>spelta</i>	<i>var.caeruleum</i>	CAN
41	UA0300388	<i>spelta</i>	<i>var.duhamelianum</i>	CAN
42	UA0300391	<i>spelta</i>	<i>var.caeruleum</i>	CAN
43	UA0300392	<i>spelta</i>	<i>var.alefeldii</i>	CAN
44	UA0300398	<i>spelta</i>	<i>var.arduini</i>	UKR
45	UA0300443	<i>spelta</i>	<i>var.caeruleum</i>	RUS
46	UA0300546	<i>spelta</i>	<i>var.caeruleum</i>	RUS
47	UA0300240	<i>compactum</i>	<i>var.erinaceum</i>	ARM
48	UA0300354	<i>compactum</i>	<i>var.pseudoicterinum</i>	GRC
49	UA0300368	<i>compactum</i>	<i>var.humboldtinflatum</i>	CHN
50	UA0300528	<i>compactum</i>	<i>var.kerkianum</i>	GEO
51	UA0300110	<i>turgidum</i>	<i>var.plinianum</i>	KGZ
52	UA0300237	<i>turgidum</i>	<i>var.rubroathrum</i>	GRC
53	UA0300376	<i>turgidum</i>	–	BGR
54	UA0300490	<i>persicum</i>	<i>var.persicum</i>	GEO
55	UA0300495	<i>persicum</i>	<i>var.rubiginosum</i>	GEO
56	UA0300402	<i>boeticum</i>	<i>var.boeticum</i>	UKR
57	UA0300224	<i>sinskajae</i>	<i>var.sinskajae</i>	RUS
58	UA0300545	<i>timopheevii</i>	<i>var.nigrum</i>	BLR
59	UA0300257	<i>militinae</i>	<i>var.militinae</i>	RUS
60	IU0700070	<i>ispahanicum</i>	<i>var.ispahanicum</i>	IRN
61	IU070589	<i>aethiopicum</i>	<i>var.nigriviolaceum</i>	ERI

Note: *RUS – Russia; UKR – Ukraine; KAZ – Kazakhstan; GRC – Greece; BGR – Bulgaria; Aze – Azerbaijan; ALB – Albania; arm – Armenia; HUN – Hungary; GEO – Georgia, SYR – Syrian Arab Republic; BLR – Belarus, IRN – Iran; KGZ – Kyrgyzstan; UZB – Uzbekistan; AUS – Australia; CAN – Canada; ERI – Eritrea

Table 3. Characteristics of the studied samples of the genus *Triticum* L.

No.	National catalogue number	Sample name	Parentage	Country of origin	Institution of origin
62	UA0500004	PAG-12	<i>T. persicum</i> x <i>T. monococcum</i>	RUS	VIPI
63	UA0500007	PAG-20	<i>T. timococcum</i> x <i>T. monococcum</i>	RUS	VIPI
64	UA0500008	PAG-31	<i>T. dicoccum</i> i-329428, Poland x <i>T. monococcum</i> k-20636, Spain	RUS	VIPI, DRS VIPI
65	UA0500009	PAG-32	<i>T. dicoccum</i> k-14055, Armenia x T. monococcum i-452639, Czech Republic	RUS	VIPI, DRS VIPI
66	UA0500010	PEAG	<i>T. dicoccum</i> i-244569, Germany x <i>Ae. Tauschii</i> l-110	RUS	VIPI, DRS VIPI
67	UA0500014	<i>Triticum</i> x <i>kiharae</i>	<i>T. timococcum</i> x <i>Ae. Tauschii</i>	JPN	

Table 3, Continued

No.	National catalogue number	Sample name	Parentage	Country of origin	Institution of origin
68	UA0500018	Haynatricum	AD (<i>T. dicoccum</i> - <i>D. villosum</i>)	RUS	Moscow Timiryazev Agricultural Academy
69	UA0500022	AD8	<i>T. dicoccum</i> x <i>Ae. triuncialis</i>	AZE	ANAS Genetic Research Institute
70	UA0500023	PAG-13	<i>T. dicoccum</i> x <i>T. monococcum</i>	RUS	VIPI
71	UA0500024	PAG-39	<i>T. dicoccum</i> x k-150007, Poland x <i>T. sinskajae</i>	RUS	VIPI, DRS VIPI
72	UA0500025	<i>Triticum</i> x <i>timococcum</i>	<i>T. timopheevii</i> x <i>T. monococcum</i>	RUS	Moscow Timiryazev Agricultural Academy
73	UA0500026	<i>Triticum</i> x <i>sinskourarticum</i>	<i>T. sinskajae</i> x <i>T. urartu</i>	ARM	Armenian Agriculture University
74	UA0500043	PAG-4	<i>T. durum</i> v. <i>Stebutii</i> k-16477 x <i>T. monococcum</i> v. <i>macedonicum</i> k-18140	RUS	VIPI
75	UA0500044	PAG-7	<i>T. durum</i> x <i>T. monococcum</i>	RUS	VIPI
76	UA0300107	-	<i>T. timopheevii</i> x <i>timopheevii</i>	-	-

Note: *RUS – Russia; AZE – Azerbaijan; ARM – Armenia; JPN – Japan

Observations were carried out in 2018-2020 in the training and experimental production centre “Doslidne pole” of the Kharkiv National Agrarian University named after V.V. Dokuchaev. Sowing was carried out at the optimal time for the crop in the first ten days of April. Collection samples were sown manually under a marker, in two rows 1 m long each with row spacing of 0.15 m, at the rate of 100 grains per linear meter. The registered area of the site for each sample was 1 m². All phenological observations were carried out in accordance with the guidelines for studying wheat collections [11; 12]. To assess the intraspecific and interspecific variability of spring wheat, 30 plants of each study sample were analysed annually. Thus, 60 plants of each spring wheat sample were analysed over three years, and the total number was 6390 plants per year.

Observation, accounting, and biometric measurements were carried out in accordance with the “methodology for conducting an examination of plant varieties of the grain group for difference, uniformity, and stability” [12]. During phenological observations, the sowing period, emergence, phases of 2-3 leaves, tillering phase, tubing phase, flag leaf, earing, flowering, milk-wax ripeness, maturation were recorded [13; 14]. To group spring wheat genotypes using cluster analysis by traits, Euclidean distances were performed in STATISTICA 10. The obtained data was encoded and entered into a matrix for further processing of the results. Statistical analysis was performed using the Statistica 10 software.

To assess the intraspecific and interspecific diversity of spring wheat, the Shannon index was used, which allows assessing the heterogeneity of populations (1):

$$H' = -\sum \frac{nt}{N} \ln \frac{nt}{N} \quad (1)$$

where H' – Shannon diversity index; nt – total number of species or intraspecific diversity; N – total number of detected individuals. The Shannon index is an informational indicator that has found wide application in the study of the species richness of biocenoses and the genetic diversity of plant organisms [15].

The frequency of morphological features was calculated in the CONVERT 1.31 software. The Shannon diversity index, Pielou alignment index, and standard deviation were calculated in Microsoft Excel. Genetic distances Nei and a phylogenetic tree were calculated using the *PhyIip-3.69* software package. The reliability of the resulting phylogenetic relationship tree was verified using *bootstrap* analysis in 1000-fold repetition.

RESULTS AND DISCUSSION

In the period from 2018-2020, the morphological variability of the spring wheat collection was assessed, which showed the presence of polymorphism in all the studied features using cluster analysis. Analysis of the phenotypic variability of collection samples of spring wheat showed the presence of polymorphism of all studied features.

The advantage of the cluster analysis method is that the mathematical apparatus allows finding and selecting a pile of objects (points) that exists in the same space based on a simultaneous grouping by a large number of features [16; 17]. Using a dendrogram, it is possible to build and analyse information about the nature of relationships between samples at cluster levels and can detail relationships within its genotype [13; 2].

The cluster analysis allowed distributing the studied samples of the genus *Triticum L.* into three clusters. In the cluster analysis, the following characteristics were

chosen as the basis of the groupings: *awnedness* – *awnlessness*, awnlessness is the dominant feature to awnedness; *pubescence of spikelet scales*, this feature is mono- or digenic; *the colour of spikelet scales*. Dark

colour is dominant relative to light; the *colour of the awns* – white, red, and black. The diversity of spring wheat varieties is controlled by one or more genes; *grain colour* – white, red, green, blue, purple (Fig. 1).

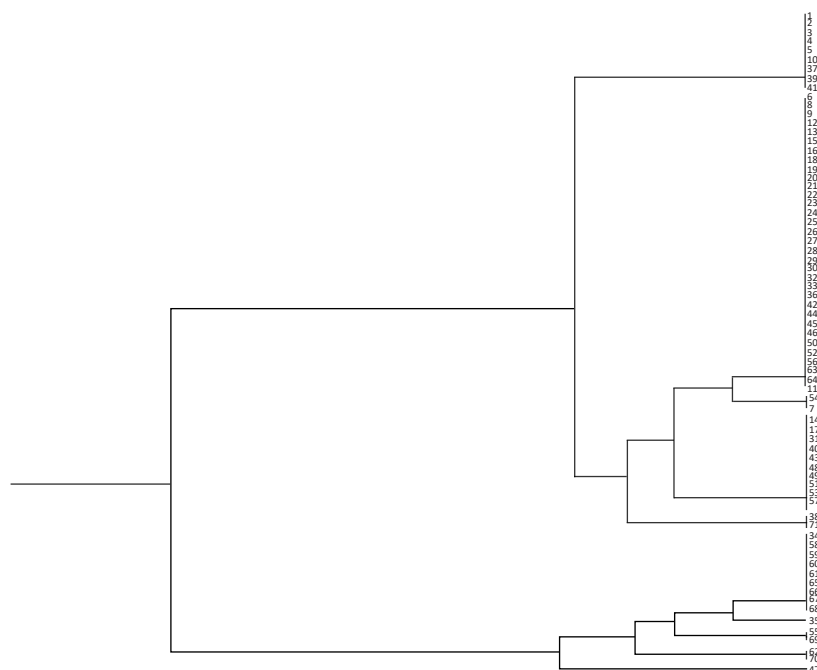


Figure 1. Dendrogram of phylogenetic relationships between the studied samples of spring wheat based on the analysis of morphological features

Note: *Triticum aestivum* 1-10; *Triticum durum* Desf 11-20; *Triticum monococcum* 21-28; *Triticum dicocum* 29-37; *Triticum spelta* 38-46; *Triticum compactum* 47-50; *Triticum turgidum* 51-53; *Triticum persicum* 54-55; Uncommon 56-61; Amphidiploid samples 62-76

The main differential factors as a result of the conducted studies were: the presence or absence of awns, the colour of awns, the pubescence of ear scales, the pubescence of the subcrown internode, the pubescence of the ear internode, the colour of caryopsis, the colour of straw, the species affiliation of samples.

The first cluster contained a large number of samples, which can be divided into two subclusters. This cluster includes samples of the following species: *Triticum aestivum*: Sunnan (Sweden); Prokhorovka (Russia); Kharkivska (Ukraine); L 501 (Russia); Simkodamyronivska (Ukraine); L 685-12 (Ukraine); *Triticum spelta* UA0300304 (Australia); UA0300388 (Canada); UA0300392 (Canada). Characteristic phenotypic features of this cluster are: absence of awns, white colour of grain, white colour of ear scales, white colour of straw, no pubescence of all organs, but in the studied populations there were samples with other gradations of features. Collection samples were characterised by the greatest similarity and within this cluster were located on the same branch of the phylogenetic tree, which can be observed on the dendrogram.

Also, a common node in this block was formed by samples of *Triticum aestivum* and *Triticum durum* species, namely: Yrym (Kazakhstan), Fito 14/08 (Ukraine), Fito 33/08 (Ukraine), Orenburgskaya 21 (Russia), Nurly (Kazakhstan); Bukuria (Ukraine); Altyn Shygys (Kazakhstan); Novatsiya (Ukraine); Diana (Ukraine); Kostanay 80 (Kazakhstan).

This cluster also includes samples of *Triticum monococcum* UA0300104 (Bulgaria); UA0300221 (Azerbaijan); UA0300223 (Albania); UA0300254 (Armenia); UA0300282 (Hungary); UA0300310 (Georgia); UA0300313 (Hungary); *Triticum dicocum* UA0300327 (Russia); UA0300407 (Ukraine); UA0300406 (Ukraine); UA0300199 (Iran); UA0300009 (Russia); *Triticum spelta* UA0300238 (Uzbekistan); UA0300387 (Canada); UA0300546 (Russia); *Triticum compactum* UA0300240 (Armenia); UA0300354 (Greece); *Triticum turgidum* UA0300376 (Bulgaria); *Triticum persicum* UA0300495 (Georgia); *Triticum timopheevii* UA0300545 (Belarus); *Triticum durum x Triticum monococcum* UA0500043 (Russia); UA0500044 *Triticum durum x Triticum monococcum* (Russia).

The second cluster contained samples of different species, namely: *Triticum durum* UA0201229 (Ukraine); a rare sample of spring wheat IU070589 (Eritrea); *Triticum aestivum* UA0105661 (Mexico); *Triticum durum* UA0201201 (Ukraine); UA0201386 (Ukraine); *Triticum dicocum* UA0300199 (Iran); *Triticum spelta* UA0300391 (Canada); *Triticum spelta* UA0300443 (Russia); *Triticum compactum* UA0300528 (Georgia); *Triticum turgidum* UA0300237 (Greece); *Triticum persicum* UA030049 (Georgia); *Triticum ispahanicum* IU0700070 (Iran); *Triticum militinae* UA0300257 (Russia); *Triticum spelta* UA0300387 (Canada); **Amphidiploid sample** UA0500010 (Russia). Characteristic features of this cluster are: the presence of awns, white colour of awns, no pubescence of all organs, white colour

of grain, white color of straw. The third cluster contained the following samples: *Triticum dicoccum* UA0300021 (Kazakhstan); *Triticum persicum x Triticum monococcum* UA0500004 (Russia); *Triticum timococcum x Triticum monococcum* UA0500007 (Russia); *Triticum dicoccum x Triticum monococcum* UA0500009 (Russia); *Triticum dicoccum x Ae. Tauschii* UA0500010 (Russia); *Triticum dicoccum-D.villosum* UA0500018 (Russia); *Triticum dicoccum x Ae. triuncialis* UA0500022 (Azerbaijan); *Triticum dicoccum* UA0500024 (Russia); *Triticum dicoccum*

IU070615 (Bulgaria); Rarte samples: UA0300224 (Russia); Amphidiploids: *Triticum x kiharae T. timococcum* UA0500014 *x Ae. Tauschii* (Japan); UA0500025 *Triticum x timococcum Triticum timopheevii x Triticum monococcum* (Russia). UA0300107 *Triticum timopheevii x Triticum timopheevii* UA0300368 *Triticum compactum* (China).

Characteristic features of this cluster are: the presence of awns, white colour of awns, white colour of ear scales, pubescence of leaves, pubescence of the ear internode, pubescence of the subcrown internode [16] (Table 4).

Table 4. Distribution of spring wheat traits by clusters

Trait	Cluster		
	I	II	III
Presence of awns	Absent	Present	Present
Awns colour	-	White	White
Ear scales colour	White	White	White
Leaf pubescence	Absent	Absent	Pubescent
Subcrown internode pubescence	Absent	Absent	Pubescent
Ear internode pubescence	Absent	Absent	Pubescent
Caryopsis colour	White	White	White
Colour of straw	White	White	White

The results obtained on the basis of an assessment of the variability of morphological features confirm the genetic closeness of the species involved in the study. This may mean that the most likely scenario for the development of spring wheat species is the presence of a common ancestor, which marked the beginning of domestication of other forms. At the same time, the distribution of populations of different spring wheat species in each cluster, phenotypically different from the main population of samples of a particular group, indicates insufficient differentiating ability of morphological features.

All studied morphological features were polymorphic in spring wheat samples. The number of gradations of manifestation of each trait varied from 2 to 8. The maximum Shannon diversity index (H') in spring wheat samples was recorded based on the colour of awns in samples of *Tr. persicum*, it was (H'=0.98). According to this feature, spring wheat samples from most of the countries were characterised by the highest level of variability. A significant level of polymorphism in the total number of spring wheat samples was also distinguished by the presence of awns. In samples of *Tr. spelta* and *Tr. aestivum* the maximum value of the Shannon index was 0.67, respectively. The least variable in the spring wheat samples were the signs of straw colour and grain colour (H'=0.0, respectively).

The total level of polymorphism of spring wheat samples by morphological features according to the Shannon index was 0.69.

Characteristics of spring wheat plants that were included in the first cluster when evaluating the indicator "presence of awns" samples of *Triticum aestivum*, namely samples of Sunnan of Swedish selection, Prokhorovka of Russian selection and Kharkivska of Ukrainian selection, have well-defined awns, also the first cluster included samples of Simkodamironivska of Ukrainian selection, L 685-12 of Ukrainian selection and sample UA0300304 of Austrian selection on the indicator pubescence of the subcrown internode and pubescence of the ear internode. According to the indicator of caryopsis straw colour, all the studied samples were included in the same cluster, because they had no differences.

According to a number of researchers, it is quite effective to conduct cluster analysis using various indicators to determine the parameters of difference and uniformity. Estimating the rearrangement of cluster structures is a rather cumbersome task and requires, in addition to morphological and morphometric, the use of other research methods [18].

CONCLUSIONS

Based on the conducted studies using cluster analysis in the technology of the breeding process during 2018-2020, samples and constant breeding lines were identified, balanced on economically useful traits, which can be used as promising breeding material, and parent components during hybridisation. The diversity of collection samples of spring wheat at the interspecific and intraspecific level was also assessed.

Based on the results of the study, it was confirmed that the advantage of cluster analysis in relation to statistical analysis is that cluster analysis allows identifying varieties and breeding lines by the balance on economically useful traits, and in the statistical analysis, it is possible to select and distinguish only certain quantitative features by their level of formedness and variability and yield.

In addition, the genetic similarity or remoteness of genotypes can be assessed using cluster analysis based on quantitative traits. The highest level of variability was observed in the sign of Awns colour in samples of *Tr.persicum*

and was 0.98. Therefore, as a result of the research, the genetic structure of the collection of spring wheat samples of various ecological and geographical origin was assessed by morphological features. During the research, it was observed that the sample of spring wheat samples has a similar level of variability in these indicators. In the process of clustering spring wheat samples of different ecological and geographical origin, groupings were analysed, and the correspondence of each wheat sample to a specific cluster was evaluated. The data obtained can complement information about the genetic collection of spring wheat.

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КЛАСТЕРНИЙ АНАЛІЗ ЗРАЗКІВ *TRITICUM L.* РІЗНОГО ЕКОЛОГО-ГЕОГРАФІЧНОГО ПОХОДЖЕННЯ

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Анотація. Стаття присвячена застосуванню кластерного аналізу для оцінки зразків м'якої ярої пшениці за елементами структури врожаю. Метою дослідження є аналіз внутрішньовидової та міжвидової мінливості морфологічних ознак колекційних зразків пшениці ярої різного еколого-географічного походження за 8 морфологічними ознаками. Спостереження проводилися в 2018–2020 роках у навчально-дослідному виробничому центрі «Дослідне поле» Харківського національного аграрного університету ім. В.В. Докучаєва. Проведений кластерний аналіз колекції зразків пшениці ярої, до якої ввійшло 76 зразків різного еколого-географічного походження, дозволив одержати оцінку таких ознак: наявність остюків, забарвлення остюків, забарвлення колосових лусок, опушеність листків, опушеність стеблового міжвузля, опушеність колосового міжвузля, забарвлення зернівки, забарвлення соломини. Викладено результати аналізу філогенії різних видів пшениці ярої методом кластерного аналізу з використанням морфологічних маркерів з метою визначення однорідних груп і сформовано уражене дерево систематичного утворення кластеризаційних груп. За результатами проведеного кластерного аналізу виділено дві окремі групи зразків пшениці ярої м'якої за комплексом елементів продуктивності рослини. У кожен кластер зразки групуються залежно від кількісних ознак структури урожаю і їх взаємодії один з одним. Загалом усі зразки за роки дослідження показали гарні результати, а саме за ознакою «забарвлення остюків», особливо варто відмітити зразки виду *Tr. persicum*. Відповідно до отриманих результатів роботи всі зразки мають гарні показники, і кластерний аналіз зразків м'якої ярої пшениці дозволив виділити групи рослин, що перевершують батьківські форми по оптимальному набору господарсько-цінних ознак, що дозволить більш цілеспрямовано вести відбір цінних форм за певними ознаками

Ключові слова: модель, кластеризація, кластер, дендрограма, оцінка, пшениця яра