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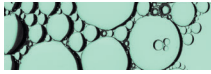
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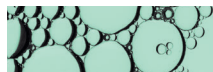
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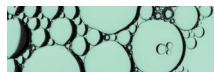
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Substantiation of the preparation technology of soft-grained wheat for deep processing

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Abstract. The process peculiarities of harvesting grain for processing and production of food products are impossible without determining the content of protein, starch, gluten, the same in the grain weight of soft-grained wheat, which comes to grain processing plants, contains grain and waste impurities. The purpose of the work was to substantiate the technologies of primary and advanced preparation of wheat grain using modern methods of storage and transportation for further use in the processes of deep grain processing. The method of identification was used for the technological features establishment, measuring with the morphological characteristics and impurities determination. Grain standards provide for the determination of moisture, test weight, waste and grain impurities, gluten content and gluten deformation index (GDI): grain batches of different varieties of spring and winter soft wheat. The obtained data met the requirements of the 2nd class, according to the indicator of crude protein content, falling number (FN) of the 2nd and 3rd classes. Commercial indicators of the qualitative composition of spring wheat and winter varieties of soft-grained wheat were experimentally determined. It was established that in the group of winter wheat varieties, the moisture content was within 10.1-11.2%, test weight was 757-773, weight per 1,000 seeds was 41.7-43.4 g, gluten content was 20.4-27.3%, GDI was 76.4-81.6 units, FN was 339-364 seconds; 11.4-12.2%, 740-755, 41.8-43.8 g, 21.8-26.2%, 71.1-80.4, 313-358, respectively, in spring wheat varieties. Regarding the nutritional qualities of wheat, in the group of winter varieties, crude protein was 20.9-21.7%, crude fat was 2.4-2.7%, crude fibre was 2.5-3.0%, nitrogen-free extractive substances were 71.1-71.5%; in spring varieties, respectively, 19.64-20.3%, 2.2-2.7%, 2.2-2.4%, 73.5-74.2%. The practical significance of the work lies in the implementation of modern methods of grain storage and transportation, which allows

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to significantly improve the quality of raw materials, increase the efficiency of food production, reduce losses during processing, and ensure compliance of products with high quality standards

Keywords: grain raw materials; equipment; impurities; peeling; separation

INTRODUCTION

The important directions for modernisation of the agro-industrial complex are the productivity growth and the technological processes intensification of complex processing of grain and grain waste. The problem of many plants, especially small ones, is the use of outdated, impractical systems of production processes automation. The development and implementation of the modern complex grain processing equipment with the possibility of computer setting and remote control significantly increases the technical level of enterprises and provides a high profitability level. Grain products are raw materials for many branches of the food and processing industry, therefore, the demand for them is constantly growing. Grain products are the basis of human nutrition and are characterised by high nutritional value and taste.

V. Khudaverdiyeva (2022) states that with export volumes of 40-45 million tons of grain per year, the transportation deficit is about 8 million tons, this potential can be used at grain processing plants for deep processing of grain. In addition, the events of 2022 led to significant limitations in the logistical possibilities for the grain raw materials export. The domestic production of seeds reached 75,000 tons or 63% of the total amount, however, taking into account the huge export flows of grain crops, the cultivated quality potential is lost due to the impossibility of processing raw materials into plant products with high added value, and only the introduction of new technologies for processing grain crops will ensure domestic market. According to H. Wieser *et al.* (2022), deep grain processing is the process of grinding raw materials into components and their effective use in products with high consumer value. As a result of the wheat grain processing technology improvement, opportunities appear not only for the production of dry wheat gluten, starch and feed products, but also for further processing into sugars, in particular glucose, fructose, mannose and galactose. The most common cereal crop, wheat, is considered as a raw material for the ethanol and biomethane production, however, modern

processing industries require a larger line of products that are obtained through deep processing.

W. Cheng *et al.* (2021) describe the hardness of the grain endosperm of soft wheat varieties, which are divided into hard grain and soft-grained, and the grain hardness indicator is determined by the consistency diagnostics of wheat endosperm. According to M. Formentini *et al.* (2021), it is known that in the leading producing countries of the USA and Canada, exporters of soft-grained wheat, classify this raw material according to the endosperm consistency, which is the main determinant of the class-forming criterion of wheat quality, both in the domestic and world grain markets. Modern technologies and methods are playing a pivotal role in the enhancement of grain processing efficiency. For instance, the integration of deep learning models, as detailed in a study by Q. Gao *et al.* (2024) have significantly improved the detection and classification of grain quality. These models facilitate rapid and accurate on-site screening, essential for ensuring the high quality of grains intended for deep processing. The precision offered by these technologies reduces labour costs and enhances impurity detection in grain products, thus supporting the production of superior quality wheat products.

V. Liubych *et al.* (2020) provide information on grain stability, which depends on the characteristics of the wheat variety, processing and storage conditions. During storage, the grain ripens, therefore, the enzymes activity decreases, the number of water-soluble substances and non-protein nitrogen decreases, the synthesis of starch from sugars and fat from glycerine occurs and the content of unsaturated fatty acids increases. Usually, grains contain active microbes and pests represented by rodents and insects. According to the characteristics of L. Li *et al.* (2022), grain processing properties can be characterised by such indicators as vitreousness, grain size, bulk or natural weight, weight per 1,000 seeds, density, ash content, grinding ability and type grain composition. According to D. Kumar & V. Kukreja (2022),



the characteristics of the flour baking properties are evaluated by indicators of nutrition, gluten quality, gas-forming capacity, dispersed composition, and physical properties of the resulting dough. N. Vasylenko & I. Pravdziva (2022) states that about 113 varieties are involved in the growing process of soft, soft-grained wheat in Ukraine.

When growing grain crops, it is important to increase not only the raw materials yield, but also technical characteristics, namely, grinding, flour-milling and baking properties, that determine the market value. The multi-stage processing technology in the agricultural industry is actively developing and can provide the end consumer with high-quality plant products. The purpose was to substantiate the preparation technologies of raw materials for processing using modern methods of storage, transportation and evaluation of the actual qualitative composition of wheat grain.

MATERIALS AND METHODS

The study was conducted in 2022 at the Institute of Plant Breeding in Ukraine and complied with the ethical standards set forth in the Convention "On Biological Diversity" (1992) and the Convention "On the Trade in Endangered Species of Wild Fauna and Flora" (1973). Ethical norms observed included sustainable use of resources to prevent depletion of wheat varieties and conservation of biological diversity by maintaining and studying various genotypes. Efforts ensured fair and equitable sharing of benefits from the use of genetic resources, ethical conduct in research, and protection of endangered species. These considerations ensured the research was conducted responsibly, aligning with international standards for biological resource conservation and use.

The object of the scientific work was soft winter wheat varieties widely grown in Ukraine – Cubus, Jersey, Palitra; varieties of spring soft wheat – Zlata, Heroinya, Kharkivska 26. Determination of grain quality was carried out according to biological and laboratory methods. Biological methods included organoleptic evaluation methods using the senses, determining the main indicators of grain freshness by colour, odour and taste. Laboratory tests were performed according to generally recognised methods in biology, based on complex biochemical studies by V. Vlizlo *et al.* (2023): on the content of total nitrogen calculated on the raw protein

of Kjeldahl pores, crude fat, crude fibre, crude ash, nitrogen-free extractive substances (NFES).

The study used theoretical methods: identification to establish the main technological features of soft-grained wheat seeds; measuring to determine morphological characteristics and the number of foreign impurities. During the course of the work, a systematic approach was applied to the uniqueness of technical and economic conditions for effective evaluation of grain seed cleaning. The list of the main indicators of nutrition and quality of winter wheat grain of different varieties for different purposes in particular commodity and seed material characteristics has been determined.

The information base of the research consisted of regulatory and legal documents, scientific and analytical articles, informational materials published in official publications and on Internet sites, as well as own developments in the breeding industry. In particular, the study took into account the following normative acts: DSTU ISO No. 13690:2003 (2003), DSTU ISO No. 21415-1:2009 (2009), DSTU No. 3768:2019 (2019), DSTU No. 8840:2019 (2019) and DSTU GOST No. 1084 0:2019 (2019). These normative documents ensure the standardization of methods of research, determination and control of the quality of grain and grain products, which allows conducting complex laboratory tests and ensuring high quality and safety of products.

The qualitative wheat indicators were determined according to the methodology of the qualification examination of plant varieties for suitability for distribution in Ukraine by S. Tkachyk *et al.* (2016) according to the following indicators: technological: moisture, colour, smell, taste, impurities content, contamination, small grain fraction content; flour-milled: vitreousness, test weight, weight per 1,000 seeds, specific gravity, ash content, grinding, actual composition of nutrients; baking properties: gluten content and quality, falling number (FN), dispersed composition, acidity, and porosity.

RESULTS

According to the Food and Agriculture Organization (FAO) (2023), national policy measures have been established to increase productivity, food security, and food products, particularly grain crops, through the effective use and processing of raw

materials from soft-grained wheat. An important issue addressed by the State Service of Ukraine for Food Safety and Consumer Protection (n.d.) is the control over the safety and quality of products of plant origin, aiming to enhance and improve existing methods of veterinary and sanitary control throughout the production cycle. These scientific implementations facilitate the application of a comprehensive set of special laboratory studies on grain crops, fodder, feed additives, and raw material systems, considering the potential productivity of different varieties. The most common methods of grain cleaning and sorting include wheat aspiration by air flow, separation by grid size, separation by length on triers according to shape, and

cleaning and sorting by density and surface properties, as well as electrical methods. These methods ensure the quality and safety of wheat grains, making them suitable for various applications.

Figure 1 illustrates trending products produced through the deep processing of soft-grained wheat, such as gluten, starch, glucose monohydrate, ethanol derivatives (bioethanol), biomethane, glucose crystals, GFS-42 (glucose-fructose syrup), GFS-55, organic acids (citric, succinic, lactic), amino acids (lysine, methionine, threonine), biopolymers, and yeast extracts. These products highlight the diverse and valuable outputs achievable through effective grain processing, supporting both national policy objectives and industry needs.

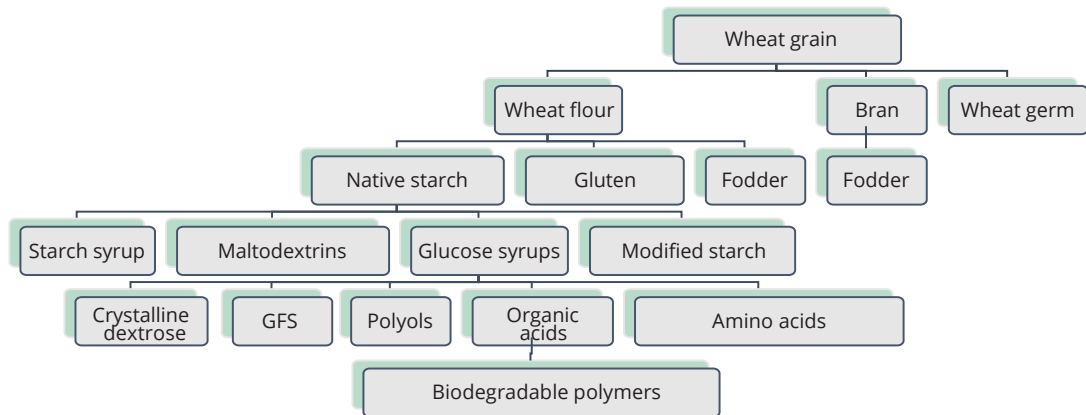


Figure 1. Products of deep wheat processing

Source: compiled by the authors based on National Academy of Agrarian Sciences of Ukraine (2021)

Wheat grain that arrives at grain processing plants always contains a certain amount of impurities in addition to the main component. Grain cleaning is conducted with the help of: dispersing units, washers, crushers, stone selectors, on pneumatic dispersing tables and air separators. Impurities are classified as: seeds of wild weeds: common wild oat, dandelion, wild radish, bitterling, bitter gourd, coronilla, curly weed; seeds of

other grain and leguminous crops: barley, corn, peas; damaged seeds: small, underdeveloped, damaged by drying, self-heating, microorganisms, grain parasites; organic impurities: straw, crumbs; inorganic impurities – small stones, sand, ore, lumps. According to the characteristics, soft wheat is divided into six classes, its quality indicators are standardised according to the current standard provided in Table 1.

Table 1. Standard quality indicators of soft wheat

Indicator	Characteristics and standards for soft wheat by classes					
	1	2	3	4	5	6
Type composition	I-IV types			I-IV types, VII types are allowed		
Test weight, g/l, not less	760	755	730	710	710	Not limited
Moisture, %, no more	14.5	14.5	14.5	14.5	14.5	14.5
Grain impurity, %, no more	5	5	8	10	15	15

Table 1. Continued

Indicator	Characteristics and standards for soft wheat by classes					
	1	2	3	4	5	6
In particular, sprouted grains	1	1	3	3	5	Within grain impurity
Waste impurity, %, no more	1.5	2	3	4	5	5
In particular: spoiled grains	0.2	0.2	0.5	0.5	1	1
Fusarium grains	0.3	0.5	1	1	1	1
Ryegrass	0.3	0.5	0.5	0.5	0.5	0.5
Mineral impurity	0.3	0.3	0.5	1	1	1
In particular, pebbles and slag	0.15	0.15	0.2	0.3	Within mineral impurity	
Harmful impurity	0.2	0.3	0.5	0.5	0.5	0.5
In particular:						
smut and crowns	0.05	0.05	0.1	0.1	0.1	0.1
Russian centaury, darnel ryegrass, Sophora alopecuroides, golden banner (in a mixture)	0.05	0.05	0.1	0.1	0.1	0.1
Crown vetch	0.1	0.1	0.1	0.1	0.1	0.1
Smut grain, %, no more	5	5	5	8	8	10
Weight part:						
Crude protein, on dry basis, %, not less	14	13	12	11	10	Not limited
Crude gluten, %, not less	30	27	23	18	18	Same
Gluten quality						-
GDI device units	45-75	45-100	45-100	20-100	20-110	-
FN, sec., over	200	200	150	100	less than 100	-

Source: compiled by the authors based on DSTU ISO No. 21415-1:2009 (2009) and DSTU No. 3768:2019 (2019)

Soft wheat of the 1-3 classes is used for the production of food products, mainly in the flour mill, bakery industry and for export. Soft wheat of the 4 class is used for non-food products. Soft wheat of the 5 and 6 classes is used for technical and fodder purposes. Soft wheat quality indicators are: test weight, vitreousness, moisture, grain impurity, waste impurity, smut grain, protein mass fraction, crude gluten mass fraction, gluten quality and FN. If the wheat seed does not meet the established quality standards according to only one of the indicators, it is transferred to a lower class. Indicators of the crude gluten mass fraction and its quality indicators are not mandatory in determining the soft wheat class, their standards are necessarily included in the wheat supply contract for processing enterprises. The preparatory stages of deep processing include the following processes:

- grain receiving, primary cleaning and storage;
- grain separation at elevators or mills and screening from impurities;
- grinding with reduction of peel and crushing;
- grain classification according to the corresponding sizes with fractional sorting of preparation raw materials;

- granulation with screening of small fractional elements;

- quality control;
- transportation and packaging.

Grain mass impurities, which differ from the main seed in terms of geometric dimensions, in particular length, width, thickness, are separated on the grids. Depending on the purpose and technical means used for grain cleaning, the following stages are distinguished: preliminary, primary and secondary cleaning and sorting. Preliminary cleaning of the grain pile consists in separating light, small and large impurities and providing favourable conditions for further technical work on post-harvest grain processing. The primary cleaning of grain consists in separating large, small and light impurities, and sorting them into the main food and seed grain and fodder fractions with minimal losses. At the same time, the main fraction meets the criteria of the basic purchasing conditions. If grain contamination and moisture is low, post-harvest processing can be started with primary cleaning. After the primary cleaning, the grain undergoes secondary processing, it is sorted into food or seed. Sorting is the division of the main

crop grain into fractions according to certain features of size and density, includes correction, which separates the seed material by size, post-harvest cleaning is a series of interrelated technical operations that ensure the grain quality for use in food, technical, fodder or sowing purposes. There is also a growing demand for cleaning to remove quarantine seeds to avoid risks during grain export.

The grain correspondence with grinding affects the biochemical wheat properties, because there are the following technical processing stages: preliminary cleaning of the grain mass from impurities, hydrothermal processing (HTP), particles surface treatment, final cleaning. Preliminary cleaning from lumps is carried out in separators, triers and aspiration shafts for the separation of small grain particles, heavy and light impurities, and stones. Grain HTP is based on the water and heat action, which reduce the endosperm strength, which leads to the grain peeling with the shells separation during sieving. Grain HTP includes the stages of moistening, steaming, drying, cooling, as a result of which it is possible to increase the strength of the grain core, and the shell, on the contrary, to make the grain brittle for quick separation from the shell. HTP equipment includes: steamers, dryers, moisturisers. When humidity and temperature change, biochemical processes develop

in the grain, the consequence of which is the redistribution of chemical substances in the anatomical parts of the grain. Properly selected grain processing modes can change the gluten properties, weak gluten can be strengthened by rapid conditioning, and strong gluten can be weakened by cold conditioning. Secondary deep cleaning is a yield of pure products of at least 99.95%, with a hard-separable impurity that cannot be removed by conventional means. Cold conditioning is a process in which grain and water are not heated at a set temperature of grain and water not lower than 18-20°C. Under such conditions, the grain and water are heated and cooled to ensure normal conditions of moisture and at the same time dehydration of the grain. The grain temperature in the heaters is set up to 20-25°C, and the water temperature is set up to 60-70°C. The disadvantage of the cold conditioning method is the larger hopper capacity due to the longer time of moistening. Equipment for the grain raw materials preparation for processing begins with a complex of grain storage hoppers, regulatory and transport equipment, separation units of weeds and magnetic impurities according to geometric dimensions, shape and density. Installations for HTP of the grain surface and the product peeling into seeds and seed coat are shown in detail in the diagram of Figure 2.

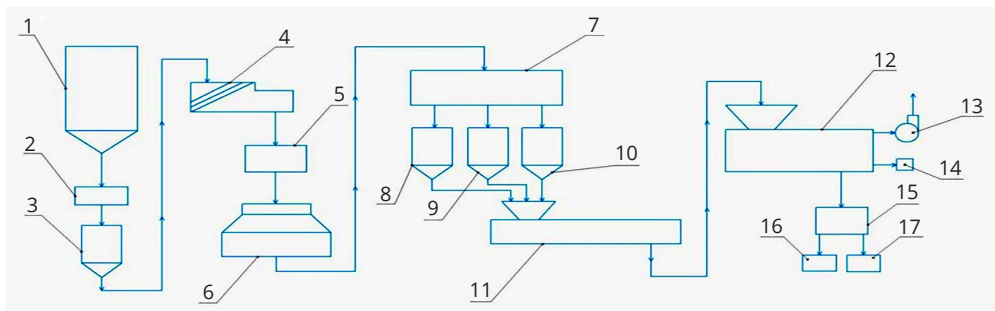


Figure 2. Technological diagram of the wheat seed peeling and cleaning plant for use in deep grain processing

Note: 1 – hopper for receiving raw materials; 2 – automated scales; 3 – intermediate bunker; 4 – grain cleaning plant; 5 – magnetic separator; 6 – trier; 7 – calibrator; 8 – small seed hopper; 9 – medium seed hopper; 10 – large seed hopper; 11 – raw material moisturiser; 12 – rotary-blade peeling installation; 13 – separation with fruit and seed coats; 14 – endosperm hopper; 15 – separator by vibrations; 16 – aleurone and subaleurone phases; 17 – seed hopper

Source: compiled by the authors based on DSTU No. 3768:2019 (2019)

Flour and water are mixed in a certain ratio in a dough-mixing unit, pumped into a homogeniser, where flour particles are fragmented. Then the

mass is put to the tricanter, where there is an effective separation into solid, heavy and light liquid phases. The solid phase produces practically pure

starch with a content of 54% in terms of an absolutely dry substance (ADS), which is already freed from gluten and contains up to 1.5% of crude protein. A-starch is dehydrated and dried to an ADS content of 88%. The heavy liquid phase consisting of gluten and B-starch, the resulting raw material is discharged from the tricanter under excess pressure using a combination of a phase separation disc and adjustable impeller. The light liquid phase that comes from the tricanter by gravity contains pentosans and non-starch polysaccharides, which

are further sent either to the production of alcohol or substrate for the fodder additives manufacture. The percentage yield of semi-finished products from wheat flour depends on the flour quality and the selected technological scheme. The A-starch content is 55%, B-starch is 14%, dry gluten is 10%, liquid fodder is 12%, sewage liquid waste is 9%. Taking into account the complex technology of deep processing of soft wheat, the requirements for the grain quality supplied for production are provided in Table 2.

Table 2. The main nutrients content in spring and winter wheat grains in terms of ADS, %

Indicator	Crude protein	Crude fat	Crude gluten	Crude ash	NFES
Winter wheat grain, Palitra variety	21.42	2.74	2.5	1.83	71.51
Winter wheat grain, Jersey variety	20.99	2.65	3.06	1.94	71.36
Winter wheat grain, Cubus variety	21.7	2.44	2.94	1.76	71.16
Spring wheat grain, Zlata variety	19.89	2.71	2.44	1.46	73.5
Spring wheat grain, Heroinya variety	19.64	2.29	2.48	1.34	74.25
Spring wheat grain, Kharkivska 26 variety	20.33	2.18	2.28	1.37	73.84

Source: compiled by the authors

Varieties of soft winter and spring wheat according to their actual composition of nutrients in the grain were determined by the high content of crude protein, crude fat and NFES, being necessary raw materials in the food industry. In the group of winter wheat varieties, crude protein was 20.9-21.7%, crude fat was 2.4-2.7%, crude fibre was 2.5-3%, NFES were 71.1-71.5%. In the group of spring wheat varieties, crude protein was 19.64-20.3%, crude fat was 2.2-2.7%, crude fibre was 2.2-2.4%,

NFES were 73.5-74.2%. Qualitative composition evaluation of wheat grain is necessary to comply with the storage indicators of plant products, however, in some cases, there are individual requirements for product monitoring, which are caused by special terms of contracts. Market qualities of wheat grain are represented by test weight indicators, weight per 1,000 seeds, GDI, FN, percentage of waste and grain impurities, data of various wheat varieties are provided in detail in Table 3.

Table 3. The main nutrients content in spring and winter wheat grains

Indicator	Moisture, %	Test weight, g/l	Weight per 1,000 seeds, g	Gluten, %	GDI, units	FN, sec.
Winter wheat grain, Palitra variety	10.15	757	42.2	24.2	78.2	364
Winter wheat grain, Jersey variety	11.25	773	41.7	20.4	76.4	339
Winter wheat grain, Cubus variety	10.15	784	43.4	27.3	81.6	345
Spring wheat grain, Zlata variety	12.32	740	43.3	26.2	71.1	358
Spring wheat grain, Heroinya variety	12.15	752	41.8	21.8	80.4	360
Spring wheat grain, Kharkivska 26 variety	11.45	755	43.8	23.1	74.7	313

Source: compiled by the authors

According to the received data on the qualitative composition in the winter wheat varieties group, the test weight varied at the level of 757-773, the weight per 1,000 seeds was 41.7-43.4 g,

gluten was 20.4-27.3%, IDC – 76.4-81.6 units, state of emergency 339-364 seconds. In the group of spring wheat varieties, the nature fluctuated at the level of 740-755, the weight of 1,000



seeds – 41.8-43.8 g, gluten – 21.8-26.2%, GDI was 71.1-80.4 units, FN was 313-358 seconds.

The studied wheat was grown according to intensive technologies, therefore, protective operations were carried out in a timely manner, under favourable weather conditions for after-ripening and harvesting, winter varieties were not damaged by frost, pests, diseases, germination deterioration, seeds blackening or mold damage. The content of waste and grain impurities was determined from the average sample without preliminary washing. The distribution and analysis of the foreign impurities showed that they included grass seeds, sand, soil, parts of stems and chaff. No grain damaged by fusarium, smut or crowns fungi was found.

DISCUSSION

The results of the current study confirm the critical role of modern grain cleaning and sorting methods in ensuring the quality and safety of wheat grain. The study highlights that by removing impurities, pathogens, and substandard grains through techniques such as aspiration, separation by density, and the use of advanced sieving technologies, it is possible to significantly enhance the purity and quality of the grain before further processing. These processes are crucial not only for maintaining the nutritional and safety standards required for food products but also for meeting the regulatory standards set by national and international food safety organizations. Implementing advanced technologies at each stage of grain processing, such as automated sorting systems, real-time quality monitoring, and precision sieving, directly contributes to achieving national goals related to food security. These technologies help in maximizing the efficiency of the food industry by reducing waste, improving the consistency of grain products, and ensuring that the final products meet the high standards expected by consumers and regulators alike. For instance, the use of computer vision and machine learning in grain sorting allows for more precise identification and removal of defective grains, thus enhancing overall product quality.

The results of this study showed that the improvement of cultivation technologies and the introduction of new high-yielding varieties significantly increased the productivity and profitability of the production of grain crops. In particular, between 2010 and 2020, the production of

agricultural products has increased by 25% due to the improvement of cultivation technologies and by 75% due to the genetic potential of new varieties. In particular, this concept is consistent with the research of S. Ostapenko (2022), which emphasises the importance of the natural value of new varieties for the growth of production. Analysis of modern equipment for grain processing revealed that the use of gravity tables, air and optical separators significantly increases the efficiency of processing with reduced energy consumption. A. Moghimi *et al.* (2020) note that such innovative technologies make it possible to improve the organoleptic and structural-mechanical characteristics of finished products. These conclusions are well-supported, as the current research also highlights that the implementation of intelligent sorting systems, regulated by computer algorithms, significantly enhances the quality of the final products.

The comparison of this study with others in the field reveals a general consensus among scientists on the necessity of adopting these advanced technologies throughout the grain processing chain. Despite variations in the specific methods and technologies employed, there is widespread agreement that these innovations are essential for maintaining high standards of food safety and quality. Moreover, the integration of these technologies into existing processing frameworks is seen as a key factor in improving the efficiency and sustainability of grain processing operations, thereby supporting broader food security objectives on a national and global scale. In a study conducted by S.D. Prakash *et al.* (2024), the emphasis on the importance of various grain processing stages and the need to ensure grain safety and quality throughout the supply chain aligns closely with the findings of this study. Both studies underscore the critical role of quality control at all stages, particularly during cleaning and sorting. Y. Lin *et al.* (2023) explored the behaviour of pathogens during the tempering of wheat grain, highlighting specific safety aspects. Although their focus differs slightly, the current study also addresses similar processing stages, emphasizing the importance of maintaining product quality. The findings from both studies underscore the necessity of technological control in preserving grain quality. The microstructure of wheat grain layers, particularly the



aleurone layer, as examined by X. Tian *et al.* (2021), has a significant impact on the efficiency of processing operations. This observation is consistent with the technological aspects discussed in the current study, which also highlights the influence of grain structure on processing outcomes.

Research by K. Chen *et al.* (2024) on the microbiological composition and enrichment of kefir grains, although not directly related to grain processing, suggests that microbiological analysis techniques could be beneficial in improving quality control measures within the grain industry. The study by A. Bianco *et al.* (2024) highlights the role of agro-food waste fermentation in promoting environmental sustainability. The findings from their research can be complemented by the results of this study, particularly regarding sustainable resource use in deep grain processing technologies. Investigations by I. El Houssni *et al.* (2024) into the microbiological quality of wheat flour and bran in Morocco resonate with the current study's focus on the need for stringent microbiological control throughout the grain processing stages. The alignment of these studies emphasizes the importance of technological oversight to maintain product safety. The work of T. Joshi *et al.* (2024) explored the use of modern technologies such as IoT and machine learning (ML) in agriculture. Integrating their findings with the current study could enhance the precision and efficiency of grain processing, particularly through the application of big data analytics.

The research by F. Jing *et al.* (2024) on reducing cadmium accumulation in wheat grain using biochar and selenium introduces important environmental considerations. Their findings, when viewed alongside the results of this study, provide a broader understanding of how different technological regimes affect grain safety and quality. The study by B. Zheng *et al.* (2021) on the impact of reduced nitrogen fertilizer rates on wheat grain quality echoes the current study's exploration of wheat classes and their applications. Their approach to balancing grain yield and quality through the adjustment of fertilizer rates and planting density offers valuable insights that could be applied to improve the grain handling methods described in this study. Research by J. Ren *et al.* (2024) on the effects of plant volatile organic compounds in preventing postharvest grain spoilage is relevant

for further refining grain safety methods discussed in this study. The work by K. Laabassi *et al.* (2021) on automating grain classification using machine learning presents promising directions for enhancing the efficiency and accuracy of the grain cleaning and sorting processes outlined in the current study. S. Ma *et al.* (2024) investigation into the use of plasma-activated water to modify wheat starch gels could lead to improvements in grain processing technologies and the development of new wheat-based products. This research complements the findings of the current study by offering potential enhancements to grain processing methods.

The biotechnology of wheat bran fermentation to increase its nutritional value, as studied by L. Fan *et al.* (2024), aligns with the goals of the current research. These insights can be integrated to create more nutritious wheat-based products and improve overall grain processing techniques. L. Verdi *et al.* (2022) assessed the ecological impact of organic versus traditional agriculture on wheat, providing a useful complement to the current study's focus on sustainability and the environmental impact of grain processing. The study by J. Zhang *et al.* (2023) on the impact of microplastics on soils with long-term organic fertilizer application raises important concerns for future research. These findings are relevant to understanding how such factors might affect grain quality and processing methods, as considered in the current study. Finally, the systematic review by D. Kumar & V. Kukreja (2024) of wheat disease recognition methods using computer vision technologies offers practical applications for improving quality control during grain processing. This approach is particularly valuable for detecting defects and contamination, which are critical stages in the processes discussed in this study. According to C. Celestina *et al.* (2023), the development of new scales for assessing the growth stages of grain crops is instrumental in refining grain processing methods. Their focus on improving measurement accuracy and analytical methods aligns well with the technological goals outlined in the current study.

In conclusion, the results of this study confirm the crucial role of modern grain cleaning and sorting methods in ensuring quality and safety. The comparison with other studies demonstrates a broad consensus on the need for advanced



technologies across all stages of grain processing, despite differing approaches. The current study offers a comprehensive framework for addressing quality assurance issues in grain processing, providing a solid foundation for further research and practical applications in this field.

CONCLUSIONS

Based on the conducted experimental studies, the levels of quality and market productivity of the varieties of soft winter and spring wheat according to their actual composition were established. Soft varieties of winter and spring wheat according to the actual nutrients' composition in the grain, according to the content of crude protein, crude fat, crude fibre, NFES, varied for winter wheat: crude protein from 20.9 to 21.7%, crude fat from 2.4 to 2.7%, crude fibre from 2.5 to 3% and NFES from 71.1 to 71.5%. In the group of spring wheat varieties, crude protein was from 19.6 to 20.3%, crude fat from 2.2 to 2.7%, crude fibre from 2.2 to 2.4%, NFES from 73.5 to 74.2%.

It was experimentally proven that the market indicators of the quality composition in the group of winter wheat varieties by moisture content varied within 10.1-11.2%, test weight within 757-773, weight per 1,000 seeds within 41.7-43.4 g, gluten content varied within 20.4-27.3%, GDI within 76.4-81.6 units, FN within 339-364 seconds. In the group of spring wheat varieties, the same

indicators varied in the following interval, respectively: 11.4-12.2%, 740-755, 41.8-43.8 g, 21.8-26.2%, 71.1-80.4 units, 313-358 seconds. Grain standards provide for the indicator's determination of moisture, test weight, waste and grain impurities, gluten content and GDI: grain batches of various varieties of spring and winter soft wheat met the requirements of the 2nd class, according to the indicator of crude protein content, falling number of the 2nd and 3rd classes.

The substantiation of priority measures for competitive production in raw material preparation for the deep processing of wheat grain in modern economic conditions is a promising approach to obtaining high-quality crop production with added value. Therefore, it is recommended to thoroughly study the chemical composition and market qualities of raw materials, as well as standards for pests and diseases in wheat seeds, to fully reveal their genetic potential and contribute to increased economic profitability. Further research in this direction will help to develop and implement new technologies that will ensure stable growth of production and improvement of product quality.

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None.

CONFLICT OF INTEREST

None.

REFERENCES

- [1] Bianco, A., Zara, G., Garau, M., Castaldi, P., Atzori, A.S., Deroma, M.A., Coronas, R., & Budroni, M. (2024). Microbial community assembly and chemical dynamics of raw brewers' spent grain during inoculated and spontaneous solid-state fermentation. *Waste Management*, 174, 518-527. [doi: 10.1016/j.wasman.2023.12.021](https://doi.org/10.1016/j.wasman.2023.12.021).
- [2] Celestina, C., et al. (2023). Scales of development for wheat and barley specific to either single culms or a population of culms. *European Journal of Agronomy*, 147, article number 126824. [doi: 10.1016/j.eja.2023.126824](https://doi.org/10.1016/j.eja.2023.126824).
- [3] Chen, K., Yang, J., Guo, X., Han, W., Wang, H., Zeng, X., Wang, Z., Yuan, Y., & Yue, T. (2024). Microflora structure and functional capacity in Tibetan kefir grains and selenium-enriched Tibetan kefir grains: A metagenomic analysis. *Food Microbiology*, 119, article number 104454. [doi: 10.1016/j.fm.2023.104454](https://doi.org/10.1016/j.fm.2023.104454).
- [4] Cheng, W., Sun, Y., Fan, M., Li, Y., Wang, L., & Qian, H. (2021). Wheat bran, as the resource of dietary fiber: A review. *Critical Reviews in Food Science and Nutrition*, 62(26), 7269-7281. [doi: 10.1080/10408398.2021.1913399](https://doi.org/10.1080/10408398.2021.1913399).
- [5] Convention "On Biological Diversity". (1992, June). Retrieved from <https://www.cbd.int/doc/legal/cbd-en.pdf>.
- [6] Convention "On the Trade in Endangered Species of Wild Fauna and Flora". (1973, June). Retrieved from <https://cites.org/eng/disc/text.php>.



- [7] DSTU GOST No. 10840:2019 "Grain. Method for Determining Bulk Density". (2019, December). Retrieved from https://online.budstandart.com/ua/catalog/doc-page?id_doc=89079.
- [8] DSTU ISO No. 13690:2003 "Cereals, Pulses, and Milled Products. Sampling". (2003, November). Retrieved from https://online.budstandart.com/ua/catalog/doc-page?id_doc=86198.
- [9] DSTU ISO No. 21415-1:2009 "Wheat and Wheat Flour. Gluten Content. Part 1. Determination of Wet Gluten by Manual Method". (2009, December) Retrieved from https://online.budstandart.com/ua/catalog/doc-page?id_doc=84541.
- [10] DSTU No. 3768:2019 "Wheat. Technical Specifications". (2019, May). Retrieved from https://online.budstandart.com/ua/catalog/doc-page?id_doc=82765.
- [11] DSTU No. 8840:2019 "Oilseed Seeds. Methods for Determining Colour and Odour". (2019, March). Retrieved from https://online.budstandart.com/ua/catalog/doc-page.html?id_doc=82152.
- [12] El Houssni, I., Zahidi, A., El Ouardi, A., Khedid, K., & Hassikou, R. (2024). Microbiological survey and physicochemical analysis of Moroccan durum, soft and red wheat landraces. *Journal of Agriculture and Food Research*, 16, article number 101199. doi: 10.1016/j.jafr.2024.101199.
- [13] Fan, L., Ma, S., Li, L., & Huang, J. (2024). Fermentation biotechnology applied to wheat bran for the degradation of cell wall fiber and its potential health benefits: A review. *International Journal of Biological Macromolecules*, 275(1), article number 133529. doi: 10.1016/j.ijbiomac.2024.133529.
- [14] Food and Agricultural Organization. (2023). *Food outlook: Biannual report on global food markets*. Rome: Food and Agriculture Organization of the United Nations.
- [15] Formentini, M., Secondi, L., Ruini, L., Guidi, M., & Principato, L. (2021). Enablers and barriers to circular supply chain management: A decision-support tool in soft wheat bread production. *Journal of Enterprise Information Management*, 35(3), 796-816. doi: 10.1108/jeim-02-2021-0069.
- [16] Gao, Q., Li, H., Meng, T., Xu, X., Sun, T., Yin, L., & Chai, X. (2024). A rapid construction method for high-throughput wheat grain instance segmentation dataset using high-resolution images. *Agronomy*, 14(5), article number 1032. doi: 10.3390/agronomy14051032.
- [17] Jing, F., Gao, Y., Li, H., Fan, G., Zhang, Q., Gao, X., & Zhou, D. (2024). Control location could confuse the evaluation of passivation effect of iron-based biochar and selenium application on wheat grain cadmium accumulation. *Pedosphere*. doi: 10.1016/j.pedsph.2023.12.017.
- [18] Joshi, T., Sehgal, H., Puri, S., Karnika, N., Mahapatra, T., Joshi, M., Deepa, P.R., & Sharma, P.K. (2024). ML-based technologies in sustainable agro-food production and beyond: Tapping the (semi) arid landscape for bioactives-based product development. *Journal of Agriculture and Food Research*, 18, article number 101350. doi: 10.1016/j.jafr.2024.101350.
- [19] Khudaverdiyeva, V. (2022). Priorities of innovative development in the agricultural sector. *International Science Journal of Engineering & Agriculture*, 1(3), 52-86. doi: 10.46299/j.isjea.20220103.6.
- [20] Kumar, D., & Kukreja, V. (2022). Deep learning in wheat diseases classification: A systematic review. *Multimedia Tools and Applications*, 81(7), 10143-10187. doi: 10.1007/s11042-022-12160-3.
- [21] Kumar, D., & Kukreja, V. (2024). Image segmentation, classification, and recognition methods for wheat diseases: Two decades' systematic literature review. *Computers and Electronics in Agriculture*, 221, article number 109005. doi: 10.1016/j.compag.2024.109005.
- [22] Laabassi, K., Belarbi, M.A., Mahmoudi, S., Mahmoudi, S.A., & Ferhat, K. (2021). Wheat varieties identification based on a deep learning approach. *Journal of the Saudi Society of Agricultural Sciences*, 20(5), 281-289. doi: 10.1016/j.jssas.2021.02.008.
- [23] Li, L., Chen, S., Deng, M., & Gao, Z. (2022). Optical techniques in non-destructive detection of wheat quality: A review. *Grain & Oil Science and Technology*, 5(1), 44-57. doi: 10.1016/j.gaost.2021.12.001.
- [24] Lin, Y., Simsek, S., & Bergholz, T.M. (2023). Fate of *salmonella* and shiga-toxin producing *Escherichia coli* on wheat grain during tempering. *Food Microbiology*, 111, article number 104194. doi: 10.1016/j.fm.2022.104194.
- [25] Liubych, V., Novikov, V., & Leshchenko, I. (2020). Technological properties of different types of wheat grain depending on the genotype. *Taurida Scientific Herald*, 114, 63-69. doi: 10.32851/2226-0099.2020.114.9.

- [26] Ma, S., Zhang, M., Wang, X., Yang, Y., He, L., Deng, J., & Jiang, H. (2024). Effect of plasma-activated water on the quality of wheat starch gel-forming 3D printed samples. *International Journal of Biological Macromolecules*, 274(1), article number 133552. doi: [10.1016/j.ijbiomac.2024.133552](https://doi.org/10.1016/j.ijbiomac.2024.133552).
- [27] Moghimi, A., Yang, C., & Anderson, J.A. (2020). Aerial hyperspectral imagery and deep neural networks for high-throughput yield phenotyping in wheat. *Computers and Electronics in Agriculture*, 172, article number 105299. doi: [10.1016/j.compag.2020.105299](https://doi.org/10.1016/j.compag.2020.105299).
- [28] National Academy of Agrarian Sciences of Ukraine. (2021). *Catalogue of varieties and hybrids*. Retrieved from <https://sgi.in.ua/data/documents/Katalog-sortiv-i-gibridiv-SGI-NCNS-2021.pdf>.
- [29] Ostapenko, S. (2022). Priority directions of food industry state regulation as a means to diversify agroexport. *Food Resources*, 10(18), 257-265. doi: [10.31073/foodresources2022-18-25](https://doi.org/10.31073/foodresources2022-18-25).
- [30] Prakash, S.D., Rivera, J., & Siliveru, K. (2024). Unit operations in wheat processing. In C.K. Sunil, K.A. Athmaselvi, N. Venkatachalapathy, C. Anandharamakrishnan & V.M. Balasubramaniam (Eds.), *Unit operations in food grain processing* (pp. 289-329). Amsterdam: Academic Press. doi: [10.1016/B978-0-443-18965-4.00010-8](https://doi.org/10.1016/B978-0-443-18965-4.00010-8).
- [31] Ren, J., Wang, Y.-M., Zhang, S.-B., Lv, Y.-Y., Zhai, H.-C., Wei, S., Ma, P.-A., & Hu, Y.-S. (2024). Terpinen-4-ol from tea tree oil prevents *Aspergillus flavus* growth in postharvest wheat grain. *International Journal of Food Microbiology*, 418, article number 110741. doi: [10.1016/j.ijfoodmicro.2024.110741](https://doi.org/10.1016/j.ijfoodmicro.2024.110741).
- [32] State Service of Ukraine for Food Safety and Consumer Protection. (n.d.). *Food safety and veterinary medicine*. Retrieved from <https://dpss.gov.ua/bezpechnist-harchovih-produktiv-ta-veterinarna-medicyna/pro-departament>.
- [33] Tian, X., Wang, Z., Yang, S., Wang, X., Li, L., Sun, B., Ma, S., & Zheng, S. (2021). Microstructure observation of multilayers separated from wheat bran. *Grain & Oil Science and Technology*, 4(4), 165-173. doi: [10.1016/j.gaost.2021.10.002](https://doi.org/10.1016/j.gaost.2021.10.002).
- [34] Tkachyk, S., Kyienko, Z., Prysiazniuk, L., Shovhun, O., Ivanytska, A., & Pavliuk, N. (2016). *Methodology for the qualification examination of plant varieties for suitability for distribution in Ukraine. Methods of determining plant production quality indicators*. Vinnytsia: D.Yu. Korzun IE.
- [35] Vasylenko, N., & Pravdziva, I. (2022). Yielding capacity and flour-milling properties of spring bread wheat varieties depending on growing environmental conditions. *Plant Varieties Studying and Protection*, 18(2), 127-135. doi: [10.21498/2518-1017.18.2.2022.265180](https://doi.org/10.21498/2518-1017.18.2.2022.265180).
- [36] Verdi, L., Marta, A.D., Falconi, F., Orlandini, S., & Mancini, M. (2022). Comparison between organic and conventional farming systems using Life Cycle Assessment (LCA): A case study with an ancient wheat variety. *European Journal of Agronomy*, 141, article number 126638. doi: [10.1016/j.eja.2022.126638](https://doi.org/10.1016/j.eja.2022.126638).
- [37] Vlizlo, V., Zelenina, O., & Kozak, M. (2023). Pegylated antimicrobials. In A. Krynski, V. Stybel, V. Vlizlo & I. Kovalchuk (Eds.), *Achievements and research prospects in animal husbandry and veterinary medicine* (pp. 24-40). Riga: Baltija Publishing. doi: [10.30525/978-9934-26-316-3-2](https://doi.org/10.30525/978-9934-26-316-3-2).
- [38] Wieser, H., Koehler, P., & Scherf, K.A. (2022). Chemistry of wheat gluten proteins: Qualitative composition. *Cereal Chemistry*, 100(1), 23-35. doi: [10.1002/cche.10572](https://doi.org/10.1002/cche.10572).
- [39] Zhang, J., Li, Z., Zhou, X., Ding, W., Wang, X., Zhao, M., Li, H., Zou, G., & Chen, Y. (2023). Long-term application of organic compost is the primary contributor to microplastic pollution of soils in a wheat-maize rotation. *Science of the Total Environment*, 866, article number 161123. doi: [10.1016/j.scitotenv.2022.161123](https://doi.org/10.1016/j.scitotenv.2022.161123).
- [40] Zheng, B., et al. (2021). Increasing plant density improves grain yield, protein quality and nitrogen agronomic efficiency of soft wheat cultivars with reduced nitrogen rate. *Field Crops Research*, 267, article number 108145. doi: [10.1016/j.fcr.2021.108145](https://doi.org/10.1016/j.fcr.2021.108145).

Обґрунтування технології підготовки м'якозерної пшениці до глибокої переробки

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Анотація. Технологічні особливості заготівлі зерна для переробки та виробництва харчових продуктів неможливі без визначення вмісту білка, крохмалю, клейковини, так само в зерновій масі м'якозерної пшениці, яка надходить на зернопереробні підприємства, міститься зернова та сміттева домішки. Метою роботи було обґрунтування технологій первинної та поглибленої підготовки зерна пшениці з використанням сучасних методів зберігання і транспортування для подальшого використання в процесах глибокої переробки зерна. Для встановлення технологічних особливостей було використано метод ідентифікації, вимірювання морфологічних характеристик та визначення домішок. Стандарти зерна передбачають визначення вологості, натури, вмісту смітної та зернової домішок, вмісту клейковини та індексу деформації клейковини (ІДК) у партіях зерна різних сортів ярої та озимої м'якої пшениці. Отримані дані відповідали вимогам 2-го класу, за показником вмісту сирого протеїну, числа падіння (ПЧ) 2-го та 3-го класів. Експериментально визначено товарні показники якісного складу зерна пшениці м'якої ярої та сортів пшениці м'якої озимої. Встановлено, що в групі сортів пшениці озимої вологість була в межах 10,1-11,2 %, натура – 757-773, маса 1000 насінин – 41,7-43,4 г, вміст клейковини – 20,4-27,3 %, ІДК – 76,4-81,6 одиниць, число падіння – 339-364 секунди; у сортів пшениці м'якої ярої відповідно 11,4-12,2 %, 740-755, 41,8-43,8 г, 21,8-26,2 %, 71,1-80,4, 313-358. Щодо харчових якостей пшениці, то в групі озимих сортів вміст сирого протеїну становив 20,9-21,7 %, сирого жиру – 2,4-2,7 %, сирій клітковини – 2,5-3,0 %, безазотистих екстрактивних речовин – 71,1-71,5 %; у ярих сортів, відповідно, 19,64-20,3 %, 2,2-2,7 %, 2,2-2,4 %, 73,5-74,2 %. Практичне значення роботи полягає у впровадженні сучасних методів зберігання та транспортування зерна, що дозволяє значно покращити якість сировини, підвищити ефективність харчового виробництва, зменшити втрати при переробці, забезпечити відповідність продукції високим стандартам якості

Ключові слова: зернова сировина; обладнання; домішки; лущення; сепарація



Assessment of the state of phytocenoses of quarry-dump complexes by remote sensing

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Abstract. One of the types of anthropogenic activities that leads to negative environmental changes and biodiversity loss is the extraction of minerals within quarry-dump complexes, which requires measures to restore ecological balance following the completion of mining operations. The search for optimal methods to identify disturbed areas, monitor the condition and recovery dynamics of exhausted lands in the context of biodiversity conservation and restoration was the aim of the study, particularly when field research was inaccessible, and there was a need to observe multiple sites simultaneously. This paper presents the results of assessing vegetation cover within territories disturbed by mineral extraction using remote sensing techniques. Methods such as scientific analysis, synthesis, statistical data processing, and the transect method were employed. It has been determined that the analysis and monitoring of Normalised Difference Vegetation Index (NDVI) values, obtained via remote sensing, enable the assessment of the quality of reclamation measures, identification of high-productivity areas, and detection of problem zones for devising effective methods to improve the ecological condition of the studied site. Within the examined Andriikovetskyi quarry-dump complex, the successional stages exhibited heterogeneity, with some areas remaining open without vegetation cover and others characterised by early successional stages and sparse vegetation. The lowest NDVI values were recorded in 2019 and 2022, while between 2020-2021 and 2023-2024, an increase in biomass productivity was observed, with the extent of areas covered by dense and moderate vegetation growing. It was noted that

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this situation was caused by height differences, surface irregularities, water and wind erosion processes (due to the absence of reclamation measures), instability of the sandy substrate, and a low capacity to supply vegetation with sufficient moisture. The findings of the study highlighted the importance of reclamation measures for post-mining areas and provided practical recommendations for the necessary engineering and technical measures to restore the quarry-dump complex to conditions that are closer to natural ones, promoting the spread of zonal species and self-recovery processes

Keywords: disturbed areas; NDVI; mineral extraction; vegetation; habitat conditions; reclamation; monitoring

INTRODUCTION

Since the beginning of the 21st century, a negative trend of increasing anthropogenic impact on natural environmental components has been observed, particularly in the last decade. Anthropogenic influence contributes to the emergence of significant areas of unauthorised landfills, pollution of soils and water bodies, a decrease in soil fertility, and a reduction in productivity. Biodiversity loss, a crucial component of the environment, is also significant on a large scale.

As highlighted by M. Horun *et al.* (2019), a primary driver of rapid biodiversity loss is the “Great Acceleration”, a period beginning in 1950 characterised by a surge in human activities. This era marks the onset of the Anthropocene, a new epoch where humanity has become the dominant force shaping climate change, biodiversity, and the environment through deforestation, soil degradation, agricultural expansion, land degradation, and landscape fragmentation. The existing network of protected areas is insufficient to safeguard species, habitats, and ecosystems. According to the State cadaster of territories and objects of the nature reserve fund (2024), as of 2023, the coverage of protected areas was 6.91%, significantly below the European average of 21%.

Reclamation activities are accompanied by monitoring of the restoration process of disturbed lands. Remote sensing systems, including aerial imagery and unmanned aerial vehicles (UAVs), are used to observe and predict changes in the state of the studied area under the influence of anthropogenic factors. As noted by N. Mironova & B. Artaimonov (2020), these systems are used to address practical tasks related to spatially distributed data, which are employed to ensure the environmental safety of regions and their sustainable development. The authors highlight several advantages of remote sensing methods, including the ability to

cover large areas, obtain information on multiple objects simultaneously, monitor areas in regions that are difficult to access for field observations, achieve a high degree of information generalisation, and transition from a discrete picture of the values of natural environment indicators at individual points within the study area to a continuous map of the spatial distribution of these indicators. According to Yu. Vikhot *et al.* (2022), the main disadvantages of using remote sensing methods include dependence on weather conditions (as satellite imaging cannot occur during cloudy or rainy weather). When employing unmanned aerial vehicles, research time is limited by weather conditions and the season, and GPS signals can be lost or degraded. Additionally, the cost of specialised software or sensors can be quite high.

In the context of monitoring post-mining areas, the obtained data can provide information on the structure and composition of the study area, the dynamics of changes in mining landscapes, and can be used to assess the effectiveness of reclamation stages (including agricultural and forest phytomelioration), the spread of hazardous phenomena or their consequences (landslides, erosion, fires), and the identification of critical conditions such as weed proliferation, vegetation thinning, changes in moisture content, and precipitation levels. Using remote sensing techniques and analysing satellite data, scientists R.M. Shevchuk (2019), V. Carabassa *et al.* (2021), and J.C. Padro *et al.* (2022) have highlighted the importance of conducting monitoring studies using remote sensing for mining sites, investigating their condition and changes, and identifying water erosion processes in disturbed areas through remote sensing.

According to data obtained by P. Prokop (2020), an assessment of long-term land use was conducted, identifying the main factors

contributing to land degradation, such as deforestation, reduction of pastures, stability of arable land cultivation, population growth, expansion of water bodies, and mining activities. Researchers M.K. Firozjahi *et al.* (2021) evaluated the actual and potential impacts of mining on the biophysical characteristics of the Earth's surface. Monitoring the Normalised Difference Vegetation Index and other plant growth indicators using remote sensing (Earth observing system, n.d.; Crop monitoring, n.d.) can reveal critical conditions and phenomena after biological reclamation or during spontaneous recovery.

The study aimed to assess the condition of the phytocoenoses in the post-mining areas of the Andriikovetskyi quarry-dump complex by analysing Normalised Difference Vegetation Index values over a five-year period, obtained using remote sensing techniques. To achieve this aim, the following tasks were undertaken: identifying the main factors influencing vegetation recovery in the quarry-dump complex and characterising the structure of the mining-industrial landscape. The study also involved zoning the area according to prevalent vegetation types, outlining problematic zones within the quarry-dump complex and determining the causes of their emergence, as well as providing recommendations for further measures to optimise the ecological state of the studied area.

MATERIALS AND METHODS

To assess the condition of the phytocoenosis within the study, various methods were employed, including field methods (transect method, aerial photography, collection of herbarium samples), scientific methods (analysis, synthesis), and statistical methods (statistical analysis of collected data). Changes in the condition of disturbed areas were identified through monitoring the NDVI (Normalised Difference Vegetation Index), one of the most widely used indices for the quantitative assessment of vegetation cover. This index was used to analyse the characteristics of primary vegetation formation and the progression of successional stages for different vegetation types within the Andriikovetskyi quarry-dump complex. The NDVI data were systematised and analysed during the active vegetation period (March to October) from 2019 to 2023, based on the Crop Monitoring system using Sentinel-2 satellite data. The

findings allowed conclusions to be drawn regarding the vegetation's projected cover.

The Andriikovetskyi sand quarry-dump complex is located near the village of Andriikivtsi in the Rozsoshanska rural territorial community of the Khmelnytskyi District in Khmelnytskyi Region. The designated study area of the quarry is 4.3 hectares. Extraction took place from 2006 to 2015, and the quarry is situated amid agricultural land where maize and sunflower are cultivated. The identification of the quarry-dump complex in the geospatial context was conducted using GPS coordinates. The results of monitoring topographical changes through UAV aerial photography led to the creation of an elevation change map, which depicts the lowest and highest points of the quarry and highlights its differences from the surrounding agricultural landscape. Based on the aerial photography, a map with a hypsometric profile was generated, which facilitated the description and identification of the main elements of the mining-industrial landscape structure. The progression of primary succession is influenced by factors such as the mechanical composition of the soil, the physical properties of the surface layer of sand, and the exposure of slopes and dumps, reflecting the edaphic conditions. The characteristics of the sandy substrate affect the distribution, anchoring, and germination of seeds, as well as the subsequent spread rate of species.

Based on archival data and Geoinform Ukraine (n.d.), the main characteristics of the substrate of the Andriikovetskyi sand quarry-dump complex were determined as of 2020 and 2022: physico-mechanical properties, mineral composition, chemical composition, and fine-grained fraction. In terms of physicommechanical properties, the sandy substrate is characterised by a dense structure, with a bulk density ranging from 1.3 g/cm³ to 1.41 g/cm³ and an average true density of 2.63 g/cm³. The proportion of fine-grained fractions of clay, silt, and mud varies from 2.4% to 19.9%. The primary mineral composition consists of quartz, with admixtures of potassium feldspar and glauconite. In terms of chemical composition, the sandy substrate contains SiO₂ (which predominates over other compounds, ranging from 81.99% to 86.03%), Al₂O₃ (alumina), and CaO (quicklime), each with contents exceeding 3%, as well as Fe₂O₃ and K₂O, both with contents greater than 1%,

and TiO_2 and MgO , with contents up to 1%. Plant names are provided according to the International plant name index (n.d.) and the system by S. Mosyakin & M. Fedoronchuk (1999). Species with high invasive potential are indicated as per V. Protopopova *et al.* (2002). The description and identification of common species were conducted under laboratory conditions based on the collected herbarium material.

RESULTS AND DISCUSSION

Post-mining areas, once mineral extraction has ceased, exhibit a range of negative environmental impacts including degraded air quality, soil contamination, depletion of natural resources, reduced groundwater levels, and altered topography. In such areas, segetal and ruderal species, and highly invasive species rapidly proliferate, hindering zonal successional processes and contributing

to the decline and loss of biodiversity in adjacent natural areas. Natural restoration can take decades or even centuries or may not occur at all, as devastated lands are low in productivity and have conditions that differ significantly from those of surrounding areas, preventing the colonisation and formation of species-rich zonal phytocoenoses.

It has been established that within the studied sand quarry-dump complex, self-restoration of the plant cover has occurred, accompanied by noticeable plant differentiation. The phytocoenosis significantly differs from those formed in undisturbed natural areas. One of the factors influencing species distribution within quarry-dump complexes is the heterogeneous conditions of the edaphotope. The results obtained from surveying the area using UAVs facilitated the construction of a height change map for the quarry-dump complex, as depicted in Figure 1.

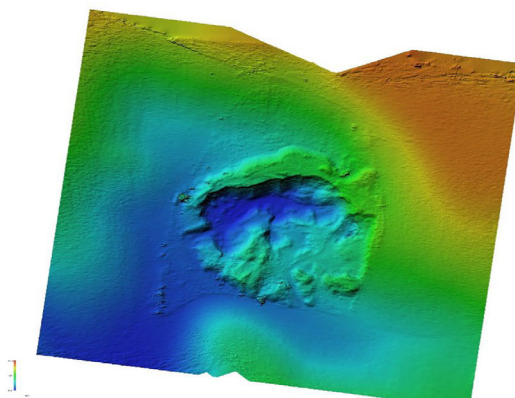


Figure 1. Height change map of the quarry-dump complex

Source: created by the authors

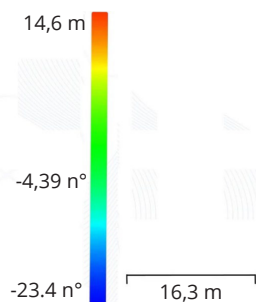


Figure 2. The scale of values for the measured contrasts

Source: created by the authors

Research findings have revealed that the anthropogenic conditions within the quarry-dump complex are characterised by significant elevation differences (the deepest point of the quarry is 328 meters above sea level, located in the north-eastern part, while the highest point is 340 meters above sea level, with a height difference within the quarry ranging from 15 to 20 meters), the presence of large embankments in the southern and south-western parts of the quarry, and steep, unvegetated sand walls and slopes (up to 80° in the northern part, up to 70° in the central, northwestern, and western parts, and more gentle, up to 40° , in the

eastern and southeastern parts). The vegetation zoning of the quarrydump complex during the period from 2019 to 2023 and its current state (2024) are presented in Figure 3.



Figure 3. Zoning of the study area

Note: ■ – dense vegetation; ■ – moderate vegetation; ■ – sparse vegetation; ■ – bare soil.

Source: created by the authors

Based on *in situ* research, the primary structure of the mining landscape was determined, taking into account the aforementioned anthropogenic conditions: the quarry floor (bottom) where clay-rich rocks have partially surfaced; hilly areas; inclined surfaces; sandy-loamy dumps and sandy-loamy areas that were not involved in mineral extraction; ridge-like rock embankments, micro-hilly surface areas and escarpments, especially the escarpment of exposed rocks (mainly fine-grained sand), as well as low-lying areas and transitional areas with sufficient moisture. Since no reclamation measures have been carried out within this quarry, and the structure of the quarry-dump complex differs significantly from natural landscape conditions, the distribution of species and the course of successional stages are

heterogeneous, with some areas lacking or virtually devoid of vegetation cover.

At the beginning of the study, a significant difference in the condition of the eastern part of the quarry and its internal slopes was observed, as they were subject to landslides and erosion, which was recorded in satellite images. Meanwhile, in the central and western parts of the quarry, the spread of woody shrub species and herbaceous plants was noted. By 2022–2023, zonal species had appeared in the species composition of the phytocoenosis. The presence of mesophytes and mesotrophs among the zonal species indicates soil-forming processes and access to the necessary nutrients. Woody shrub species are common in depressions with sufficient moisture, on the slopes of the northern part, while in the micro-hilly escarpments of the northwestern part, the distribution of herbaceous-grassy plant communities with solitary woody species was recorded. Within the asymmetrical hollows of the central part of the quarry, segetal and ruderal, and herbaceous vegetation predominates with a moderate projective cover.

Over the study period from 2019 to 2024, plant colonisation did not occur in certain areas, primarily the eastern part of the quarry and the internal slopes of the western, north-central, and north-eastern parts. However, the total area of land with absent or nearly absent vegetation cover decreased. Several monocarpic herbs appeared, dominated by the pioneer species *Tussilago farfara* L., which is characteristic of the initial stage of succession. A small number of polycarpic herbs, represented by species of the genus *Fabaceae*, were also present, which will positively impact the enrichment of the sandy substrate with nitrogen (Didur & Shevchuk, 2020). The largest area of land not covered by vegetation or with insignificant projective cover – 1.08 hectares, accounting for 25% of the total quarry area – was observed in 2022. The change in the area of vegetation-covered areas and areas with bare ground (sandy substrate) is presented in Table 1.

Table 1. Changes in the area of vegetation-covered territories

Year Indicator	2019		2020		2021		2022		2023	
	Area, ha	In %	Area, ha	In %	Area, ha	In %	Area, ha	In %	Area, ha	In %
Dense vegetation ■	1.09	26	1.31	31	1.58	37	1.16	27	1.41	33
Dense vegetation ■	1.49	35	2.16	51	1.38	32	1.26	30	1.76	41

Table 1. Continued

Year Indicator	2019		2020		2021		2022		2023	
	Area, ha	In %	Area, ha	In %	Area, ha	In %	Area, ha	In %	Area, ha	In %
Moderate vegetation 	1.22	28	0.56	13	0.97	23	0.77	18	0.79	18
Sparse vegetation 	0.36	8	0.19	4	0.26	6	0.88	21	0.29	7
Bare soil 	0.11	3	0.05	1	0.08	2	0.2	4	0.02	1

Source: calculated by the authors

Analysis of the retrospective data over a five-year period allows for the tracking of the dynamics

of plant biomass development. The average NDVI values for the study period are depicted in Figure 3.

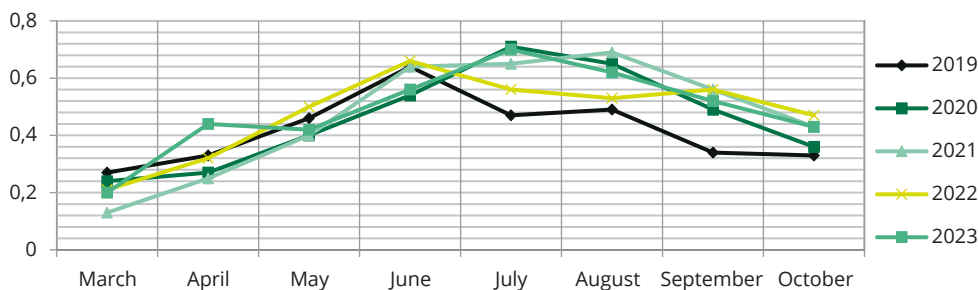


Figure 4. Average NDVI values during the active vegetation period 2019-2023

Source: developed by the authors based on the study

An increase in the NDVI was recorded from May to June, with peak values occurring in July. The lowest values were recorded in 2019, which is associated with the presence of larger areas not covered by vegetation and landslides on the slopes. The highest biomass productivity values were obtained in 2020-2021: in July-August 2020, the values reached 0.65-0.71; in 2021, 0.65-0.69. However, in 2022, a sharp decline in plant biomass productivity was recorded: during the period from July to August, values were within the range of 0.53-0.56. In 2023, the situation improved – NDVI values increased (0.62-0.7), as did the areas covered by dense vegetation (the area value in 2022 was 1.16 ha and 1.26 ha, in 2023 this value was 1.41 ha and 1.76 ha), however, despite the increase in productive areas, landslides continue in the eastern part of the quarry.

It has been established that within devastated lands, negative phenomena can occur, timely identification of which will allow for the implementation of preventive measures or measures to mitigate the consequences and continue the restoration of disturbed territories. The identification

of these factors is carried out through thermal contrasts, which are recorded by infrared and thermal spectra. Scientist S. Alpert (2024) has substantiated that using the NDVI index, problem areas with probable oil pollution sites can be identified in this way. In the case of the study of the Andriikovetskyi quarry-dump complex, changes in spectra have allowed for the determination of a sharp decline in plant cover productivity, increasing the area of bare ground and sparse vegetation. After inspecting the territory of the sand quarry, it was found that the decrease in productivity was associated with the appearance of several fire outbreaks, caused by possible spontaneous combustion or arson of unauthorised landfills, which spread to adjacent territories.

The pyrogenic factor poses a significant threat and its monitoring is crucial not only in human-disturbed ecosystems but also in natural ones. Researchers Ye. Suetnov & A. Lazebna (2020) have determined that in areas where landfills are located, spontaneous combustion can occur due to the disposal of waste in unauthorised sites, the absence of proper waste disposal procedures,



and the formation of biogas, the accumulation of which in large volumes can lead to massive fires. In the case of the studied quarry, the most likely cause of fires is the intentional burning of waste by humans for disposal purposes, as the size of the formed landfills and the insignificant composition of organic waste are insufficient for the accumulation of excessive amounts of biogas and its subsequent combustion. As noted by O. Mudrak & D. Andrusiak (2022), the impact of the anthropogenic factor is decisive in the occurrence of fires. Climatic conditions, highly flammable plants and their dry residues play a crucial role, as they can lead to the rapid spread of fires and increase the risk of emergencies that are no longer dependent on human factors. This is what happened within the Andriikovetskyi quarry – due to the burning of landfills, the fire spread to vegetation-covered areas, resulting in a massive wildfire of dead wood.

Large-scale mining sites such as peatlands are particularly susceptible to fires. According to research by L. Lischenko *et al.* (2022), seasons with the highest risk of fires and the primary risks associated with anthropogenic factors were identified: within the two study areas, fires most frequently occurred in autumn (September–October). In the Andriikovetskyi quarry, a massive fire broke out in July, during peak temperatures, confirming the influence of climatic conditions on the spread of fire in the study area. In some areas, the spread of segetal and ruderal vegetation was observed, including species such as *Elytrigia repens* (L.) P. Beauv., *Capsella bursa-pastoris* L., *Artemisia absinthium* L., *Cirsium vulgare* (Savi) Ten, *Tripleurospermum inodorum* (L.) Sch. Bip, *Erysimum cheiranthoides* L., *Chenopodium album* L., etc. Some species have a high invasive potential (*Solidago canadensis* L., *Stenactis annua* L. Cass, *Acer negundo* L., *Amaranthus retroflexus* L.).

As of 2023, the hilly and sloping surfaces, the quarry floor, the rampart-like embankments, and the sandy-loamy surfaces are dominated by ruderal vegetation, herbaceous plants, grasses, and a small number of woody species. The inner slopes are characterised by the absence of phytocoenoses or are covered with sparse herbaceous vegetation and are subject to frequent landslides of sandy substrate. The eastern part of the quarry is characterised by the almost complete absence of vegetation, particularly within the sandy escarpment where

unauthorised sand extraction occurs, and the surrounding area – the monolithic sandy bottom and individual sections of sandy-loamy spoil heaps. A small amount of herbaceous vegetation is represented by species such as *Astragalus onobrychis* L., *Tanacetum vulgare* L., *Pimpinella saxifraga* L., *Myosotis micrantha* Pall. ex Lehm, *Taraxacum officinale* Weber ex F.H. Wigg. s. l., is formed on the steep slopes of the quarry, with *Tussilago farfara* L. as the dominant species in the plant cover of this area. The process of quarry restoration is directly dependent on its location, the degree of disturbance, the formed edaphic conditions, the type of rock and its properties, as demonstrated by the results of the study conducted on different types of quarries.

The overall condition of the quarry and its vegetation cover has been assessed as satisfactory. Similar findings were reported by I. Vorovencii (2021), who investigated the state of areas following reclamation efforts, noting the establishment of spontaneous vegetation and forest regeneration over several years. The development of vegetation cover has also been deemed satisfactory within the titanium ore extraction site, as indicated by the results of an EIA conducted by B.V. Borysiuk *et al.* (2022). The identified biogeocenoses of forests, meadows, and wetlands are considered to be quite resilient and suitable for supporting plant and animal life. However, it has been noted that the forested areas are densely populated with underbrush, which may adversely affect the overall biogeocenosis of the forest. A similar negative factor has been identified in the studies of the Andriikovetskyi sand quarry-dump complex, where a significant number of segetal and ruderal species are prevalent, thereby impacting the formation of vegetation cover within the studied area and hindering the spread of zonal flora species.

Y. Wang *et al.* (2022), through NDVI analysis of a vacant lot with limestone soil, found that the ecological condition of the area was improving but only reached a moderate level of vegetation cover, indicating the need for additional reclamation measures. According to the obtained monitoring results, a general improvement in the situation has occurred within the Andriikovetskyi quarry-dump complex; however, the situation within the eastern part of the quarry remains unsatisfactory, requiring restoration work. When studying a limestone quarry in India, scientists V. Kumar &



K. Yarrakula (2022) analysed data from 1997 to 2017 and found an increase in built-up and agricultural areas, while natural water bodies and forest areas decreased. Within the studied Andriikovetskyi quarry, on the contrary, using the NDVI index, an increase in the total area covered by vegetation was determined (indicating a sequence of successional stages). However, destructive processes within the quarry do not cease, and areas of bare ground (sandy substrate) are still localised within the study object. A similar situation was found by scientists L. Suresh *et al.* (2021) in granite quarries: within the study area, areas were found where vegetation was destroyed and there are areas of bare substrate, although vegetation was preserved on most of the study area. Researchers A. Buczyńska *et al.* (2023) found, through an analysis of vegetation index values within brown coal extraction quarries, a general improvement in vegetation cover, except in a specific area in the north-west, where a decrease in the vegetation index was observed. Within the eastern part of the studied quarry-dump complex, a section with the worst vegetation cover indices was identified, significantly differing from the sections in the western, central, and southern parts.

In the studies conducted by S. Huang *et al.* (2021), the overall trend of using NDVI and the limitations of the method that may impact the assessment of vegetation cover were examined. The researchers noted that this vegetation index would continue to be the dominant index for vegetation studies; however, its effective application depends on the quality of the multispectral data obtained and its subsequent interpretation. Furthermore, the need for training users of NDVI was highlighted to minimise uncontrolled usage of the data acquired. An important factor identified for the accurate recording and interpretation of data is the influence of sensor and atmospheric effects. During the analysis of data from the Andriikovetskyi quarry-dump complex, the atmospheric effect was noted as the most frequently recurring factor that hampers proper registration of remote sensing data on certain days of the growing season.

Monitoring disturbed areas using remote sensing is more effective when combined with other research methods and measures that contribute to improving the restoration processes of devastated sites. Researchers V. Adjiski & V. Zubíček (2023)

combined the Google Earth Engine (n.d.). computational platform with Landsat time series data, NDVI, the RandomForest (RF) algorithm, and LandTrendr to monitor the impact of mining, reclamation measures, and solar power plant activities at a coal mine from 1984 to 2021. In this study, remote sensing monitoring was combined with *in situ* research within the quarry, making it possible to identify the prerequisites and trends in changes in vegetation and landscapes in the study area, characterise the factors influencing the formation of vegetation cover at the time of the study, and forecast possible ways to implement conservation measures. The study has determined that the Andriikovetskyi quarry requires a mining engineering stage of reclamation (grading, slope stabilisation, formation of slopes, covering with a layer of fertile or potentially fertile soil, removal and disposal of waste) using environmentally friendly methods to bring the conditions of the quarry-dump complex closer to natural ones, which will contribute to accelerating zonal successional transformations.

CONCLUSIONS

Biodiversity is a crucial component of the natural environment, and its preservation is a prerequisite for the sustainable development of any region. Since 2014, the risk of its loss has increased, especially in heavily disturbed areas of mining landscapes, necessitating the adoption of new technologies for monitoring and observing the state of the environment. Monitoring the NDVI index has enabled the assessment of the condition of phytocoenoses in the studied areas and the timely identification of problem areas during reclamation or the monitoring of self-recovery of post-mining territories.

Remote sensing results and the transect method of the territory have confirmed that due to elevation differences, surface irregularities, frequent water and wind erosion processes (resulting from the lack of reclamation measures), instability of the sandy substrate, and its low ability to provide plants with the necessary amount of moisture, plant differentiation has formed within the quarry. Some areas within the eastern part of the quarry are not covered by vegetation, while the inner slopes of the western and central parts of the quarry are characterised by the course of primary successional stages, distinguished by sparse vegetation. In 2023, the total area of plots where

primary colonisation by species did not occur decreased: the area of bare ground is 0.02 ha, which is 5.5 times less than the values recorded at the beginning of the study in 2019.

The sparse vegetation cover in transitional areas includes the appearance of ruderal and segetal species, and species with high invasive potential, such as *Solidago canadensis* L., *Stenactis annua* L. Cass, *Acer negundo* L., and *Amaranthus retroflexus* L., which may hinder the spread of zonal species and the formation of stable phytocoenoses. Continued monitoring will allow tracking the dynamics of vegetation cover, and reducing the impact of negative processes in the edaphic environment through necessary engineering measures will ensure the formation of zonal natural flora.

Measures aimed at the self-recovery of quarries and the formation of vegetation cover will contribute to the establishment of quarries as objects that will represent natural zonal flora in the context of biodiversity conservation and sustainable development. Further research aimed at finding and identifying similar objects in the geospatial realm, determining ways to improve the condition of disturbed areas, and ways of their further profitable use is promising.

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CONFLICT OF INTEREST

None.

REFERENCES

- [1] Adjiski, V., & Zubíček, V. (2023). Continuous monitoring of the mining activities, restoration vegetation status and solar farm growth in coal mine region using remote sensing data. *Mining Review*, 29(1), 26–41. doi: [10.2478/minrv-2023-0003](https://doi.org/10.2478/minrv-2023-0003).
- [2] Alpert, S. (2024). An application of the modern methods for satellite image processing for solution of problems of environmental monitoring. *Ukrainian Journal of Remote Sensing*, 11(2), 13–18. doi: [10.36023/ujrs.2024.11.2.260](https://doi.org/10.36023/ujrs.2024.11.2.260).
- [3] Borysiuk, B., Hurelia, V., & Statnyk, I. (2022). Study of the influence of activities on flora during the construction and operation of the titanium ore quarry. *Herald of the National University of Water and Environmental Engineering: Agriculture Science*, 3(99), 15–24. doi: [10.31713/vs320222](https://doi.org/10.31713/vs320222).
- [4] Buczyńska, A., Blachowski, J., & Bugajska-Jędraszek, N. (2023). Analysis of post-mining vegetation development using remote sensing and spatial regression approach: A case study of former “Babina” mine (Western Poland). *Remote Sens*, 15(3), article number 719. doi: [10.3390/rs15030719](https://doi.org/10.3390/rs15030719).
- [5] Carabassa, V., Montero, P., Alcañiz, J.M., & Padró, J.C. (2021). Soil erosion monitoring in quarry restoration using drones. *Minerals*, 11(9), article number 949. doi: [10.3390/min11090949](https://doi.org/10.3390/min11090949).
- [6] Crop monitoring. (n.d.). Retrieved from <https://crop-monitoring.eos.com>.
- [7] Didur, I., & Shevchuk, V. (2020). Increasing soil fertility as a result of the accumulation of nitrogen by leguminous crops. *Agriculture and Forestry*, 16(1), 48–60. doi: [10.37128/2707-5826-2020-1-4](https://doi.org/10.37128/2707-5826-2020-1-4).
- [8] Earth observing system. (n.d.). Retrieved from <https://eos.com/uk/products/crop-monitoring/key-functions/satellite-monitoring>.
- [9] Firozjaei, M.K., et al. (2021). A historical and future impact assessment of mining activities on surface biophysical characteristics change: A remote sensing-based approach. *Ecological Indicators*, 122, article number 107264. doi: [10.1016/j.ecolind.2020.107264](https://doi.org/10.1016/j.ecolind.2020.107264).
- [10] Geoinform Ukraine. (n.d.). Retrieved from <http://geoinf.kiev.ua>.
- [11] Google Earth Engine. (n.d.). Retrieved from <https://earthengine.google.com/>.
- [12] Horun, M., Pyrih, H., Faifura, V., & Fedirko, M. (2019). *Ecology*. Ternopil: Ternopil National Economic University.
- [13] Huang, S., Tang, L., Hupy, J. P., Wang, Y., & Shao, G. (2021). A commentary review on the use of normalized difference vegetation index (NDVI) in the era of popular remote sensing. *Journal of Forestry Research*, 32, 1–6. doi: [10.1007/s11676-020-01155-1](https://doi.org/10.1007/s11676-020-01155-1).
- [14] International plant name index. (n.d.). Retrieved from <https://www.ipni.org/>.
- [15] Kumar, V., & Yarrakula, K. (2022). Environmental impact assessment of limestone quarry using multispectral satellite imagery. *Earth Science Informatics*, 15, 1905–1923. doi: [10.1007/s12145-022-00845-0](https://doi.org/10.1007/s12145-022-00845-0).

- [16] Lischenko, L., Shevchuk, R., & Filipovych, V. (2022). The technique for satellite monitoring of peatlands in order to determinate their fire hazard and combustion risks. *Ukrainian Journal of Remote Sensing*, 9(1), 16-25. [doi: 10.36023/ujrs.2022.9.1.210](https://doi.org/10.36023/ujrs.2022.9.1.210).
- [17] Mironova, N., & Artamonov, B. (2020). [The use of GIS technology in the study of mineral deposits of sedimentary origin of the Khmelnytskyi Region](#). *Herald of Khmelnytskyi National University: Technical Science*, 3(285), 7-11.
- [18] Mosyakin, S., & Fedoronchuk, M. (Eds.). (1999). *Vascular plants of Ukraine: A nomenclatural checklist*. Kyiv: M.G. Kholodny Institute of Botany. [doi: 10.13140/2.1.2985.0409](https://doi.org/10.13140/2.1.2985.0409).
- [19] Mudrak, O., & Andrusiak, D. (2022). Influence of the pyrogenic factor on natural ecosystems of Podilski Tovtry National Nature Park. *Agroecology Journal*, 2, 124-138. [doi: 10.33730/2077-4893.2.2022.263328](https://doi.org/10.33730/2077-4893.2.2022.263328).
- [20] Padro, J.C., et al. (2022). Drone-based identification of erosive processes in open-pit mining restored areas. *Land*, 11(2), article number 212. [doi: 10.3390/land11020212](https://doi.org/10.3390/land11020212).
- [21] Prokop, P. (2020). Remote sensing of severely degraded land: Detection of long-term land-use changes using high-resolution satellite images on the Meghalaya Plateau, northeast India. *Remote Sensing Applications: Society and Environment*, 20, article number 100432. [doi: 10.1016/j.rsase.2020.100432](https://doi.org/10.1016/j.rsase.2020.100432).
- [22] Protopopova, V., Mosyakin, S., & Shevera, M. (2002). [Phytoinvasions in Ukraine as a threat to biodiversity: Current state and tasks for future](#). Kyiv: M.G. Kholodny Institute of Botany.
- [23] Shevchuk, R.M. (2019). Monitoring of myliatyn Granular phosphorite quarry current state using remote sensing data. *Geological Journal*, 2(367), 73-78. [doi: 10.30836/igs.1025-6814.2019.2.169937](https://doi.org/10.30836/igs.1025-6814.2019.2.169937).
- [24] State cadaster of territories and objects of the nature reserve fund. (2024). Retrieved from https://data.gov.ua/dataset/mepr_05.
- [25] Suetnov, Ye., & Lazebna, A. (2020). Legal regulation of waste management: Analysis, problems and directions of solution. *Man and Environment*, 33, 102-108. [doi: 10.26565/1992-4224-2020-33-09](https://doi.org/10.26565/1992-4224-2020-33-09).
- [26] Suresh, L., Jothibas, A., & Anbazhagan, S. (2021). [Assessment of land use and land cover changes in the granite mining area of Krishnagiri district, South India using remote sensing data](#). *Indian Journal of Natural Sciences*, 12(67), 32976-32988.
- [27] Vikhot, Yu., Bubniak, I., Kril, S., & Fourman, V. (2022). Using unmanned aerial vehicles (UAV) for geophysical observations. *Herald of the Lviv University: Geology*, 36, 100-105. [doi: 10.30970/vgl.36.08](https://doi.org/10.30970/vgl.36.08).
- [28] Vorovencii, I. (2021). Changes detected in the extent of surface mining and reclamation using multitemporal Landsat imagery: A case study of Jiu Valley, Romania. *Environmental Monitoring and Assessment*, 193(30). [doi: 10.1007/s10661-020-08834-w](https://doi.org/10.1007/s10661-020-08834-w).
- [29] Wang, Y., Qiao, L.F., Yao, Z.Y., Qi, A.G., & Zhang, Y.C. (2022). Analysis of the change in vegetation coverage of chalk soil wasteland during the growing season based on UAV sequence image. *Applied Ecology & Environmental Research*, 20(4), 3311-3322. [doi: 10.15666/aeer/2004_33113322](https://doi.org/10.15666/aeer/2004_33113322).



Оцінка стану фітоценозів кар'єрно-відвальних комплексів засобами дистанційного зондування

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Анотація. Одним із видів антропогенної діяльності людини, який спричиняє негативні зміни природних умов середовища та втрату біорізноманіття, є видобування корисних копалин у межах кар'єрно-відвальних комплексів, які потребують заходів з відновлення екологічної рівноваги після завершення видобувних робіт. Пошук оптимальних методів для виявлення порушених ділянок, моніторингу стану та динаміки відновлення відпрацьованих земель у контексті збереження та відновлення біорізноманіття, становив мету дослідження, особливо в умовах недоступності для проведення натурних досліджень та за необхідності спостереження за кількома об'єктами одночасно. В статті представлено результати оцінки стану рослинного покриву в межах порушених видобуванням корисних копалин територій за допомогою засобів дистанційного зондування Землі. Застосовано такі методи як наукові (аналіз, синтез), статистична обробка даних, маршрутний метод. Визначено, що аналіз та моніторинг значень нормалізованого диференційного вегетаційного індексу (NDVI), отриманих засобами дистанційного зондування Землі, дає змогу оцінити якість проведених заходів із рекультивації, визначити високопродуктивні ділянки та виявити проблемні зони для пошуку ефективних методів покращення екологічного стану досліджуваної ділянки. В межах досліджуваного Андрійковецького кар'єрно-відвального комплексу відзначено неоднорідність перебігу сукцесійних стадій, на території локалізовані відкриті ділянки без рослинного покриву та ділянки, які характеризуються перебігом первинних сукцесійних стадій та розрідженою рослинністю. Зафіксовано найнижчі показники NDVI в 2019 та в 2022 роках, у період з 2020 по 2021 рр. та з 2023 по 2024 роки відбулось збільшення продуктивності біомаси, площа ділянок із густою та помірною рослинністю збільшилась. Відзначено, що дана ситуація спричинена наявністю перепадів висот, нерівностей поверхні, процесами водної і вітрової ерозії (що є наслідком відсутності рекультиваційних заходів), нестабільністю піщаного субстрату та низькою здатністю до забезпечення рослин необхідною кількістю вологи. Результатами проведеного дослідження підкреслено важливість рекультиваційних заходів пост-майнінгових територій та надано практичні рекомендації щодо проведення необхідних інженерно-технічних заходів для наближення умов кар'єрно-відвального комплексу до природних, що сприятиме поширенню зональних видів та процесам самовідновлення

Ключові слова: порушені території; NDVI; видобування корисних копалин; рослинність; умови місцезростань; рекультивація; моніторинг





Methods of computer modelling of the transcription factor of stress resistance WRKY2 in *Triticum Aestivum*: A comparative analysis

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Abstract. The aim of this work was to compare the efficiency of modern computer modelling methods for constructing the three-dimensional structure of the transcription factor TaWRKY2 from *Triticum aestivum*, which plays a key role in plant stress resistance. The study used traditional homology approaches and machine learning-based methods, including AlphaFold, RoseTTaFold, ESMFold, and OmegaFold. The model obtained with AlphaFold2 (MMseqs2) was the best in terms of Clashscore (99th percentile), MolProbity Score, and ERRAT. The complex with zinc ions and DNA generated by AlphaFold3 showed better results in terms of Z-Score. The AlphaFold method provided biologically relevant structures with the correct location of functional sites. ESMFold provided fast modelling, but showed deviations in the structure, including additional α -helices and lower quality in most metrics. The RoseTTaFold model had an elongated shape with a higher content of α -helices and required additional verification of functional activity. OmegaFold, although it provided the best QMEAN score (0.4), was inferior in other metrics. Additional tools, such as Amber and Chimera, allowed for structure relaxation and analysis of key features, including the spatial arrangement of the zinc fingers (18.7 Å). Evaluation by Verify 3D, ERRAT, Ramachandran Plot, and other metrics revealed the advantages and disadvantages of each approach. The findings confirmed the advantages of machine learning methods for modelling proteins with high functional plasticity. In particular, AlphaFold was recognised as the most effective approach for building models with high accuracy. At the same time, the use of several methods allows considering alternative conformations and interactions, which is important for a deeper understanding of the functional mechanisms of the protein

Keywords: bioinformatics; three-dimensional protein structure; machine learning methods; model evaluation metrics; zinc fingers

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INTRODUCTION

Molecular biology often focuses on studying the mechanisms of plant adaptation to stressful conditions, in particular with the involvement of transcription factors (TFs). The WRKY transcription factors are one of the key groups of proteins that regulate plant responses to biotic and abiotic stresses. These factors function by interacting with the W-boxes of target gene promoters, activating or repressing their expression. Significant progress in the understanding of WRKY proteins in woody plants was achieved in the studies of L. Long *et al.* (2023), who focused on the functional features of these proteins, but their structure and mechanisms of interaction remain poorly understood.

Computer modelling technologies have opened up new perspectives in the study of protein structures, in particular, machine learning methods such as AlphaFold have demonstrated high accuracy in predicting protein conformations. A study by M. Baek *et al.* (2021) showed that three-layer neural networks can achieve accuracy comparable to experimental methods such as X-ray crystallography. At the same time, AlphaFill, proposed by M.L. Hekkelman *et al.* (2023), extended the capabilities of AlphaFold by allowing the inclusion of ligands and cofactors in protein models, which increases their biological relevance. However, the accuracy of the interactions of WRKY proteins with metal ions, such as zinc, is still a challenge due to the lack of specialised tools. In this context, the MIB2 server, according to C.H. Lu *et al.* (2022), provides metal binding site prediction, which is promising for improving WRKY protein models. In addition to AlphaFold, other methods such as RoseTTaFold, ESMFold, and OmegaFold have also been shown to be effective in structural modelling. The study by Z. Lin *et al.* (2023) found that transformer models such as ESMFold can predict protein structures at the evolutionary level, providing speed and scale. However, their accuracy in complex proteins remains lower than that of AlphaFold. The study of WRKY transcription factors is a promising area of molecular biology that may open up new opportunities to increase crop resistance to abiotic and biotic stresses. For example, the study by D. Upadhyay *et al.* (2024) demonstrated the importance of WRKY2 in wheat drought tolerance, but the structural aspects of this protein are still poorly understood.

Structural biology methods, in particular machine learning, have greatly expanded the possibilities of predicting protein structures. AlphaFold, developed by DeepMind, has already proven to be effective in predicting the three-dimensional structure of proteins at the atomic level (Wu *et al.*, 2022). At the same time, other tools, such as RoseTTaFold and ESMFold, offer alternative approaches to modelling structures, including protein-DNA complexes. PyDockDNA, described by L.A. Rodríguez-Lumbreras *et al.* (2022), provides accurate modelling of protein-DNA interactions, which is important for WRKY proteins that can affect multiple stressor pathways. Despite significant progress, gaps in the research remain. In particular, the structural features of WRKY proteins, such as the interaction of their zinc fingers with DNA, metals, and other proteins, are not well understood. The study by P. Ranjan *et al.* (2024) demonstrated the potential of combined approaches that include molecular dynamics to analyse protein stability, but there is still a need to compare the effectiveness of modern modelling tools. Another important gap is the insufficient consideration of the effect of ligands and metals, which can significantly change the conformation of WRKY proteins. For example, S. Li *et al.* (2024) emphasised that the integration of metal and cofactor interactions into models can significantly improve the accuracy of predictions. However, this requires the additional use of tools such as AlphaFill or MIB2, which allow the inclusion of ligands and metal ions in protein models.

The aim of this study was to comparatively analyse modelling methods for building the structure of the transcription factor TaWRKY2 from *Triticum aestivum*, including the use of modern machine learning tools. Particular emphasis was placed on determining the effectiveness of methods for modelling protein-DNA interactions, as well as taking into account key functional regions of the protein, such as zinc fingers.

MATERIALS AND METHODS

The amino acid sequence of the transcription factor TaWRKY2 from the GenPept database of the National Center for Biotechnology Information (NCBI) (2024) server was used for comparative analysis of computer modelling methods for



protein molecules. The sequence was accessed using the protein number ACD80357.1, which contains 468 amino acid residues. This sequence was chosen because of its key role in the response of *Triticum aestivum* to stress conditions, making it an important target for research. Modelling methods. The following approaches were used to build a structural model of the protein: homology modelling methods (SWISS-MODEL, Modeller and Phyre2), ab initio methods (I-TASSER, D-I-TASSER and QUARK – used to build structures in cases where no relevant templates are available), and machine learning methods.

Among the methods based on machine learning, the following were selected: AlphaFold is a tool developed by DeepMind (2024) that uses neural networks to predict structures with high accuracy (Abramson *et al.*, 2024); to refine the protein structure, the modelling was performed in the Google Colab environment on a Google T4 GPU. When the modelling was performed using MMseqs2, the authors additionally performed structure relaxation using Amber. RoseTTAFold, which integrates machine learning and homology modelling methods to predict three-dimensional structures, was modelled using the Robetta service; ESMFold, based on transformer models for fast and accurate protein structure prediction; and OmegaFold, a tool that uses generative models to create highly accurate protein structures. Chimera software was used to analyse the structural characteristics of the TaWRKY2 model, namely to determine the distance between the domains of the zinc fingers. The Robetta service was used to model TaWRKY2 using the RoseTTAFold method, which provides integration of modern machine learning approaches to protein structure prediction. To evaluate the accuracy and quality of the created TaWRKY2 protein models, a set of metrics was used, each of which provides specific information about various aspects of the structural model, its stability and correspondence to known protein structures.

Verify 3D is a metric that assesses the stereochemical quality of a model by comparing the three-dimensional structure of a protein with its primary amino acid sequence. The analysis is performed by creating profiles for each amino acid residue in the structure and comparing them with expected values. ERRAT is based on the statistical analysis of energy mismatches in the

protein structure. It allows identifying regions of the model that show significant deviations from the typical values of energy interactions. Ramachandran Plot Analysis is one of the key tools for checking the geometric correctness of protein models. The Ramachandran diagram displays the conformational angles φ (phi) and ψ (psi) for each amino acid residue. G-factor is a metric that determines the geometric quality of a model based on the distribution of conformational parameters such as bond angles and bond lengths. The G-factor reflects the deviation from the expected values obtained from empirical data.

QMEAN is a comprehensive metric that takes into account several model quality parameters, including surface entropy, global interaction energy, interactions between residues, etc. The QMEAN value is normalised to facilitate comparison between different models. Z-Score is a metric used to statistically compare the obtained model with experimentally determined structures in the PDB database. Z-Score determines how much the model deviates from the average values for known protein structures. MolProbity analyses models based on the geometric quality and accuracy of atomic coordinates. In particular, this metric takes into account the presence of steric collisions between atoms in the protein structure, which are evaluated through Clashscore. The predicted local distance difference test (pLDDT) is an indicator of the local accuracy of protein structure prediction used in the AlphaFold method. It reflects the model's confidence in the accuracy of predicting the spatial location of each amino acid residue. As part of this work, several models of the TaWRKY2 protein were created using different approaches. However, the main focus was on machine learning-based methods (AlphaFold, RoseTTAFold, ESMFold, OmegaFold), as they provided the most accurate and reliable results. The resulting models were compared using the aforementioned metrics to determine their quality and stability.

While each of the approaches has its advantages, there are limitations. Homology modelling methods (programs such as SWISS-MODEL, Modeller and Phyre2) show limitations in cases where there are no suitable templates in the PDB database. This reduces their effectiveness for proteins with significant structural differences or unique elements, such as metal-dependent domains.

Ab initio methods (I-TASSER, D-I-TASSER, and QUARK) provide greater independence from templates, but often lack the accuracy of machine learning methods, especially for complex proteins with metal centres where there is insufficient data on metal interactions. AlphaFold2, while demonstrating the highest accuracy in predicting structures, models the protein as an isolated molecule, without taking into account interactions with metal ions, ligands, or other proteins. This can limit the realism of the model, especially for proteins where metals are functionally important. RoseTTAFold can generate structures with excessive plasticity, which does not always correspond to biological realities. ESMFold and OmegaFold are fast and efficient, but their accuracy for complex proteins with numerous unstructured regions or metal centres remains lower than AlphaFold2.

RESULTS AND DISCUSSION

Modelling of TaWRKY2 using the AlphaFold method. At the first stage of modelling, the

AlphaFold database was searched to obtain the theoretically predicted structure of TaWRKY2 (Yang *et al.*, 2023). The ChimeraX-1.7.1 software was used for this purpose. Among several analysed structures, the model with the index B3GAU3 was selected, which was further evaluated by the quality of regions using the pLDDT metric (Figs. 1, 2). This can be due to several factors: unstructured or flexible regions – many proteins have regions that do not form a clear three-dimensional structure. This is especially true for transcription factors, which often contain flexible binding domains or activator regions. Another factor is the absence of structural analogues in the training data: since AlphaFold is based on machine learning using experimentally determined structures, poor prediction quality can arise from the absence of close analogues for a particular protein or its individual fragments in the training set.

The analysis showed that the majority of the structure, except for two zinc finger domains, is characterised by low pLDDT values.

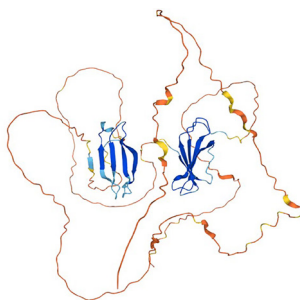


Figure 1. Structure of B3GAU3_WHEAT

Note: the image shows regions with different pLDDT: blue – pLDDT > 90, blue – 90 > pLDDT > 70, yellow – 70 > pLDDT > 50, orange – pLDDT < 50. Some areas with low pLDDT may be isolated unstructured

Source: created by the authors

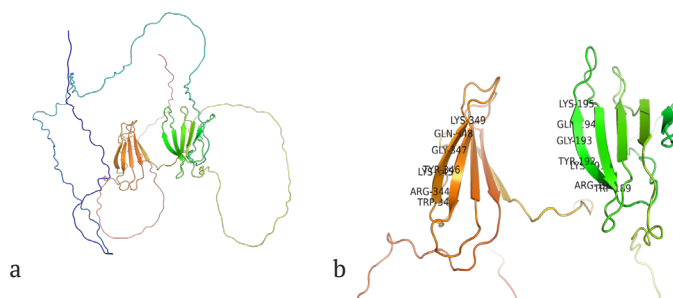


Figure 2. Structural Features and DNA Binding Characteristics of B3GAU3_WHEAT WRKY Transcription Factor

Note: a) Structure of B3GAU3_WHEAT and b) location of WRKYGQK sequences

Source: created by the authors

As shown in the study, the two zinc fingers in the protein structure are located at a distance of 18.7 Å from each other, which is less than the diameter of B-shaped DNA (20 Å). In addition, one of the key areas of WRKY responsible for binding to DNA is oriented “inwards” (Fig. 2b). This makes it difficult for the DNA molecule to be positioned between the domains, although it does not exclude this possibility, as transcription factors have sufficient flexibility to perform their functions. Interaction with other molecules. According to the results obtained, many proteins, especially transcription factors, are characterised by dynamic changes in structure when interacting with other molecules, such as DNA, RNA, or partner proteins. These changes include conformational transformations that allow the protein to adapt to specific bonds or functions. For example, the WRKY transcription factors undergo a significant reorganization of their zinc fingers during DNA binding, which ensures specific recognition of W-boxes in gene promoter sequences.

AlphaFold models the protein structure as isolated, which is a significant limitation for proteins with high functional plasticity. In the case of the TaWRKY2 model, zinc atoms, which critically affect the stability and functionality of the zinc fingers, were missing. This led to incomplete or less realistic reconstruction of functional domains. Since zinc fingers play a key role in protein binding to DNA, taking such details into account is important for accurate prediction of protein structure and function. It has also been found that in addition to interacting with DNA, WRKY proteins can form protein-protein complexes that affect their regulatory activity. For example, interaction with suppressor proteins or cofactors can change the accessibility of WRKY domains to DNA. Such complex interactions are not taken into account in the structural predictions generated by AlphaFold.

Technical limitations. Although AlphaFold significantly outperforms traditional homology modelling methods, this approach has a number of technical limitations. In particular, the accuracy of predictions decreases for proteins that have rare or unique structural elements that are not present in the algorithm’s training sets. For example, non-standard conformational changes that occur during protein-protein or protein-ligand interactions are often not reflected in isolated models. In

addition, machine learning-based methods such as AlphaFold rely on pre-formed training data, so their performance is reduced if the protein structure or functional domains differ from known templates. In the case of TaWRKY2, this can manifest itself in a less accurate reconstruction of flexible or unstructured regions that play an important role in the functional adaptation of the transcription factor. Another problem is modelling multicomponent complexes. For proteins that work as part of large protein machines, such as WRKY2, the accuracy of predictions by AlphaFold may be limited due to the lack of data on specific interprotein contacts. To improve the accuracy of such models, additional tools, such as docking or experimentally obtained interaction data, should be integrated.

The Chimera software was used to analyse the structural characteristics of the TaWRKY2 model, in particular to determine the distance between the zinc finger domains. In the case of the B3GAU3 model, the software made it possible to visualise the spatial arrangement of the key domains and measure the distance between the zinc fingers, which was 18.7 Å (indicated by the yellow dashed line in Fig. 3). This distance is an important parameter for assessing the functional ability of a protein to interact with DNA, given that the diameter of a DNA molecule in the B-form is approximately 20 Å.

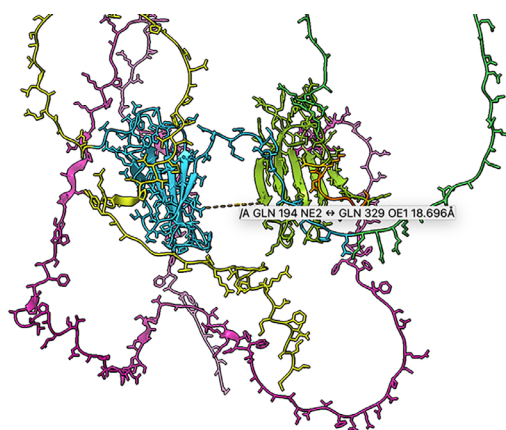


Figure 3. Distance between domains in B3GAU3 (yellow dashed line)

Source: created by the authors

To clarify the structure of the TaWRKY2 transcription factor, the authors performed modelling using AlphaFold in the Google Colab environment

on a Google T4 GPU. This approach provides the ability to perform calculations relatively quickly on a remote server with limited computing resources. As part of the work, various versions of Jupyter Notebook were used to simplify the work with AlphaFold. In addition, other state-of-the-art modelling tools such as ESMFold and RoseTTaFold, which also provide protein structure prediction, were used for comparison. In the case of AlphaFold, a model was obtained using MMseqs2, for which the structure was additionally relaxed using Amber. Figure 4 shows this structure, which demonstrates the distinctive arrangement of the domains. In particular, the zinc fingers form a dimer, and the functional regions of WRKY are oriented “outwards”. This conformation potentially facilitates binding to DNA, creating conditions for the formation of a stable loop during the transcription process. The validity of this model is confirmed by the similarity of the zinc fingers to

the corresponding domains found in the experimentally determined structures. For example, as can be seen in Figure 4b, a similar organization of zinc fingers was observed in the AtWRKY2 model (PDB ID: 6J4F), although in this case the fingers belong to different protein chains.

This feature of the model indicates its potential functional relevance, as the structure may facilitate interaction with DNA and active loop formation necessary for transcription initiation. An additional analysis of the model showed that the arrangement of the domains allows for effective stabilization of the protein structure when it works in a complex with DNA. This approach to modelling using a combination of AlphaFold and MMseqs2 followed by relaxation provides flexible opportunities for detailed study of proteins, especially those that play an important role in plant stress adaptation (Fig. 4). The structure quality assessment in ProSA is shown in Figure 5.

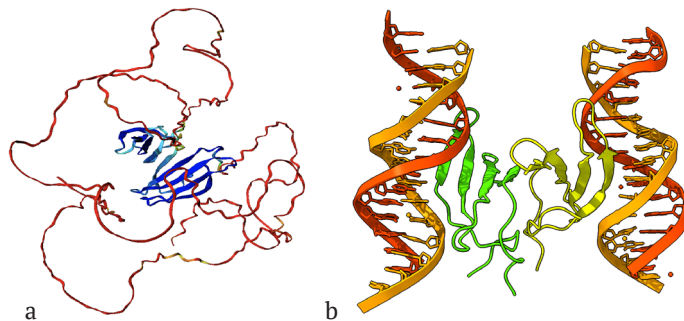


Figure 4. Predicted structure of TaWRKY2 (AlphaFold, MMseqs2, Amber)

Note: a) coloured according to pLDDT; b) structure of 2 zinc fingers from AtWRKY2 with PDB ID 6J4F, confirming the high confidence of the structure modelled by AlphaFold

Source: created by the authors

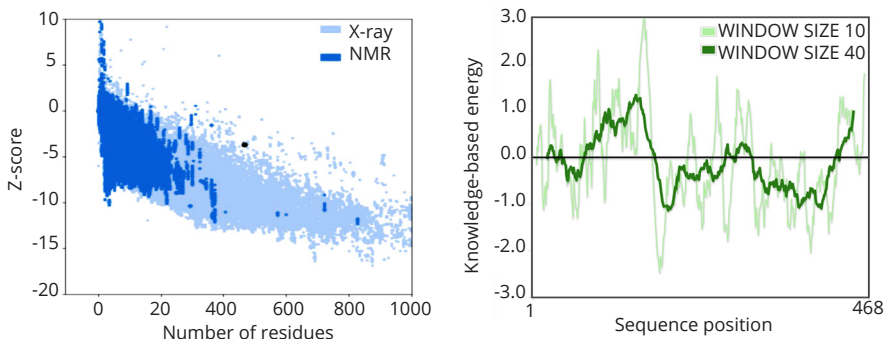


Figure 5. Structure quality assessment of TaWRKY2 (AlphaFold, MMseqs2)

Source: created by the authors

The data obtained indicate that the best quality in the model is the β -folding of the zinc fingers, as in the structure from the AlphaFold database according to the local values in QMEAN. With respect to the global Z-score, the model falls within the range of X-crystallographic structures of the same polypeptide chain length, while the local evaluation revealed some fluctuations. The blue averaged line on the Verify3D graph shows the overall trend, which is high and hovers around 0.2, indicating that the model is of fairly good quality (although it contains residues of lower quality). The model's Clashscore is superb at 2.31, which falls in the 99th percentile. The MolProbity Score is acceptable: 2.35, with a score in the 56th percentile.

Another variant of Jupyter Notebook, offered by DeepMind, does not use MMseqs2 and is a simplified version of AlphaFold2 itself, with a focus on multimer construction. However, the structure modelled using this approach was largely similar to the previous one, with an additional β -sheet appearing between the zinc finger domains (Fig. 6). However, this new β -sheet is not of high quality, as can be seen from the pLDDT value (the additional β -sheet is marked in orange on the left of Figure 6).

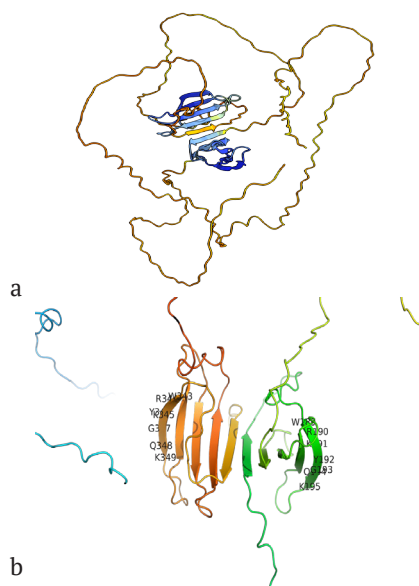


Figure 6. Predicted structure of TaWRKY2 (from DeepMind)

Note: coloured according to a) pLDDT and b) the location of WRKYGQK sequences; 10 β -sheets are visible (instead of 9 in the previous model)

Source: created by the authors

When comparing the number of β -sheets, the additional 10th sheet in the AlphaFold (DeepMind) model may, on the one hand, contribute to greater stability of the TF domain dimer structure, but on the other hand, this feature is not observed in the experimental data (Fig. 4(b)). Nevertheless, since the structure of 6J4F is based on AtWRKY2 from Arabidopsis, it is likely that wheat has specific folding features for TaWRKY2. This additional β -sheet can serve as another example of the difference in modelling approaches: in a homology method, where there is no corresponding template, it would be impossible to predict such a structure. Additionally, if the authors look at the number of hydrogen bonds connecting the two zinc fingers, the AlphaFold (DeepMind) model has significantly more of them, which can provide additional stability to the structure. It is also important to note that when docking the structure with AlphaFold (MMseqs2), the interaction of the W-box with the WRKYGQK motif was less efficient compared to the model built with AlphaFold (DeepMind). In particular, there was no interaction of arginine in the N-terminal domain with tryptophan in the C-terminal domain with DNA.

The only significant drawback of the AlphaFold2 method compared to homology modelling is the inability to directly add ligands during the modelling process, unlike platforms such as SWISS-MODEL, where heteroatoms can be incorporated from template structures. However, over time, additional tools have been developed, such as AlphaFill, which allow filling structures from the AlphaFold database with appropriate ligands. In the case of TaWRKY, however, this resource was unable to add zinc atoms, which is a limitation. In addition, it is worth noting that the process of protein structure prediction using AlphaFold2 requires significantly more time and computational resources compared to homology modelling. This is due to the complexity of the model and high hardware requirements. To simplify this process, the study used Jupyter Notebooks offered by the developers instead of directly running local AlphaFold with full databases, as this approach requires much more computing power. The study also used a new version of AlphaFold3, which is capable of modelling not only protein molecules with standard amino acid residues, but also constructing DNA/RNA (including modified nucleotides),

finding binding sites for metal ions, engaging a specific set of ligands, and applying post-translational modifications to proteins. For comparison, the modelling of an isolated protein and a complex was performed. The values of the complex metrics were better than those of the isolated model.

In the complex of TaWRKY2 with zinc ions and two DNA fragments with W-boxes, it is clear that a dimer of zinc fingers is present, as in the case of AlphaFold2 (Fig. 7). However, unlike previous models, an α -helix between the domains is also observed, which may stabilise the structure. Internal quality metrics showed the following results: ipTM = 0.89; pTM = 0.45. They are both based on the template modelling score (TM), which measures the accuracy of the entire structure. A score of pTM > 0.5 means that the predicted complex may be similar to the real structure. The ipTM score measures the accuracy of the relative positions of subunits in the complex. Values > 0.8 indicate high-quality predictions. The structure quality score in ProSa is shown in Figure 8.

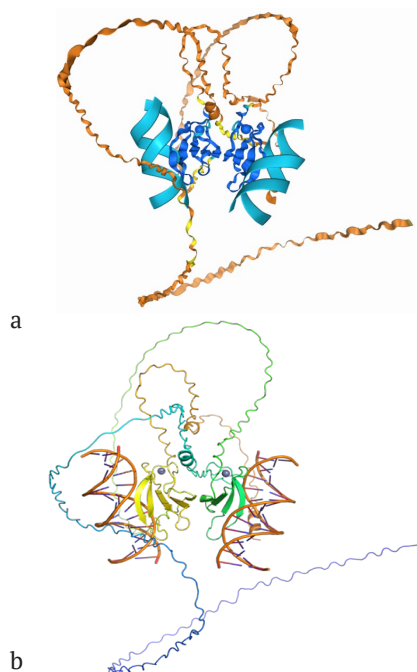


Figure 7. The TaWRKY2 complex predicted in AlphaFold3, 2 Zn²⁺, 2 DNA fragments with W-boxes

Note: stained a) according to pLDDT and b) according to N→C ends from red to blue

Source: created by the authors

The TaWRKY2 model from AlphaFold3 generally performs worse than AlphaFold2, except for the Z-Score. This may be due to less flexibility in setting up the modelling process on the server. When comparing AlphaFold2 (DeepMind) and AlphaFold3, the authors also observe that the latter model is less compact.

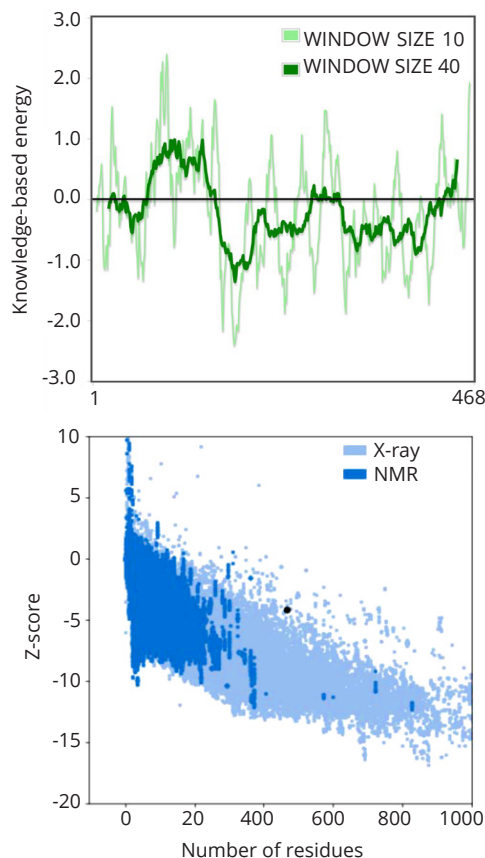


Figure 8. Structure quality assessment of TaWRKY2 (AlphaFold3)

Source: created by the authors

Modelling the TaWRKY2 structure using ESMFold. To create a model of TaWRKY2 using ESMFold, the authors used Jupyter Notebook, developed by the authors of the tool, in the Google Colab environment using a Google T4 GPU (Fig. 9). This approach provided a fast prediction of the protein structure, although the quality of the model obtained was significantly different from the results obtained with AlphaFold.

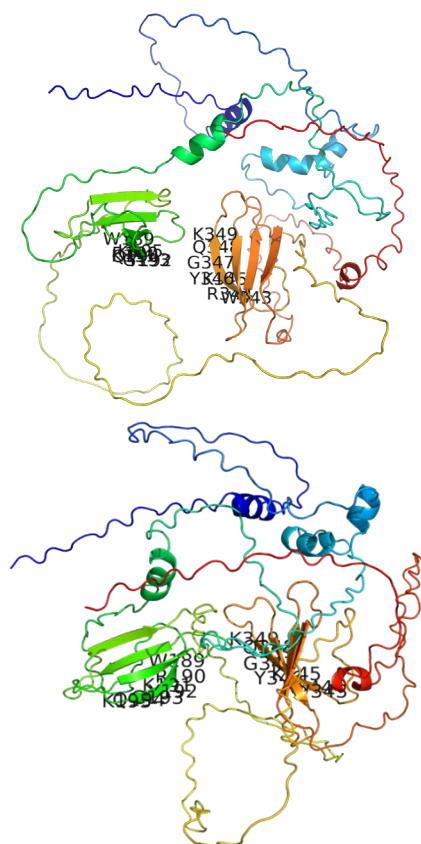


Figure 9. TaWRKY2 model in ESMFold from 2 angles

Source: created by the authors

The resulting structure shows a different arrangement of zinc fingers compared to the AlphaFold model. Additional α -helices are observed in the ESMFold model, which are practically absent in the AlphaFold versions (only a small α -helix is present in the AlphaFold-MMseqs2 model). These differences may indicate an alternative conformation of the protein, which could theoretically occur under specific conditions. Despite the structural features, the model's metrics are significantly inferior to AlphaFold. In particular, the Clash-score value corresponds to only the 22nd percentile (compared to the 99th for AlphaFold-MMseqs2). Other metrics, such as Ramachandran Plot Percentage and MolProbity Score, also indicate lower quality. It is worth noting that the QMEAN metric (0.39) was slightly better than the same indicator in the AlphaFold models (Fig. 10).

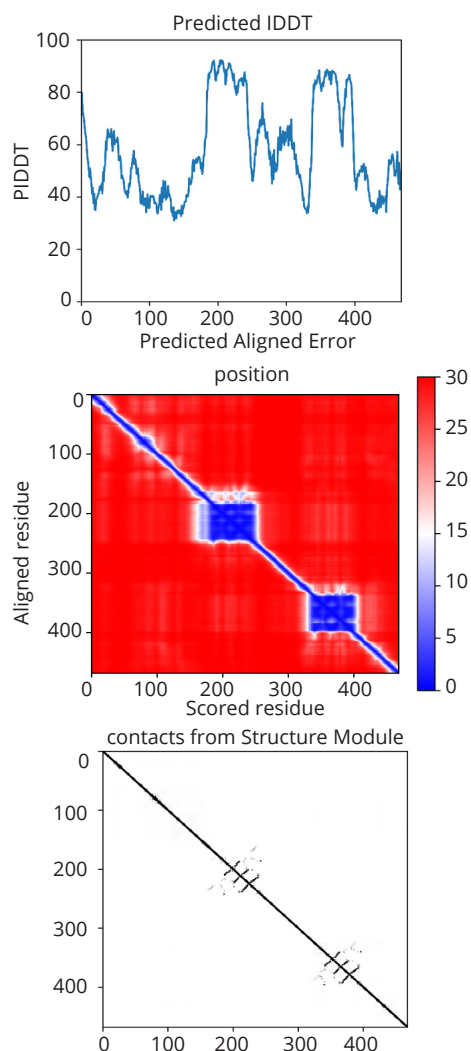


Figure 10. Evaluation of the ESMFold model quality

Source: created by the authors

Despite these shortcomings, the ESMFold model provides useful information about possible protein conformations, especially in cases where traditional methods fail or create overly idealised models. However, the resulting structure has certain drawbacks: the WRKY domains of the N- and C-termini are located opposite each other, which can potentially create steric conflicts when interacting with DNA, making it difficult to implement transcriptional activity. Modelling with RoseTTaFold. For modelling TaWRKY2 with

RoseTTaFold, the authors used the Robetta service, which integrates modern machine learning approaches to protein structure prediction. The

modelling result (Fig. 11) shows a structure that is significantly different from the previous models created by AlphaFold and ESMFold.

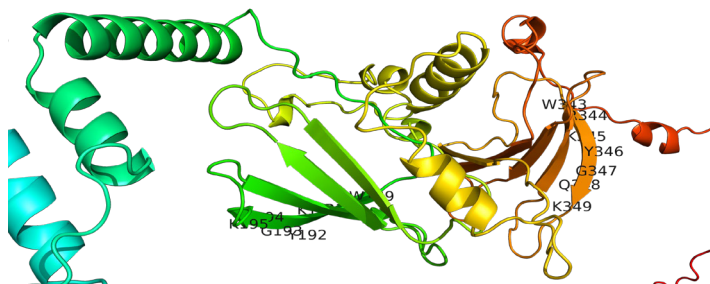


Figure 11. Location of the WRKYGQK sequence in the RoseTTaFold model (internal Confidence metric is 0.35 out of 1)

Source: created by the authors

The main feature of the RoseTTaFold model is its “elongated” shape, in contrast to the compact structures obtained by other methods. In this model, the WRKYGQK sequence of the N-terminus is in an accessible position for DNA binding, while the C-terminal sequence is partially overlapped by a loop with a small α -helix. In general, the structure contains more α -helices compared to AlphaFold or ESMFold. In some cases, the model’s metrics have very good values, in particular MolProbity Score and Clashscore, which even exceed those of previous models, and

ProSA score also has better values (Fig. 12). Other metrics are comparable to previous models. However, despite this, such folding seems less likely when compared to the experimentally determined structure and according to Confidence’s internal quality assessment. Of course, the tertiary structure of a protein can change during its function (e.g., before and after binding to DNA) and the unstructured regions of the AlphaFold models in TaWRKY2 may actually contain alpha helices, but accepting the model without critical analysis may be a mistake.

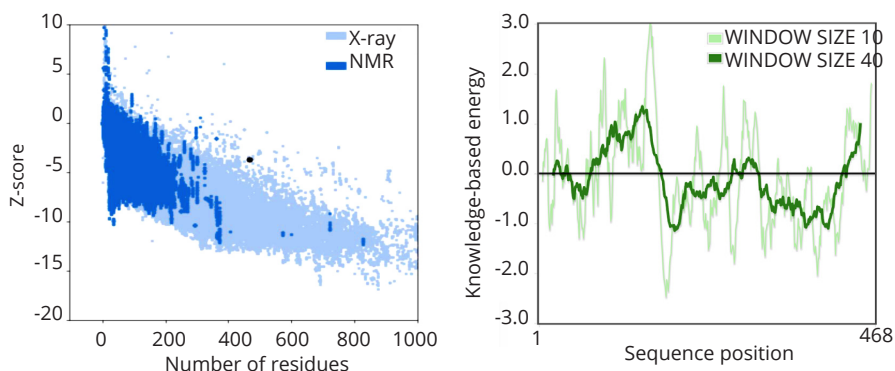


Figure 12. Quality assessment of the TaWRKY2 RoseTTaFold model

Source: created by the authors

Therefore, even with high metrics, each model must be validated against known biochemical data and against possible conformational changes

that may occur in the real cellular environment. This is especially important for protein regions responsible for binding and regulation, where



the correct conformation is critical for functional activity. Modelling with OmegaFold. The OmegaFold tool, which is positioned as an improvement over AlphaFold and RoseTTaFold, was also used for modelling TaWRKY2. The code from the GitHub repository was adapted for the Google

Colab environment, where the modelling was performed on the basis of the downloaded fasta file. The resulting model (Fig. 13) showed the presence of alpha-helical structures, although their number was smaller than in the RoseTTaFold model.

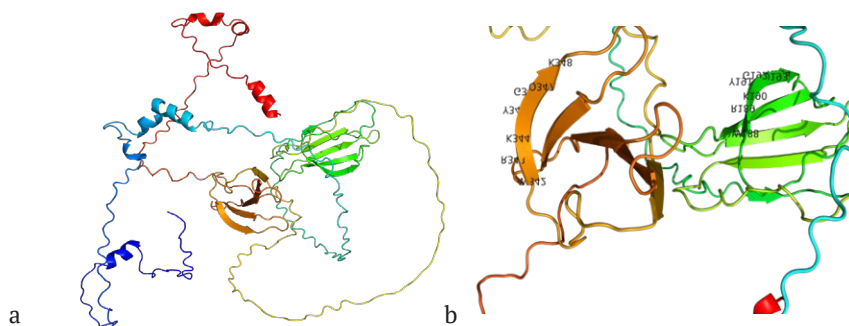


Figure 13. Model of a) TaWRKY2 in OmegaFold and b) relative position of the WRKYGQK sequence
Source: created by the authors

In this structure, no steric hindrance was observed in WRKYGQK sequences for DNA binding. However, quality metrics such as Clashscore and Ramachandran Plot Percentage were found to be worse compared to AlphaFold and RoseTTaFold. The only exception is the QMEAN metric, which

is 0.4, which is the best value among all models. As a result of the modelling performed using the methods described above, the obtained models were analysed and the obtained metrics were evaluated (Table 1). This makes it possible to assess the quality of the obtained models and their viability.

Table 1. Resulting table comparing metrics of models created by different methods

Method\Metric	Verify 3D, %	ERRAT	Ramachardran, %	G-factor	QMEAN	Z-Score	Molprobability Score/%ile		Clashscore /%ile	
SWISS-MODEL	44.32	82.05	79.4	-0.38	0.35 ± 0.05	-3.23	1.82,	84	0.59	99
Phyre2	69.66	3.91	57.6	-0.92	0.35 ± 0.05	0.05	3.65	6	221.26	0
AlphaFold (MMseqs2)	45.73	93.43	61.8	-0.75	0.38 ± 0.05	-3.72	2.19	65	0.72	99
AlphaFold (DeepMind)	48.93	85.23	62.8	-0.7	0.35 ± 0.05	-3.62	2.35	56	2.31	99
AlphaFold3	53.42	69.37	58.4	-0.61	0.35 ± 0.05	-4.37	2.84	29	12.55	60
AlphaFold3 (in the complex)	45.94	74.53	58.9	-0.52	0.36 ± 0.05	-4.14	2.63	40	7.1	86
ESMFold	46.79	61.63	40.8	-2.4	0.39 ± 0.05	-4.13	3.64	6	24.15	22
RoseTTaFold (Robetta)	67.09	89.32	83.7	0.27	0.35 ± 0.05	-5.03	1.40	97	2.16	99
OmegaFold	46.37	32.72	44.7	-2.11	0.40 ± 0.05	-3.68	3.49	9	31.19	14
D-I-Tasser	50	65.42	51.4	-0.35	0.34 ± 0.05	-4.08	2.73	35	22.35	26
Modeller (TaWRKY19 template)	55.13	63.29	86.6	-0.31	0.40 ± 0.05	-2.98	2.21	64	16.15	45

Note: the %ile-value indicates the percentile in which a particular model was included

Source: created by the authors



The analysis confirms that each of the methods used has its advantages and limitations. AlphaFold provides the best results for most metrics and is the most reliable method for modelling proteins with known structural features. RoseTTaFold and OmegaFold can also be effective, especially for complex structures, but the resulting models require additional verification. The ESMFold method, despite its lower model quality, shows potential in cases where an alternative protein conformation needs to be quickly obtained for further analysis. All models show that a thorough evaluation of both the structural and dynamic properties of the obtained models is necessary to ensure the functional activity of the protein.

The results of this study, based on modelling the structure of TaWRKY2 using modern methods, confirm the high potential of machine learning in structural biology. However, a comparison with previous works reveals both the advantages and limitations of different approaches. The work of A. Singh *et al.* (2019) emphasised the importance of structural diversity of WRKY proteins for efficient DNA binding, which is also confirmed by the results of the present study. In particular, the AlphaFold modelling revealed the optimal orientation of WRKY domains and the stable interaction of zinc fingers with W-boxes. At the same time, steric conflicts were observed in the ESMFold and RoseTTaFold models, which may reduce the binding efficiency, consistent with hypothesis A. Singh *et al.* about the importance of the specific conformation of proteins for their functionality. The study by S. Hassan *et al.* (2019) focuses on the role of WRKY proteins in the salt stress response. It was found that the accuracy of modelling the structure of such proteins depends on the consideration of specific factors, such as metal ions. In this study, the integration of metals through AlphaFill was only partially performed, which may explain the lower metrics in some models. However, the use of MIB2 to predict metal binding sites can significantly improve the accuracy of predictions, which is promising for future studies.

In this study, the models revealed a high plasticity of TaWRKY2 flexible regions, which may explain their adaptive role. In particular, additional α -helices were observed in the RoseTTaFold models, which may play a key role in stabilising the structure under stress. Similar conclusions were

reached by a team led by J.N. Amoah *et al.* (2019), who demonstrated that stressful conditions, including drought, cause significant changes in the expression of WRKY proteins. The conclusions about the need to further consider functional protein-environment interactions, such as complexes with DNA and ligands, are consistent with the studies of F.F. Theisen *et al.* (2024), who emphasised the importance of post-translational modifications in the regulation of transcription factors. The absence of such modifications in most current models, in particular the isolation of the protein in the AlphaFold2 environment, may limit the biological relevance of the obtained structures; while AlphaFold3 has a number of advantages in this context.

R. Blanc-Mathieu *et al.* (2024) created a structural classification of plant TFs, which confirms the importance of WRKY domains conservation for functional activity. The studied models confirmed this conservation, especially in the versions generated by AlphaFold, but in ESMFold, significant deviations in the orientation of functional regions were observed, which requires additional analysis. This study also confirmed the role of metals in the stabilization of WRKY domains. In particular, the models built with AlphaFold with the inclusion of zinc fingers showed higher MolProbity Score metrics than other approaches, which is consistent with the hypothesis of S. Banerjee *et al.* (2023) about the key role of these interactions in structural stability; the authors emphasised the importance of WRKY proteins under stress conditions, in particular their interaction with metals and partner proteins. The results of X. Chen *et al.* (2019) demonstrate that the evolution of WRKY proteins ensures their functional plasticity. The studied models showed differences in the structural organization of WRKY2, especially in the location of domains, which may reflect the evolutionary adaptations of this protein to specific conditions. This confirms the need to integrate several methods to account for different conformations.

Molecular dynamics methods and protein-ligand interactions are explored in the work by R. Shukla & T. Tripathi (2020), where the authors emphasise the importance of molecular dynamics in predicting the stability of protein structures and their interactions with ligands. In this study, based on the use of AlphaFold, RoseTTaFold and



ESMFold, models with high metrics such as Mol-Probity Score and Clashscore were obtained at the initial stages, which ensures the relevance of the results without additional lengthy simulations. This reduces computational costs while maintaining model accuracy, although molecular dynamics remains a promising approach for deeper analysis of protein functional mechanisms. The structural features of the interaction of WRKY proteins with DNA were studied by B. Pandey *et al.* (2018) noted that the interaction of WRKY domains with W-boxes can vary significantly depending on the specificity of the DNA sequence. The results of the present study confirm these findings: modelling with AlphaFold3 provided the best orientation of the domains relative to DNA, while ESMFold models showed steric conflicts that could reduce binding efficiency. Compared to previous work, the use of AlphaFold resulted in to achieve higher accuracy without the need for further optimization.

S.H. Wani *et al.* (2018) point out the importance of WRKY transcription factors in the regulation of osmotic stress in wheat. The study focused on the structural dynamics of TaWRKY2, which revealed significant plasticity of individual protein regions. The RoseTTaFold models revealed the presence of additional α -helices, which, according to previous studies, can stabilise the protein under adverse conditions. This suggests that structural changes are a key factor in adaptation to stressful conditions. The evolutionary adaptation of WRKY proteins is discussed in the study by C.M.M. Dinusha (2019), in particular, the evolutionary mechanisms of protein structure formation, including WRKY domains, are analysed. In contrast, the results of this study demonstrate specific features of TaWRKY2 that may be unique to *Triticum aestivum*. Comparison of the AlphaFold and RoseTTaFold models suggests that these features are important for plant adaptation to stress, which opens up opportunities for further evolutionary studies of WRKY proteins in cereals.

In this study, the use of the AlphaFill and MIB2 tools enabled the identification of metal binding sites in TaWRKY2. These results confirm that the integration of metal ions during modelling significantly improves the accuracy and biological relevance of structures. Compared to previous studies, such as S. Li *et al.* (2024), which pointed out the importance of metal ions for the

stability of WRKY proteins, this approach is more comprehensive and provides important information for future research. Non-coding RNAs in stress responses have been the subject of studies by N. Li *et al.* (2022); they emphasise the role of non-coding RNAs in the regulation of WRKY proteins. Although the structural aspects in this study do not cover the direct interaction with non-coding RNAs, the models obtained can serve as a basis for further modelling of protein-RNA complexes. Z. Du *et al.* (2021) highlight the effectiveness of the trRosetta server for fast and accurate protein structure prediction. In this study, models with high accuracy rates were obtained using AlphaFold and RoseTTaFold. Although trRosetta performs well for proteins with simple structural features, its application to complex proteins such as TaWRKY2 may be limited due to the lower detail of functional domains. The AlphaFold approach (MMseqs2) demonstrated higher accuracy in predicting the spatial location of WRKY domains.

Various sequence search methods were proposed by M. Steinegger & J. Söding (2017), in particular, they used MMseqs2 as a tool for highly sensitive protein sequence search, which is key for modelling the structure of proteins from poorly understood families. In this study, MMseqs2 was integrated into the AlphaFold modelling process, which significantly improved the prediction accuracy by using more relevant evolutionary data. Compared to other methods, this approach provides more detail in the prediction of structurally conserved elements, in particular zinc fingers in TaWRKY2. In the present study, the results also confirm the conservation of WRKY domains, which is particularly evident in the AlphaFold models. This is in line with the findings of X. He *et al.* (2019), who conducted a genome-wide analysis of WRKY proteins in buckwheat (*Fagopyrum tataricum*) and found that most WRKY domains show high conservation. At the same time, the models created by RoseTTaFold showed greater variability in the conformation of the domains, which may be due to the specificity of the algorithm, but requires further experimental confirmation.

Novel protein families in *Triticum aestivum* were studied by M. Zaheer *et al.* (2021), who emphasised the importance of their transcriptional profile for adaptation to stressful conditions. In the present study, the WRKY2 models obtained



confirm that structural changes in proteins can ensure their functional adaptation. RoseTTaFold models revealed the presence of additional α -helices, which, A. Tripathi *et al.* (2023) proposed Tempred as a new tool for protein pattern discovery, which allows for improved prediction accuracy. In this study, it was shown that the integration of AlphaFill and MMseqs2 already provides high accuracy of structural models. Although Tempred can offer additional benefits, its practical use for WRKY proteins still needs to be explored, as the accuracy of AlphaFold remains significantly higher for complex proteins such as TaWRKY2. The analysis of VQ family proteins in plants was performed by J. Tian *et al.* (2023), who emphasised the importance of identifying new protein families in plants. A similar approach may be useful for the study of WRKY proteins, but in this study, the emphasis was placed on the use of structural modelling to clarify functional features. The results show that WRKY2 exhibits high plasticity, which may be relevant for adaptive mechanisms.

The analysis shows the benefits of using several machine learning methods for structural modelling. Compared to previous works, the models created in this study demonstrate high accuracy and relevance for functional research. The differences with previous studies are explained by the emphasis on a comprehensive approach that includes a detailed analysis of structural features, which provides greater depth and accuracy in the study of WRKY2 functions. The main limitations of the study are the lack of experimental verification of the models, the isolation of the protein in the modelling process by most methods without taking into account its interactions with DNA or partner proteins, insufficient integration of metal ions, as well as the lack of dynamic analysis and focus on only one member of the WRKY family. Further research should be aimed at experimental confirmation of the obtained structures, integration of protein-protein and protein-DNA interactions, application of molecular dynamics, and extension of the analysis to other WRKY proteins to form a holistic view of their role in plant stress adaptation.

CONCLUSIONS

The amino acid sequence of the transcription factor TaWRKY2 from *Triticum aestivum* has been successfully used to construct and analyse a

three-dimensional structure using modern computer modelling methods. This protein, which is important for stress resistance mechanisms, has become an effective object for comparing different approaches in structural bioinformatics. AlphaFold, as a representative of the latest machine learning methods, demonstrated the best results in most metrics, such as Clashscore (99th percentile), ERRAT, MolProbity Score (AlphaFold2), and Z-Score (AlphaFold3). The model obtained with AlphaFold (MMseqs2) was the highest quality and closest to the biologically relevant structure. The models obtained with ESMFold had significant differences in structure, including additional α -helices and different arrangement of zinc fingers. Despite the lower quality of most metrics, this method shows potential for rapid protein modelling, especially in the absence of experimental data. RoseTTaFold produced a structure with unique features, such as an elongated shape and a higher number of α -helices. Although this method outperformed AlphaFold by some metrics (MolProbity Score, Clashscore), the resulting model requires additional confirmation of its functional relevance. OmegaFold, despite the improvements claimed by the developers, demonstrated model quality lower than AlphaFold and RoseTTaFold. Only the QMEAN metric indicated a certain advantage of this approach.

Additional tools, such as Amber and Chimera, provided structure relaxation and analysis of key features of the models. The Chimera analysis revealed important features such as the location of domains and the distance between zinc fingers (18.7 Å), which directly affects the functional activity of the protein. Evaluation of the models using Verify 3D, ERRAT, Ramachandran Plot, Z-Score, QMEAN and other metrics enabled the identification of the advantages and disadvantages of each modelling method. In general, for proteins with high functional plasticity, such as TaWRKY2, the most relevant approach is to use machine learning methods, such as AlphaFold. Using multiple methods with different modelling approaches, including RoseTTaFold, OmegaFold and ESMFold, can be useful for testing alternative conformations and interactions. Further modelling of multicomponent complexes, including interactions with ligands or other proteins, requires the use of experimental data and docking methods.



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None.

CONFLICT OF INTEREST

None.

REFERENCES

- [1] Abramson, J., *et al.* (2024). Accurate structure prediction of biomolecular interactions with AlphaFold 3. *Nature*, 630, 493-500. [doi: 10.1038/s41586-024-07487-w](https://doi.org/10.1038/s41586-024-07487-w).
- [2] Amoah, J.N., Ko, C.S., Yoon, J.S., & Weon, S.Y. (2019). Effect of drought acclimation on oxidative stress and transcript expression in wheat (*Triticum aestivum* L.). *Journal of Plant Interactions*, 14(1), 492-505. [doi: 10.1080/17429145.2019.1662098](https://doi.org/10.1080/17429145.2019.1662098).
- [3] Baek, M., DiMaio, F., Anishchenko, I., Dauparas, J., Ovchinnikov, S., Lee, G.R., & Baker, D. (2021). Accurate prediction of protein structures and interactions using a three-track neural network. *Science*, 373(6557), 871-876. [doi: 10.1126/science.abj8754](https://doi.org/10.1126/science.abj8754).
- [4] Banerjee, S., Mukherjee, A., Khatun, M., Roy, P., Nandi, S., & Roy, S. (2023). Exploring the critical function and molecular mechanism of WRKY transcription factor family in regulating plant response under abiotic stress conditions. In T. Aftab (Ed.), *New frontiers in plant-environment interactions: Innovative technologies and developments* (pp. 121-142). Cham: Springer. [doi: 10.1007/978-3-031-43729-8_6](https://doi.org/10.1007/978-3-031-43729-8_6).
- [5] Blanc-Mathieu, R., Dumas, R., Turchi, L., Lucas, J., & Parcy, F. (2024). Plant-TFClass: A structural classification for plant transcription factors. *Trends in Plant Science*, 29(1), 40-51. [doi: 10.1016/j.tplants.2023.06.023](https://doi.org/10.1016/j.tplants.2023.06.023).
- [6] Chen, X., Li, C., Wang, H., & Guo, Z. (2019). WRKY transcription factors: Evolution, binding, and action. *Phytopathology Research*, 1, article number 13. [doi: 10.1186/s42483-019-0022-x](https://doi.org/10.1186/s42483-019-0022-x).
- [7] DeepMind. (2024). *AlphaFold has revealed millions of intricate 3D protein structures, and is helping scientists understand how life's molecules interact*. Retrieved from <https://deepmind.google/technologies/alphafold/>.
- [8] Dinusha, C.M.M. (2019). *The evolution of reproductive development in angiosperms*. (Doctoral thesis, University of California, Riverside, USA)
- [9] Du, Z., Su, H., Wang, W., Ye, L., Wei, H., Peng, Z., & Yang, J. (2021). The trRosetta server for fast and accurate protein structure prediction. *Nature Protocols*, 16, 5634-5651. [doi: 10.1038/s41596-021-00628-9](https://doi.org/10.1038/s41596-021-00628-9).
- [10] Hassan, S., Lethin, J., Blomberg, R., Mousavi, H., & Aronsson, H. (2019). In silico based screening of WRKY genes for identifying functional genes regulated by WRKY under salt stress. *Computational Biology and Chemistry*, 83, article number 107131. [doi: 10.1016/j.compbiolchem.2019.107131](https://doi.org/10.1016/j.compbiolchem.2019.107131).
- [11] He, X., Li, J.-J., Chen, Y., Yang, J.-Q., & Chen, X.-Y. (2019). Genome-wide analysis of the WRKY gene family and its response to abiotic stress in buckwheat (*Fagopyrum tataricum*). *Open Life Sciences*, 14(1), 80-96. [doi: 10.1515/biol-2019-0010](https://doi.org/10.1515/biol-2019-0010).
- [12] Hekkelman, M.L., de Vries, I., Joosten, R.P., & Perrakis, A. (2023). AlphaFill: Enriching AlphaFold models with ligands and cofactors. *Nature Methods*, 20, 205-213. [doi: 10.1038/s41592-022-01685-y](https://doi.org/10.1038/s41592-022-01685-y).
- [13] Li, N., Liu, T., Guo, F., Yang, J., Shi, Y., Wang, S., & Sun, D. (2022). Identification of long non-coding RNA-microRNA-mRNA regulatory modules and their potential roles in drought stress response in wheat (*Triticum aestivum* L.). *Frontiers in Plant Science*, 13, article number 1011064. [doi: 10.3389/fpls.2022.1011064](https://doi.org/10.3389/fpls.2022.1011064).
- [14] Li, S., Khoso, M.A., Xu, H., Zhang, C., Liu, Z., Wagan, S., Dinislam, K., & Liu, L. (2024). WRKY transcription factors (TFs) as key regulators of plant resilience to environmental stresses: Current perspective. *Agronomy*, 14(10), article number 2421. [doi: 10.3390/agronomy14102421](https://doi.org/10.3390/agronomy14102421).
- [15] Lin, Z., Akin, H., Rao, R., Hie, B., Zhu, Z., Lu, W., & Rives, A. (2023). Evolutionary-scale prediction of atomic-level protein structure with a language model. *Science*, 379(6637), 1123-1130. [doi: 10.1126/science.ade2574](https://doi.org/10.1126/science.ade2574).

- [16] Long, L., Gu, L., Wang, S., Cai, H., Wu, J., Wang, J., & Yang, M. (2023). Progress in the understanding of WRKY transcription factors in woody plants. *International Journal of Biological Macromolecules*, 242(Part 1), article number 124379. doi: [10.1016/j.ijbiomac.2023.124379](https://doi.org/10.1016/j.ijbiomac.2023.124379).
- [17] Lu, C.H., Chen, C.C., Yu, C.S., Liu, Y.Y., Liu, J.J., Wei, S.T., & Lin, Y.F. (2022). MIB2: Metal ion-binding site prediction and modeling server. *Bioinformatics*, 38(18), 4428-4429. doi: [10.1093/bioinformatics/btac534](https://doi.org/10.1093/bioinformatics/btac534).
- [18] National Center for Biotechnology Information (NCBI). (2024). *Protein database*. Retrieved from <https://www.ncbi.nlm.nih.gov/protein/>.
- [19] Pandey, B., Grover, A., & Sharma, P. (2018). Molecular dynamics simulations revealed structural differences among WRKY domain-DNA interaction in barley (*Hordeum vulgare*). *BMC Genomics*, 19, article number 132. doi: [10.1186/s12864-018-4506-3](https://doi.org/10.1186/s12864-018-4506-3).
- [20] Ranjan, P., Yadav, A., Behera, A.K., Singh, D.K., Singh, P., & Singh, G.P. (2024). Structural, functional and evolutionary analysis of wheat WRKY45 protein: A combined bioinformatics and MD simulation approach. *Cereal Research Communications*, 52, 489-499. doi: [10.1007/s42976-023-00399-x](https://doi.org/10.1007/s42976-023-00399-x).
- [21] Rodríguez-Lumbreras, L.A., Jiménez-García, B., Giménez-Santamarina, S., & Fernández-Recio, J. (2022). pyDockDNA: A new web server for energy-based protein-DNA docking and scoring. *Frontiers in Molecular Biosciences*, 9, article number 988996. doi: [10.3389/fmolb.2022.988996](https://doi.org/10.3389/fmolb.2022.988996).
- [22] Shukla, R., & Tripathi, T. (2020). Molecular dynamics simulation of protein and protein-ligand complexes. In D.B. Singh (Ed.), *Computer-aided drug design* (pp. 133-161). Singapore: Springer. doi: [10.1007/978-981-15-6815-2_7](https://doi.org/10.1007/978-981-15-6815-2_7).
- [23] Singh, A., Sharma, A.K., Singh, N.K., Sonah, H., Deshmukh, R., & Sharma, T.R. (2019). Understanding the effect of structural diversity in WRKY transcription factors on DNA binding efficiency through molecular dynamics simulation. *Biology*, 8(4), article number 83. doi: [10.3390/biology8040083](https://doi.org/10.3390/biology8040083).
- [24] Steinegger, M., & Söding, J. (2017). MMseqs2 enables sensitive protein sequence searching for the analysis of massive data sets. *Nature Biotechnology*, 35(11), 1026-1028. doi: [10.1038/nbt.3988](https://doi.org/10.1038/nbt.3988).
- [25] Theisen, F.F., Prestel, A., Elkjær, S., Leurs, Y.H., Morffy, N., Strader, L.C., & Skriver, K. (2024). Molecular switching in transcription through splicing and proline-isomerization regulates stress responses in plants. *Nature Communications*, 15, article number 592. doi: [10.1038/s41467-024-44859-2](https://doi.org/10.1038/s41467-024-44859-2).
- [26] Tian, J., Zhang, J., & Francis, F. (2023). Large-scale identification and characterization analysis of VQ family genes in plants, especially gymnosperms. *International Journal of Molecular Sciences*, 24(19), article number 14968. doi: [10.3390/ijms241914968](https://doi.org/10.3390/ijms241914968).
- [27] Tripathi, A., Mondal, R., Lahiri, T., Chaurasiya, D., & Pal, M.K. (2023). TemPred: A novel protein template search engine to improve protein structure prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(3), 2112-2121. doi: [10.1109/TCBB.2022.3233846](https://doi.org/10.1109/TCBB.2022.3233846).
- [28] Upadhyay, D., Budhlakoti, N., Kumari, J., Chaudhary, N., Padaria, J.C., Sareen, S., & Kumar, S. (2024). In-silico characterization of drought stress related WRKY2 transcription factor in wheat crop (*Triticum aestivum* L.): Study of its physico-chemical properties and structural dynamics. *Genetic Resources and Crop Evolution*, 71, 1481-1492. doi: [10.1007/s10722-023-01706-5](https://doi.org/10.1007/s10722-023-01706-5).
- [29] Wani, S.H., Tripathi, P., Zaid, A., Challa, G.S., Kumar, A., Kumar, V., & Bhatt, M. (2018). Transcriptional regulation of osmotic stress tolerance in wheat (*Triticum aestivum* L.). *Plant Molecular Biology*, 97, 469-487. doi: [10.1007/s11103-018-0761-6](https://doi.org/10.1007/s11103-018-0761-6).
- [30] Wu, R., Ding, F., Wang, R., Shen, R., Zhang, X., Luo, S., Su, C., Wu, Z., Xie, Q., Berger, B., Ma, J., & Peng, J. (2022). High-resolution de novo structure prediction from primary sequence. doi: [10.1101/2022.07.21.500999](https://doi.org/10.1101/2022.07.21.500999).
- [31] Yang, Z., Zeng, X., Zhao, Y., & Chen, R. (2023). AlphaFold2 and its applications in the fields of biology and medicine. *Signal Transduction and Targeted Therapy*, 8, article number 115. doi: [10.1038/s41392-023-01381-z](https://doi.org/10.1038/s41392-023-01381-z).

- [32] Zaheer, M., Rehman, S.U., Khan, S.H., Shahid, S., Rasheed, A., Naz, R., & Sajjad, M. (2021). *Genome-wide identification and transcriptional profiling of new cobra-like genes in bread wheat (Triticum Aestivum)*. doi: [10.21203/rs.3.rs-796690/v1](https://doi.org/10.21203/rs.3.rs-796690/v1).

Методи комп'ютерного моделювання транскрипційного фактора стресостійкості WRKY2 у *Triticum Aestivum*: порівняльний аналіз

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Анотація. Метою роботи було порівняння ефективності сучасних методів комп'ютерного моделювання для побудови тривимірної структури транскрипційного фактора TaWRKY2 із *Triticum aestivum*, який відіграє ключову роль у стресостійкості рослин. У дослідженні використано традиційні гомологічні підходи та методи, засновані на машинному навчанні, зокрема AlphaFold, RoseTTaFold, ESMFold та OmegaFold. Модель, отримана за допомогою AlphaFold2 (MMseqs2), виявилася найякіснішою за метриками Clashscore (99-й перцентиль), MolProbity Score та ERRAT. Комплекс з іонами цинку та ДНК, згенерований AlphaFold3, виявив кращі результати за Z-Score показником. Метод AlphaFold забезпечив біологічно релевантні структури з правильним розташуванням функціональних ділянок. ESMFold забезпечив швидке моделювання, однак продемонстрував відхилення у структурі, включаючи додаткові α -спіралі та нижчу якість за більшістю метрик. Модель RoseTTaFold мала витягнуту форму з більшим вмістом α -спіралей та потребувала додаткової верифікації функціональної активності. OmegaFold, хоча й забезпечив найкраще значення за QMEAN (0,4), поступився за іншими показниками. Додаткові інструменти, такі як Amber і Chimera, дозволили провести релаксацію структур та аналіз ключових характеристик, зокрема просторового розташування цинкових пальців (18,7 Å). Оцінка за метриками Verify 3D, ERRAT, Ramachandran Plot та іншими виявила переваги та недоліки кожного підходу. Висновки підтвердили переваги методів машинного навчання для моделювання білків із високою функціональною пластичністю. Зокрема, AlphaFold було визнано найефективнішим підходом для побудови моделей з високою точністю. Разом із цим, використання кількох методів дозволяє врахувати альтернативні конформації та взаємодії, що важливо для глибшого розуміння функціональних механізмів білка

Ключові слова: біоінформатика; тривимірна структура білка; методи машинного навчання; метрики оцінки моделей; цинкові пальці



Biochemical blood parameters in cattle exposed to radiation

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Abstract. Under contemporary conditions, the study of adaptive processes in living organisms remains highly relevant, particularly in relation to the biochemical blood parameters of cattle kept for extended periods in areas contaminated with radionuclides. This study aimed to determine blood biochemical parameters, analyse characteristic changes, assess their impact on animal health, and evaluate the degree of damage caused by radioactive iodine isotopes. The study examined biochemical parameters – including the activity of amylase, aspartate and alanine aminotransferases (AST and ALT), glutathione peroxidase (GPx), the concentration of lipid hydroperoxides (LHP), the level of ceruloplasmin, and total plasma protein – using standard biochemical methods. The results revealed a wide range of parameter values; however, no significant differences were observed between the groups of cattle exposed to various doses of ionising radiation (1 Gy to the body, 2 Gy to the gastrointestinal tract, and up to 40 Gy to the thyroid gland) resulting from Chernobyl radioactive fallout, including radioactive iodine affecting the thyroid and those kept in relatively uncontaminated areas exposed to only minimal doses of radiation (within a few mGy). Characteristic changes in biochemical parameters and potential alterations in health status were analysed. It was established that under conditions of high-dose thyroid irradiation (40 Gy to the thyroid gland), powerful adaptive mechanisms are activated in the body. These mechanisms counteract the harmful effects of ionising radiation at the organismal level and help preserve important productive traits such as fertility and productivity. These findings may serve as a basis for developing a system of measures aimed at regulating the adaptive responses of organisms exposed to ecopathogenic factors

Keywords: stable iodine (^{127}I); radioactive iodine (^{131}I); radionuclide-contaminated area; thyroid gland; blood; enzymatic activity; biochemical parameters

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INTRODUCTION

The vast scale of radionuclide contamination in Ukraine following the Chornobyl nuclear power plant (ChNPP) accident led to the exposure of the country's population and livestock to radiation. This prompted scientists to study various aspects and consequences of ionising radiation's impact on people and other biological entities. A clear consequence of the Chornobyl radioactive fallout on human health was the increase in thyroid gland pathologies within the first five years after the accident. This was largely due to cows' milk being contaminated with radioactive iodine isotopes. While medical issues related to radioactive iodine exposure in humans have received significant attention from scientists worldwide, the biological effects of radioactive iodine isotopes on livestock have been comparatively understudied. Therefore, research into the molecular mechanisms of ionising radiation on animals and the development of radiation-induced adaptive processes for living organisms to withstand chronic ionising radiation exposure remains highly relevant. Crucial studies on the aftermath of the mentioned accident, particularly examining the patterns of radionuclide transfer through trophic chains from soil to food products, have been conducted in Ukraine, Germany, and England (von Zallinger & Tempel, 1988). These studies highlight the ongoing relevance of the Chornobyl radionuclides' impact, even 30 years after the accident (Mushawwir *et al.*, 2020).

The research results presented in this article, focusing on cattle under production conditions and the artificial introduction of radioactive iodine, logically extend the experiments of M.M. Lazarev & A.V. Klepko (2023). Their study assessed the haematological blood parameters of cattle experiencing "iodine" pathology observed post-Chornobyl accident. That study analysed data on ^{127}I content in the Ukrainian Polissia region, an area with radioactive contamination, and examined the health consequences for cattle due to insufficient natural stable iodine, including characteristic physiological changes. M. Haque *et al.* (2024) highlight that the Polissia region is characterised by a deficiency in biogenic microelements, particularly iodine, due to the region's specific soil and climatic conditions. These authors emphasise that low iodine levels in the soil

directly affect its concentration in plants and, consequently, in the organisms that consume these plants as feed. This creates a predisposition for iodine deficiency conditions in both animals and humans residing in this region.

O. Pareniuk & N. Yasuda (2021) emphasised that radioactive iodine is a key factor in damaging biological systems following nuclear accidents. This is because it rapidly integrates into biological cycles, particularly in the thyroid gland, leading to acute and chronic radiation effects. They highlight that during the Chornobyl accident, the ^{131}I isotope was the primary source of population exposure in the initial weeks after the explosion. This isotope accumulates in humans and animals through the inhalation of radioactive aerosols and the consumption of contaminated food products. M. Bartusková *et al.* (2023) described the diagnostic signs and clinical picture of radioactive iodine-induced radiation damage in animals. However, they did not adequately address cases where animal populations affected by ^{131}I were in regions endemic for stable iodine deficiency.

M.M. Talerko *et al.* (2020) noted in their research that ^{127}I deficiency in cattle leads to stunted growth, low body weight, reduced productivity, and characteristic changes in the hair coat, such as curliness and excessive hair length. Similar health deviations in cattle were observed in radioactively contaminated areas during the acute phase of the Chornobyl accident (Labunska *et al.*, 2021). D. Horikami *et al.* (2022) investigated the impact of ^{131}I on the thyroid gland of cattle following the Fukushima nuclear accident. They confirmed that thyroid gland damage leads to systemic changes, including bradycardia, rumen hypotonia, impaired erythropoiesis and leukopoiesis, and reduced reproductive functions. M.M. Lazarev & A.V. Klepko (2023), in their experimental studies, corroborated that the artificial introduction of ^{131}I into the cattle's body causes pathological changes similar to those observed with stable iodine deficiency. Thus, research results indicate a close relationship between physiological disturbances in animals and iodine deficiency, regardless of whether it is radioactive or stable.

Consequently, determining both haematological and biochemical blood parameters can not only characterise the health status of animals but

also provide a basis for assessing the extent of radioactive iodine isotope damage to the body. This can then be used to develop a system of measures to regulate the body's adaptive mechanisms when exposed to ecopathogenic factors. Therefore, this study aimed to investigate the biochemical blood parameters that characterise the key parameters of the physiological state of cattle in iodine-deficient and radionuclide-contaminated areas.

MATERIALS AND METHODS

The study was conducted on two groups of Black-and-White cows, with 25 heads in each group, in their 3rd to 5th lactation periods under production conditions. The first group of animals was evacuated from the exclusion zone (village of Volodymyrivka, Poliske District, Kyiv Region) three weeks after the Chernobyl accident, which occurred on 26 April 1986. At the time of the accident, the animals were kept on pasture. The first group of cows was formed from a herd that was evacuated from the village of Volodymyrivka. These cows were transferred to a farm located in the urban-type settlement of Poliske, Kyiv Region, where the radioactive contamination density was more than 20 times lower than in the village of Volodymyrivka. This difference in radioactive contamination density led to a significant difference in the radiation doses received by the animals' bodies as a whole and specifically by the cows' thyroid glands.

This study was based on the conclusions and data obtained in the research of N.A. Beresford *et al.* (2000), which formed the basis for further analysis. The observation of the cows and their offspring was conducted from 1987 to 1995. This research presents the results of biochemical status studies of the cows for the year 1989.

Cows from a farm whose territory was not considered radioactively contaminated according to the Law of Ukraine No. 791a-XII (1991) were used as a control group. The animals were kept under identical conditions on a standard farm diet but were exposed to varying doses of ionising radiation to the thyroid gland (TG). The first group of cows received 40 Gy of radioactive ¹³¹I radiation to the TG, and the second group received 10 Gy. The study assessed the overall clinical condition of the animals, recorded cow productivity (using the control milking method before the start of the experiment and monthly thereafter),

haematological parameters (Lazarev & Klepko, 2023), thyroid hormone levels using radioimmunoassay in test systems for thyroxine (T₄RIA-Pg) and triiodothyronine (T₃-RIA-Pg), and a range of biochemical parameters. These parameters showed a characteristic dependence of the observed changes on the thyroid gland radiation doses and on the keeping conditions, particularly related to the deficiency of biogenic microelements in the animals' diets. For biochemical (as well as haematological) studies, cattle blood treated with the anticoagulant heparin was used, and collected from 5–6 animals in each group.

To evaluate the biochemical profile in the animals' blood plasma, the activity of enzymes (amylase, aspartate and alanine aminotransferases (AST, ALT), glutathione peroxidase (GP)), as well as the levels of ceruloplasmin, total protein, cholesterol, sialic acids, lipid hydroperoxides (LPO), and thyroid hormones (T₃ and T₄) were determined. The studies were conducted using methods described in L.I. Ostapchenko *et al.* (2019), and the results were compared with the normative values provided in V.V. Vlizlo *et al.* (2012). Statistical analysis was performed using methods of variational statistics (Hruzieva *et al.*, 2020).

RESULTS AND DISCUSSION

Given that radioactive iodine was the primary factor in radiation damage to livestock, the functional activity of the thyroid gland was assessed by measuring thyroid hormone levels in blood plasma (Giovanella *et al.*, 2022; Lazarev *et al.*, 2024). Comparing the hormonal status of animals in the first group, which experienced the greatest radiation exposure (40 Gy to the TG and approximately 1 Gy to the whole body), with those in the second group (10 Gy to the TG) revealed a trend towards decreased concentrations of thyroid hormones (T₃ and T₄) in the blood of animals exposed to higher doses of thyroid radiation. However, in both groups, thyroid hormone levels were below the physiological norm (Table 1). The physiological range of T₄ and T₃ concentrations in cow blood varies throughout the year: before calving, it is 46–90 nmol/L and 1.2–1.6 nmol/L; at the beginning of lactation, 43–125 nmol/L and 2.0–6.0 nmol/L; at peak lactation, 57–103 nmol/L and 2.3–3.5 nmol/L; and at the end of lactation, 43–86 nmol/L and 2.4–3.2 nmol/L.

Table 1. Thyroid hormone levels in blood plasma of experimental cows (nmol/L)

Cow groups	Parameter	Time of assessment, months after ¹³¹ I exposure					
		6	8	10	13	15	20
1	T ₃	0.33 ± 0.05	0.47 ± 0.1	0.49 ± 0.01	0.69 ± 0.06	1.4 ± 0.5	0.96 ± 0.2
2	T ₃	0.43 ± 0.03*	0.53 ± 0.07	0.51 ± 0.07	0.61 ± 0.04	1.37 ± 0.04	1.0 ± 0.03
1	T ₄	27.7 ± 3.3	29.5 ± 6.4	43.1 ± 4.7*	44.3 ± 3.6	63.7 ± 4.8	38.0 ± 3.8*
2	T ₄	29.6 ± 1.2	30.1 ± 2.7	34.6 ± 1.8	46.1 ± 0.8	61.5 ± 4.3	44.5 ± 3.8

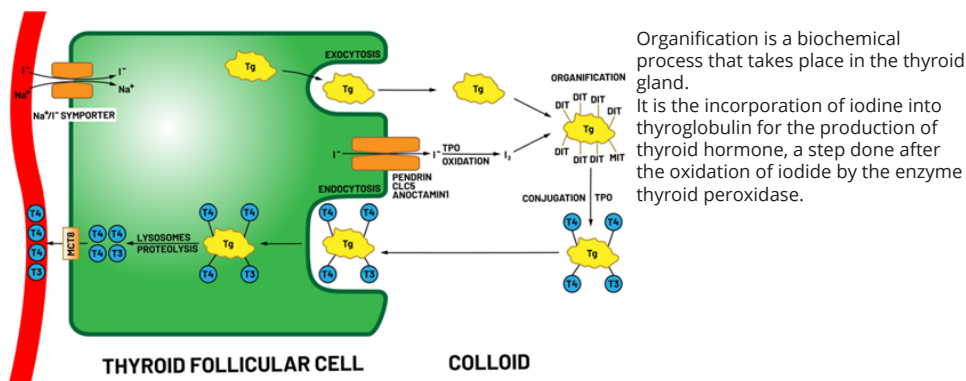
Note: ¹³¹I – radioactive iodine, T₃ – triiodothyronine, and T₄ – thyroxine, * – p < 0.05

Source: developed by the authors

The analysis of thyroid hormone levels in the blood plasma of the experimental cows indicates that the hormone levels in cows from groups 1 and 2 fluctuate with a nearly identical pattern. However, a significant difference in triiodothyronine levels is observed six months after radioactive iodine exposure, and in thyroxine levels, at 10- and 20-months post-exposure.

Thyroid hormones (T₃ and T₄) are synthesised in the follicular cells of the thyroid gland (Fig. 1) by attaching iodine to the residues of the amino acid tyrosine, which is a component of thy-

roglobulin (TG), a soluble glycoprotein (660 kDa). The daily secretion of T₄ by the thyroid gland is 80–100 µg, and that of T₃ is approximately 5 µg. T₃ is significantly more active, making a substantial portion of T₄ a precursor to T₃. While some triiodothyronine is synthesised in the thyroid gland, it is also produced in peripheral body cells through the monodeiodination of thyroxine, catalysed by the enzyme 5'-monodeiodinase (requiring the trace element selenium). Consequently, T₃ levels in serum or plasma do not always accurately reflect thyroid gland dysfunction.

**Figure 1.** Thyroid hormone production

Note: T₃ – triiodothyronine; T₄ – thyroxine; Tg – thyroglobulin; TPO – thyroid peroxidase; MIT – moniodotyrosine; DIT – diiodotyrosines; CLC5 – chloride channel 5; Na⁺/I⁻ symporter; pendrin; anoctamin1; MCT8 – monocarboxylate transporter 8

Source: L. Giovanella *et al.* (2022)

Through the action of proteases and peptidases in the lysosomes of follicular cells, Tg is broken down, and T₃ and T₄ are secreted into the blood, where they bind to plasma proteins. T₄ has a high affinity for globulin (thyroxine-binding globulin – TBG), a lower affinity for prealbumin, and a very weak affinity for albumin (approximately 75%

binds to TBG and 15%–20% to prealbumin and albumin, respectively). Only 0.5% of T₄ remains in a free (unbound) state. T₃ binds almost exclusively to TBG, with its free fraction accounting for 0.05%. The biological half-life of T₄ is 7–9 days, and that of T₃ is 2 days. Both bound and free forms of the hormones exist in dynamic equilibrium. Free forms of

triiodothyronine penetrate cell membranes relatively easily, influencing all types of metabolism.

T_4 and T_3 levels increase in the blood during hyperthyroidism, while a decrease in T_3 and T_4 levels can be observed in hypothyroidism, liver diseases, kidney diseases, lipomobilisation syndrome, ketosis, sepsis, pneumonia, peritonitis, malignant tumours, and also with the administration of iodine preparations, corticosteroids, certain antibiotics and sulfonamides, and heparin. This is why liver dysfunction can be one of the factors contributing to changes in the cows' condition, as evidenced by the data presented in Table 1.

Biochemical blood analysis, a key method of laboratory diagnosis, is used to study the function of internal organs and their systems, including metabolic processes occurring in the body. In environments contaminated with substances harmful to animal health, particularly radioactive substances, pathological changes are primarily observed in the liver – a natural barrier against toxic substances (ICRP Publication..., 2023). Deviations in liver function are indicated by altered activity levels of enzymes such as ALT, AST, and bilirubin, while kidney pathology is indicated by an increase or decrease in creatinine and urea levels in the blood. The dysfunction of organs and their systems also leads to inflammatory processes, which are indicated by changes in C-reactive protein and sialic acid levels (Vlizlo *et al.*, 2012). In addition to these parameters, other markers (over 500 substances) are studied to assess the

physiological state of the organism. The analysis of the aforementioned enzyme activities and substance levels reveals whether the chemical reactions of metabolic processes are proceeding normally or with deviations.

Biochemical analysis can indicate the development of diabetes mellitus in cases of elevated blood glucose levels, suggest myocardial infarction or hepatitis with changes in aminotransferase activity, and point to atherosclerosis and cardiovascular diseases with increased cholesterol levels. Liver dysfunction and bile flow obstruction are indicated by changes in bilirubin levels; kidney function abnormalities are suggested by elevated or decreased creatinine and urea levels; severe pathological changes are reflected in changes in total protein levels; and pancreatitis is indicated by increased amylase activity (Ostapchenko *et al.*, 2019).

A definitive diagnosis is confirmed by analysing specific biochemical blood parameters, considering their changes in the context of the mentioned deviations, which affect the overall physiological state of the organism and the metabolic processes of tissue cells in internal organs. These changes are reflected in the characteristic variations of the biochemical parameters presented above. Tables 2 and 3 present the results of biochemical parameter analysis, demonstrating diverse deviations influenced by the time of year and varying levels of thyroid gland radiation in cows. Blood from cows not exposed to radioactive iodine is used as a control.

Table 2. Enzyme activity in cow blood with varying levels of TG radiation

Enzymes, units of activity →	Amylase, mg/ hour · mL	AST, μmol/ hour · mL	ALT, μmol/ hour · mL	GP, μmol glutathione/min
Animal groups↓				
March				
1	137.7±16.0	1.6±0.08*	1.3±0.2	0.87±0.13*
2	105.7±22.0	1.13±0.05*	0.78±0.09	10.0±0.1*
Control	125.1±17.8	3.65±0.07	1.04±0.03	0
July				
1	66.5±9,2*	0.8±0.06*	0.21±0.03	7.2±0.2
2	46.2±9.0	0.8±0.06*	0.3±0.04	8.2±0.06
Control	40.0±5.2	0.3±0.03	0.06±0.01	6.7±0.08

Note: * – $p < 0.05$; significant difference between experimental and control groups; enzyme activity: amylase, aspartate aminotransferase (AST), alanine aminotransferase (ALT), glutathione peroxidase (GP)

Source: developed by the authors

Table 3. Levels of selected biochemical parameters in cow blood with varying levels of TG radiation

Content → Animal groups↓	Ceruloplasmin, mg%	Cholesterol, mg%	Sialic acids, mmol/L	Protein, mg/mL	LPO, arb. unit
March					
1	18.0 ± 3.0	112.0 ± 9.7	141 ± 4.6*	131.8 ± 7.5*	0.15 ± 0.04
2	20.2 ± 1.3	82.5 ± 10.4*	183.0 ± 9.5*	115.0 ± 7.3*	0.3 ± 0.08
Control	22.2 ± 1.05	147.8 ± 8.0	236.0 ± 3.3	90.5 ± 3.3	0.43 ± 0.07
July					
1	24.5 ± 1.2*	235.0 ± 8.8	150.0 ± 11.4	114.6 ± 5.7	1.5 ± 0.07*
2	24.2 ± 3.4*	254.0 ± 23.2	136.0 ± 10.8	11.6 ± 8.4	1.3 ± 0.07
Control	6.5 ± 0.3	212.0 ± 16.0	145.0 ± 9.3	97.9 ± 3.8	1.26 ± 0.07

Note: * – $p < 0.05$; in cattle blood, ceruloplasmin levels are 25.0–36.0 mg%; concentration of ceruloplasmin, total protein, cholesterol, sialic acids, and lipid hydroperoxides (LPO; arb. unit – arbitrary units)

Source: developed by the authors

As clearly seen from the results presented in Table 2, the activity of the studied enzymes varies not only under the influence of radioactive iodine but also shows a pronounced influence of feeding conditions during the summer and spring periods. The AST and ALT activity data in cow blood are within the normal range or lower. Seasonal changes in these parameters are particularly noticeable: in July, the activity of these enzymes in the blood of both the experimental and control groups is lower than in March and below the normal range (as shown below). In some cases, reduced AST activity can indicate pathological conditions: liver rupture, severe necrotic damage, and chronic vitamin B6 deficiency. It is difficult to conclude liver damage as other evidence is needed. A rapid decrease in ALT activity with a simultaneous significant increase in bilirubin and an increase in prothrombin time indicates a poor prognosis and suggests severe necrotic changes in liver tissue. However, without information on the latter two parameters, only predictions can be made, which should be considered in future studies.

AST (48–108 U/L or 2.8–6.5 $\mu\text{mol}/(\text{hour} \cdot \text{mL})$, or 0.80–1.80 $\mu\text{mol}/(\text{s} \cdot \text{L})$) and ALT (17–40 U/L or 1.02–2.39 $\mu\text{mol}/(\text{hour} \cdot \text{mL})$, or 0.28–0.67 $\mu\text{mol}/(\text{s} \cdot \text{L})$) represent the activity of enzymes in cattle blood (Vlizlo *et al.*, 2012; Ostapchenko *et al.*, 2019). These enzymes, located in the cells of most organs and systems, transfer amino groups from aspartic acid and alanine to alpha-ketoglutaric acid. Since aminotransferases are not specific tests for evaluating the condition of individual organs, the site of enzyme release into the blood is determined. They exhibit high activity in the cytoplasm of cells (AST

also in mitochondria), and even minor tissue damage increases their activity in serum (plasma). The determination of AST and ALT activity in blood serum is performed for the diagnosis of liver diseases (hepatitis, hepatosis, etc.). AST activity is determined in the blood serum of cattle and horses, while both AST and ALT are determined in the blood serum of pigs, dogs, and cats, which depends on the degree of activity of these enzymes in the hepatocytes of different animal species. This is because the cells of large and small animals exhibit correspondingly high AST and ALT activity.

A comprehensive assessment of animal health involves the dynamic study of the most common biochemical blood parameters, which characterise the functional activity of metabolic processes in the body as a whole and in its individual organs. Table 3 presents the parameters for assessing the state of metabolic processes in the bodies of cows exposed to varying doses of thyroid gland radiation from radioactive iodine exposure. The primary focus was on biochemical parameters that monitor the pro- and antioxidant activity of cattle blood plasma and the activity of specific metabolites responsible for the functional state of individual organs, particularly the liver and other hepato-associated deviations. Biochemical blood parameters are quite labile parameters of the biochemical state and can fluctuate within a wide range depending on environmental conditions and animal husbandry practices. Logically, it was hypothesised that the additional impact of ionising radiation on the thyroid gland could cause significant changes in the biochemical state of the experimental animals' bodies.

The results of the biochemical studies confirm the understanding of many researchers regarding the significant compensatory capabilities of organisms' biochemical status and the strain on certain biochemical parameters during unfavourable times of the year, particularly spring. This is when a significant deviation of blood parameters in experimental animals from the control group is observed. It should be noted that the impact of radiation is less pronounced than the influence of animal husbandry conditions. Amylase activity (g/hour · L) in cows of group 1 (which received a higher dose of TG radiation) was similar to the control, while the values for animals in group 2 (with a 4-fold lower radiation dose) were lower in the spring period (March). Amylolytic activity for all three groups of cows in March was higher than in July, which was likely primarily due to the cows' diet in the spring and summer periods. It should be noted that animals fed with high-starch feeds have higher amylolytic activity than those fed with low-starch feeds. Researchers H. Yang *et al.* (2012) noted that the activity of bacterial amylolytic enzymes is influenced by certain amino acids. Methionine at a concentration of 1-2 mg/mL stimulates, while lysine inhibits bacterial amylase activity and growth.

In cattle blood, the ceruloplasmin content is 25.0-36.0 mg%, as per the normal range specified in the study by V.V. Vlizlo *et al.* (2012). The relative ceruloplasmin content in the blood of animals in the experimental groups was slightly below this normal range, regardless of the TG radiation dose (except for the control group in July). Ceruloplasmin, mg%, is a key factor in neuroendocrine regulation and the body's natural defence against stress, inflammation, allergic reactions, and other diseases. This protein is a Cu-containing glycoprotein that belongs to the acute phase proteins. It participates in iron metabolism and haematopoiesis and acts as an antioxidant. It has oxidase activity, which allows it to break down biogenic amines and other substrates, thus playing a role in neuroendocrine regulation. Changes in ceruloplasmin activity usually correlate with changes in copper ions. A sharp disturbance in copper metabolism is observed in anaemia, where its concentration in the blood significantly increases due to a decrease in deionised copper content in liver tissue.

The reference values for total cholesterol in blood serum, according to V.V. Vlizlo *et*

al. (2012), range from 2.3-6.6 mmol/L or 88.93-255.189 mg%. Generally, cholesterol levels in all groups (experimental and control) fall within these reference values. Elevated cholesterol concentrations are observed in liver diseases with impaired bile acid formation (hepatitis) and bile secretion (cholestasis), lipid nephrosis, renal failure, ketosis, hypothyroidism, and excessive carbohydrate and fat consumption by animals. Hypocholesterolaemia occurs with prolonged deficiencies in dietary fats and carbohydrates, as well as in hyperthyroidism and liver diseases.

Researchers L.I. Ostapchenko *et al.* (2019) observed a decrease in cholesterol content (mg%) in spring and an increase in summer. They noted that cholesterol is a steroid synthesised mainly in the liver and also enters the blood from the intestine. Cholesterol in the blood exists in free and bound forms. Its content in blood serum depends on liver function. M.C. Bell (1985) indicated that elevated cholesterol concentrations (hypercholesterolemia) are observed in hyperlipidaemia, increased serum triacylglycerol levels in liver diseases with impaired bile acid formation (hepatitis, hepatodystrophy) and bile secretion (cholestasis), glomerulonephritis, lipid nephrosis, chronic renal failure, pancreatic tumours, ketosis, diabetes mellitus, hypothyroidism, gout, and excessive carbohydrate and fat consumption by animals.

S. Pegolo *et al.* (2023) noted that a decrease in serum cholesterol concentration, particularly its esterified fraction (hypocholesterolaemia), is observed in hepatitis, hepatodystrophy, and cirrhosis due to the impaired synthetic function of hepatocytes, deficiencies in dietary fats and carbohydrates, and reduced lipoprotein synthesis. They also emphasised that in hyperthyroidism, energy metabolism is increased, leading to higher cholesterol consumption and, consequently, its reduction in blood serum. Thus, changes in cholesterol levels can be important markers of liver and endocrine metabolic disorders.

S.M. Razavi *et al.* (2023) indicated that sialic acids are important components of glycoconjugates and play a key role in cellular processes, including immune response, inflammation, and intercellular interaction regulation. The observed trend of decreased sialic acid levels in the experimental animal groups compared to the control may result from degenerative processes in the

central nervous system associated with impaired biosynthesis of carbohydrateprotein complexes. Furthermore, S.M. Razavi *et al.* (2023) and V. Kasich *et al.* (2021) highlighted that changes in sialic acid concentration can indicate acute phase inflammatory response disorders occurring in various pathological conditions, including infectious and parasitic diseases. The authors also emphasised the significance of sialic acids as potential biomarkers for neurodegenerative and metabolic disorders in animals, which aligns with other studies establishing their role in the pathogenesis of several systemic diseases.

Protein (mg/mL) in cattle blood primarily demonstrates hyperproteinaemia in the experimental animal groups compared to the control, although there is an isolated case of hypoproteinaemia in group 2 in July. Based on the analysis of these parameters and considering general information on protein metabolism (Koch *et al.*, 2023), it can be inferred that hypoproteinaemia arose from prolonged malnutrition, alimentary osteodystrophy, hypokobaltosis, chronic gastrointestinal disorders, nephritis and nephrosis, liver cirrhosis, or tuberculosis. Conversely, hyperproteinaemia occurs due to protein overfeeding, ketosis, secondary osteodystrophy, toxicosis, liver dystrophy and inflammation, or severe forms of diarrhoea, dehydration, or acute inflammatory processes.

T. Liu *et al.* (2020) indicated that glutathione peroxidase (GPx or GP, μmol glutathione/min·mg protein) activity data suggest that biochemical processes tend to stabilise during the summer. As highlighted by S. Diyabalanage *et al.* (2020), GP is a selenoprotein found in the cytosol (70%) and mitochondria (20%-30%). The enzyme's highest activity is in the liver, lens, adrenal glands, erythrocytes, and pancreas, while the lowest is in muscles, the gastrointestinal tract, testes, and connective tissue. The enzyme protects erythrocytes from methaemoglobin formation, premature ageing, and haemolysis, and neutrophils and macrophages during the "respiratory burst". Inducers of the enzyme include selenium ions (which are part of the enzyme's active site), copper, vitamins A, E, C, B2, female sex hormones, and catecholamines. GP is activated in the initial stages of stress, vitamin E deficiency, exposure to ionising radiation, and the consumption of alcohol and fatty foods. GP activity is high in the mother's liver and lungs, placenta, and foetal liver.

The concentration of lipid hydroperoxides (LPO, arbitrary unit) remains within control values, as the excessive intake and consumption of oxygen, characteristic of all types of stress, leads to an increase in primary molecular products of lipid peroxidation (LPO), particularly lipid hydroperoxides. Researchers S. Diyabalanage *et al.* (2020) emphasise that most LPO is formed from polyunsaturated fatty acids and total lipids, and their synthesis occurs in significantly larger quantities than the synthesis of malondialdehyde (MDA), although they decompose rapidly. The maximum concentration of LPO can only be determined at the initial stage of the reaction. LPO levels are high in old age and increase with physical exertion. LPO increases intracellular calcium concentration, which is associated with glutathione oxidation.

From the analysis of biochemical parameters such as AST and ALT, ceruloplasmin concentration, total protein, cholesterol, sialic acids, GP, and LPO, it can be concluded that the observed deviations indicate impaired functioning of the body as a whole and its organs, particularly the liver, which is involved in detoxification processes. These deviations are the result of the formation of possible adaptive mechanisms in response to ionising radiation and other exogenous factors and require additional attention and study.

CONCLUSIONS

The studies conducted on the levels of thyroid hormones triiodothyronine (T_3) and thyroxine (T_4), and biochemical blood parameters in cows exposed to radioactive iodine, which resulted in varying doses of thyroid gland radiation (40 and 10 Gray), showed that, unlike haematological parameters, these blood parameters are less informative in terms of assessing their radiosensitivity.

The analysis of T_3 and T_4 levels in the blood plasma of the experimental cows demonstrated that their levels in animals of groups 1 and 2 fluctuated with a nearly identical pattern. However, a significant difference in triiodothyronine levels was observed six months after radioactive iodine exposure ($0.43 \pm 0.03^*$ nmol/L; $p < 0.05$), and in thyroxine levels, at 10- and 20-months postexposure ($43.1 \pm 4.7^*$ and $38.0 \pm 3.8^*$ nmol/L, respectively; $p < 0.05$). This is considering the physiological ranges of T_3 and T_4 concentrations

in cow blood, which vary throughout the year: before calving, 1.2-1.6 and 46-90 nmol/L; at the beginning of lactation, 2.0-6.0 and 43-125 nmol/L; at peak lactation, 2.3-3.5 and 57-103 nmol/L; and the end of lactation, 2.4-3.2 and 43-86 nmol/L. At 20 months post-radioactive iodine exposure decreased T_3 and T_4 levels in the blood were observed in hypothyroidism and liver dysfunction, which may be contributing factors to changes in the cows' condition.

The studied individual biochemical parameters (enzyme activities of amylase, aspartate and alanine aminotransferase, glutathione peroxidase, lipid hydroperoxide content, ceruloplasmin, and total protein levels in the plasma of cattle) fluctuate within wide ranges. However, they do not always significantly and consistently differ between groups of animals that have been exposed to different doses of thyroid gland irradiation and those that have not received significant doses of irradiation (at levels of a few mGy) to this important organ. A notable example is the activity of aspartate aminotransferase in the blood of groups 1 and 2 of cows, exposed to different doses of ^{131}I thyroid irradiation (40 and 10 Gy, respectively), as well as the control animals in spring and summer, which were within the normal range ($2.8\text{--}6.5\text{ }\mu\text{mol/hour}\cdot\text{mL}$) or lower (in March – $1.6 \pm 0.08^*$; $1.13 \pm 0.05^*$;

3.65 ± 0.07 , and in July – $0.8 \pm 0.06^*$; $0.8 \pm 0.06^*$; $0.3 \pm 0.03\text{ }\mu\text{mol/hour}\cdot\text{mL}$, $p < 0.05$)

The obtained results indicate that even under conditions of high-dose thyroid gland radiation (40 Gy to the TG, which would be absolutely lethal if applied to the whole animal), the body activates powerful compensatory (adaptive) mechanisms. These mechanisms allow for the neutralisation of the negative effects of ionising radiation at the organism level and the preservation of crucial agricultural traits such as reproduction and productivity. Research into changes in the body's antioxidant defence system and the assessment of oxidative stress levels under chronic radiation exposure is promising. Furthermore, the identification of specific biomarkers that can serve as early indicators of radiation damage in cattle is crucial.

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CONFLICT OF INTEREST

None.

REFERENCES

- [1] Bartusková, M., Selivanova, A., Malátová I., Hůlka J., Škrkal, J., Rosmus, J., Kapyltsova, A., & Rulík, P. (2023). A comparison of different detection techniques for ^{137}Cs measurements of cattle *in vivo*. *Radiation Protection Dosimetry*, 199(19), 2373-2382. doi: 10.1093/rpd/ncad252.
- [2] Bell, M.C. (1985). [Radiation effects on livestock: Physiological effects, dose response](#). *Veterinary and human toxicology*, 27(3), 200-207.
- [3] Beresford, N.A., et al., (2000). The transfer of ^{137}Cs and ^{90}Sr to dairy cattle fed fresh herbage collected 3.5 km from the Chernobyl nuclear power plant. *Journal of Environmental Radioactivity*, 47(2), 157-170. doi: 10.1016/s0265-931x(99)00037-5.
- [4] Diyabalanage, S., Dangolla, A., Mallawa, C., Rajapakse, S., & Chandrajith, R. (2020). Bioavailability of selenium (Se) in cattle population in Sri Lanka based on qualitative determination of glutathione peroxidase (GSH-Px) activities. *Environmental Geochemistry and Health*, 42(2), 617-624. doi: 10.1007/s10653-019-00395-3.
- [5] Giovanella, L., Avram, A.M., Ovčariček, P.P., & Clerc, J. (2022). Thyroid functional and molecular imaging. *Medical Functional Imaging*, 51(2), article number 104116. doi: 10.1016/j.lpm.2022.104116.
- [6] Haque, M., Binte Dayem, S., Tabassum Tasnim, N., Islam, M.R., & Shakil, M.S. (2024). Biological impact of Chornobyl radiation: A review of recent progress. *International Journal of Radiation Biology*, 100(10), 1405-1415. doi: 10.1080/09553002.2024.2391813.
- [7] Horikami, D., et al. (2022). The effect of exposure on cattle thyroid after the Fukushima Daiichi nuclear power plant accident. *Scientific Reports*, 12, article number 21754. doi: 10.1038/s41598-022-25269-0.

- [8] Hruzieva, T.S., et al. (2020). *Biostatistics*. Vinnytsia: Nova Knyga.
- [9] ICRP Publication 153: Radiological Protection in Veterinary Practice. (2023). *Annals of the ICRP*, 51(4), (9-95). doi: [10.1177/01466453221142702](https://doi.org/10.1177/01466453221142702).
- [10] Kassich, V., Kasianenko, O., Zazharskyi, V., Yatsenko, I., & Klishchova, Zh. (2021). Influence of ionizing radiation on the allergic reactivity of tuberculosis-infected laboratory animals. *Scientific Horizons*, 24(10), 17-27. [https://doi.org/10.48077/scihor.24\(10\).2021.17-27](https://doi.org/10.48077/scihor.24(10).2021.17-27).
- [11] Koch, F., Otten, W., Sauerwein, H., Reyer, H., & Kuhla, B. (2023). Mild heat stress-induced adaptive immune response in blood mononuclear cells and leukocytes from mesenteric lymph nodes of primiparous lactating Holstein cows. *Journal of Dairy Science*, 106(4), 3008-3022. doi: [10.3168/jds.2022-22520](https://doi.org/10.3168/jds.2022-22520).
- [12] Labunska, I., Levchuk, S., Kashparov, V., Holiaka, D., Yoschenko, L., Santillo, D., Johnston, P. (2021). Current radiological situation in areas of Ukraine contaminated by the Chernobyl accident: Part 2. Strontium-90 transfer to culinary grains and forest woods from soils of Ivankiv district. *Environment International*, 146, article number 106282. doi: [10.1016/j.envint.2020.106282](https://doi.org/10.1016/j.envint.2020.106282).
- [13] Law of Ukraine No. 791a-XII "On the Legal Regime of the Territory that has been Subjected to Radioactive Contamination as a Result of the Chernobyl Disaster". (1991, February). Retrieved from <https://zakon.rada.gov.ua/laws/show/791%D0%B0-12>.
- [14] Lazarev, M., Klepko, A., & Kalachniuk, L. (2024). *Biochemical blood parameters of cattle during long-term detention in a radionuclide-contaminated territory*. Kyiv: NULES of Ukraine.
- [15] Lazarev, M.M., Klepko, & A.V. (2023). Assessment of hematological and immunological blood parameters in cattle with "Iodine" pathology after the Chernobyl accident. *Biological Systems: Theory and Innovations*, 14(1-2), 5-12. doi: [10.31548/biologiya14\(1-2\).2023.008](https://doi.org/10.31548/biologiya14(1-2).2023.008).
- [16] Liu, T., et al. (2020). Ultrasmall copper-based nanoparticles for reactive oxygen species scavenging and alleviation of inflammation related diseases. *Nature Communications*, 11(1), article number 2788. doi: [10.1038/s41467-020-16544-7](https://doi.org/10.1038/s41467-020-16544-7).
- [17] Mushawwir, A., Arifin, J., Darwis, D., Puspitasari, T., Pengerteni, D.S., Nuryanthi, N., & Perman, R. (2020). Liver metabolic activities of Pasundan cattle induced by irradiated chitosan. *Biodiversitas Journal of Biological Diversity*, 21(12), 5571-5578. doi: [10.13057/biodiv/d211202](https://doi.org/10.13057/biodiv/d211202).
- [18] Ostapchenko, L.I., Kalachniuk, L.H., Garmanchuk, L.V., Kuchmerovska, T.M., Arnauta, O.V., Arnauta, N.V., & Smirnov, O.O. (2019). *Theoretical and methodical fundaments of the study of metabolic processes in human and animals using blood indicators*. Kyiv: NPE Yamchynskyi O.V.
- [19] Pareniuk, O., & Yasuda, N. (2021). Chernobyl exclusion zone: Current status and challenges. *Annals of the ICRP*, 50(1), 201-208. doi: [10.1177/01466453211028032](https://doi.org/10.1177/01466453211028032).
- [20] Pegolo, S., Giannuzzi, D., Piccioli-Cappelli, F., Cattaneo, L., Ganesella, M., Ruegg, P.L., Trevisi, E., & Cecchinato, A. (2023). Blood biochemical changes upon subclinical intramammary infection and inflammation in Holstein cattle. *Journal of Dairy Science*, 106(9), 6539-6550. doi: [10.3168/jds.2022-23155](https://doi.org/10.3168/jds.2022-23155).
- [21] Razavi, S.M., Yaghoobpour, T., & Nazifi S. (2023) A review on acute phase response in parasitic blood diseases of ruminants. *Research in Veterinary Science*, 165, article number 105055. doi: [10.1016/j.rvsc.2023.105055](https://doi.org/10.1016/j.rvsc.2023.105055).
- [22] Talerko, M.M., Lev, T.D., Drozdovitch, V.V., & Masiuk, S.V. (2020). Reconstruction of the radioactive contamination of the territory of Ukraine by Iodine-131 during initial period of the Chernobyl accident using the results from numerical model WRF. *Problems of Radiation Medicine and Radiobiology*, 25(8), 285-299. doi: [10.33145/2304-8336-2020-25-285-299](https://doi.org/10.33145/2304-8336-2020-25-285-299).
- [23] Vlizlo V.V., et al. (2012). *Laboratory research methods in biology, animal husbandry and veterinary medicine*. Lviv: SPOLOM.
- [24] von Zallinger, C., & Tempel, K. (1998). The physiologic response of domestic animals to ionizing radiation: A review. *Veterinary Radiology & Ultrasound*, 39(6), 495-503. doi: [10.1111/j.1740-8261.1998.tb01639.x](https://doi.org/10.1111/j.1740-8261.1998.tb01639.x).
- [25] Yang, H., Liu, L., Wang, M., Li, J., Wang, N.S., Du, G., & Chen, J. (2012). Structure-based engineering



of methionine residues in the catalytic cores of alkaline amylase from *alkalimonas amylolytica* for improved oxidative stability. *Applied and Environmental Microbiology*, 78(21), 7519-7526. doi: [10.1128/AEM.01307-12](https://doi.org/10.1128/AEM.01307-12).

Біохімічні показники крові великої рогатої худоби за дії радіаційного опромінення

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Анотація. У сучасних умовах актуальним є вивчення адаптаційних процесів живих організмів, особливо дослідження біохімічних показників крові великої рогатої худоби (ВРХ) за її тривалого утримання на забрудненій радіонуклідами території. Метою роботи було визначити біохімічні показники крові, проаналізувати характерні зміни, їхній вплив на стан здоров'я тварин та оцінити ступень ураження організму радіоактивними ізотопами йоду. Визначено біохімічні показники (активність амілази, аспартат – і аланінамінотрансфераз (АСТ і АЛТ), глутатіонпероксидази (ГПО), концентрацію гідроперекисів ліпідів (ГПЛ), вмісту церулоплазміну, рівень загального білка у плазмі крові великої рогатої худоби за традиційними методами визначення біохімічних показників) і встановлено, що їхні значення коливаються в широких межах, але вони суттєво не відрізняються між групами тварин, котрі зазнали впливу різних доз іонізуючого опромінення (1 Гр на організм, 2 Гр на шлунково-кишковий тракт і до 40 Гр на щитоподібну залозу) за рахунок чорнобильських радіоактивних випадань, враховуючи радіоактивний йод на щитоподібну залозу, і тварин, що утримувалися на відносно чистій території, тобто без суттєвих доз опромінення (на рівні декількох мГр). Проаналізовано характерні зміни біохімічних показників та ймовірні зміни стану здоров'я і встановлено: за умов опромінення щитоподібної залози у великих дозах (40 Гр на ЩЗ) в організмі спрацьовують потужні механізми адаптації, які нівелюють на організменному рівні негативну дію іонізуючої радіації і зберігають такі важливі господарські ознаки як відтворювання і продуктивність. Звідси, дані дослідження можуть бути підґрунтям для формування системи заходів регуляції механізмів адаптації організмів за впливу екопатогенних факторів

Ключові слова: йод стабільний (^{127}I); йод радіоактивний (^{131}I); забруднена радіонуклідами територія; щитоподібна залоза; кров; ензимна активність; біохімічні показники





The current state of species diversity of insect geobionts in disturbed biotopes of Kyiv Polissya

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Abstract. Soil insects (geobionts), which live in the soil and subsoil permanently or for a certain period of their life cycle are central in the biodiversity of entomofauna. Preservation and rational use of natural biodiversity are becoming one of the priority tasks for biologists, ecologists, and entomologists. The study aimed to conduct faunal analysis of the entomological biodiversity of geobionts in the disturbed biotopes of Kyiv Polissya due to anthropogenic activity. The study determined the current state of the entomological biodiversity of geobionts in the disturbed biotopes of Kyiv Polissya, in particular within the settlements of Lyutizh, Demydiv, Kozarovychi, Huta Mezhyhirska and Gostomel, located in the floodplain of the Irpin River (Vyshhorod district, Kyiv region, Ukraine). The dynamics of species in the period 2022-2024 was analysed, their systematic affiliation was established, and the impact of anthropogenic factors on the composition of the entomofauna of the studied territories was assessed. In the context of reduced biodiversity levels biocenoses, it is relevant to conduct research on the real state and distribution of species, as well as create a list of existing entomological biodiversity. For research on entomological diversity, traditional methods of accounting for entomofauna were used. As a result of the research and analysis of the current state and the compilation of a list of entomological biodiversity of geobionts in biotopes disturbed as a result of anthropogenic activity, 56 species of geobiont insects from 11 families of 4 orders were identified. The dominant order in terms of families and species was the Coleoptera order, which included 53 species from 8 families, which accounted for 94.6% of the total amount of studied entomological biodiversity. The conducted studies of the records of the entomological biodiversity of geobionts will contribute to the preservation and restoration of natural biodiversity in Kyiv Polissya Ukraine

Keywords: analytical studies; faunal studies; structure of entomofauna; order; family; monitoring

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INTRODUCTION

Analysis of the current state of species diversity of insect-geobionts in damaged biotopes of Kyiv Polissya is relevant for determination of the ecological processes occurring in these regions in the context of changes caused by anthropogenic impact, climate change and degradation of natural environments. Disturbed biotopes, such as deforestation, agricultural land and other anthropogenic changes, can significantly affect the structure of biocoenoses, including the number and composition of insect species, which are several components of these ecosystems. Other aspects, such as mechanisms of adaptation and migration of insects, and their role in the restoration of damaged biotopes, are also noteworthy. Analysis of these processes can be used to assess the impact of human activity on biodiversity and develop measures to preserve natural environments. Research into the species diversity of geobiont insects can not only determine the state of the ecosystem but also develop strategies for restoring biodiversity in the face of changes occurring in the ecosystems of Kyiv Polissya.

Insects account for more than half of the planet's biodiversity. According to R. McLellan *et al.* (2020), the presence of entomological biodiversity in an optimal amount in a biogeocenosis ensures ecological stability. Among the entire biodiversity of entomofauna, soil insects (geobionts), which live in the ground, soil and subsoil permanently or for a certain period of their life cycle are central (Pivtoraiko *et al.*, 2022; Vagaliuk *et al.*, 2024). As noted by C.A. Hallmann *et al.* (2021), and F. Bocchi *et al.* (2022), some insect species spend their entire life cycle in the soil, and some only during certain periods of ontogenesis or at certain intervals. A.Y. Kawahara *et al.* (2021), and O.L. Klyachenko *et al.* (2022) have studied that many species of geobiont insects spend their larval and some pupal periods in the soil. Among insects with incomplete transformation, *Gryllotalpa gryllotalpa* (Linnaeus, 1758) was noted. Among insects with complete metamorphosis are many species of the families Carabidae, Staphylinidae, Elateridae, Tenebrionidae, Scarabaeidae, Crysomelidae (species of the genus *Sagrinae*), some species of the families Cerambycidae, Curculionidae, Myrmeleonidae, Bibionidae, Tipulidae, Stratiomyidae, Tabanidae,

Asilidae, Therevidae, as well as species from the genera *Apodea*, *Sphecodea*, etc.

According to a study by T.A. Hallman & W.D. Robinson (2020), conducted in the soil environment, the number of entomofauna geobionts on average in 1 m² of soil contains from several tens to several hundred. According to C. Lopez-Vaamonde *et al.* (2021), the impact of insects on the soil is substantial. It is determined by their nutrition and burrowing ability. By moving in the soil, insects affect its aeration, structure, etc. Insects can mix the soil, carry its particles from deeper layers to the upper horizons, and vice versa, bring them deeper. S. Seibold *et al.* (2019) noted that many soil insects are exclusively saprophages or caprophages, most others also partially feed on organic residues. This helps accelerate the destruction of organic residues and has a positive effect on soil humification processes. A study by A.D. Barnosky *et al.* (2012), as well as special laboratory studies, confirmed that in the absence of soil invertebrates, the accumulation of humic substances occurs very slowly or stops altogether.

The aforementioned indicates that insect geobionts are substantial in the biological cycle of organic matter movement in nature under normal conditions of existence for insects. To determine the significance and impact of the entomological biodiversity of geobionts on the soil environment, studies were conducted in various biotopes: natural and disturbed by human activity. Review of the sources on the selected topic determined that the current state of the entomological biodiversity of the entomofauna of geobionts in the biotopes of Kyiv Polissya that were affected by human activity were not studied sufficiently. The study aimed to conduct faunal studies of the entomological biodiversity of geobionts in the biotopes of Kyiv Polissya that have been disturbed as a result of anthropogenic activity.

MATERIALS AND METHODS

The study was conducted in two stages. The first stage included an analysis of literature sources (Didukh, 2017; Kuzemko *et al.*, 2018; Minyailo *et al.*, 2020), which established the composition of the entomofauna of geobionts of the Kyiv Polissya biotopes in the 20th century. The second stage was faunal collections conducted from 2022 to





June 2024, which determined the species diversity of the entomocomplex of geobionts of the disturbed biotopes of Kyiv Polissya.

The studied biotopes of Kyiv Polissya, affected by anthropogenic activity, were located in the Vyshgorod district of Kyiv region. These areas included flooded and waterlogged ones near the settlements of Lyutizh, Demydiv, Kazarovychi, Huta Mezhyhirska, and Hostomel, within the floodplain of the Irpin River. The research was conducted from 2022 to June 2024. The following soil types occurred in the research area: gray podzolised chernozem, and typical weakly humus-rich light loams (Lisovoy *et al.*, 1999; Sozinov, 2005). The vegetation cover of the studied biotopes was represented mainly by wild vegetation. The terrain was slightly undulating.

Regarding the study of entomofauna in areas negatively affected by anthropogenic activity: following the Russian invasion of the Kyiv region, the water pumping station from the Irpin River to the Dnieper River in the village of Kazarovychi lost power and thus stopped. As a result, the channel and floodplain of the Irpin River were flooded to a depth of more than 2 meters. These changes created difficult conditions for free movement in the area and for conducting entomological biodiversity surveys. The flooding caused significant damage to the natural environment and biodiversity: trees, shrubs, and grassy vegetation were soaked; adults,

larvae, pupae, and eggs of soil insects perished; and many small, mouse-like rodents also died.

The identification and determination of the systematic affiliation of the entomological biodiversity of geobionts was conducted at the National University of Life and Environmental Sciences of Ukraine, the Department of Ecobiotechnology and Biodiversity (chamber studies). During the research, analytical, statistical and experimental methods were used, approved and recommended for field, forest and laboratory research in entomology, ecology and plant protection (Sozinov, 2005; Minyailo *et al.*, 2020; Klyachenko *et al.*, 2022).

The collection and registration of the entomological biodiversity of geobionts were conducted using generally accepted methods (Hallman & Robinson, 2020; Vagaliuk *et al.*, 2024) once every 7-10 days at stationary sites. The taxonomic affiliation of biological collections was determined using an entomological identifier (Lisovoy *et al.*, 1999). The research was conducted following ethical standards and compliance with relevant requirements and standards, in particular, complying with the requirements of the Convention on Biological Diversity (1992).

RESULTS AND DISCUSSION

Based on the results of analytical and faunal studies, a list of the biodiversity of insect geobionts was compiled (Table 1).

Table 1. List of known and existing biodiversity of geobiont insects in the biotopes of Kyiv Polissya (presence (+) or absence (–) of the species during faunal studies

Order, family, insect species	Presence+/absence– of species
Orthoptera; Gryllotalpidae	
1. <i>Gryllotalpa gryllotalpa</i> (Linnaeus, 1758)	+
Dermatoptera; Forficulidae	
2. <i>Forficula auricularia</i> (Linnaeus, 1758)	+
3. <i>Forficula tomis</i> (Kolenati, 1846)	–
Homoptera; Cixiidae	
4. <i>Pentastiridius leporinus</i> (Linnaeus, 1761)	–
Diptera; Tipulidae	
5. <i>Tipula paludosa</i> (Meigen, 1830)	+
Coleoptera; Silphidae	
6. <i>Silpha obscura</i> (Linnaeus 1758)	+
Carabidae	
7. <i>Pterostichus vernalis</i> (Panzer, 1795)	+
8. <i>Harpalus distinguendus</i> (Duftschmid, 1812)	+
9. <i>Harpalus luteicornis</i> (Duftschmid, 1812)	+
10. <i>Broscus cephalotes</i> (Linnaeus, 1758)	+
11. <i>Calathus erratus</i> (Sahlberg, 1827)	+





Table 1. Continued

Order, family, insect species	Presence+/absence- of species
12. <i>Bembidion properans</i> (Stephens, 1828)	+
13. <i>Amara aenea</i> (De Geer, 1774)	+
14. <i>Amara familiaris</i> (Duftschmid, 1812)	+
15. <i>Pterostichus cupreus</i> (Linnaeus, 1758)	+
16. <i>Pterostichus melanarius</i> (Illiger, 1798)	+
17. <i>Amara plebeja</i> (Gyllenhal, 1810)	+
18. <i>Amara similata</i> (Gyllenhal, 1810)	+
19. <i>Amara spreta</i> (Dejean, 1831)	+
20. <i>Amara bifrons</i> (Gyllenhal, 1810)	+
21. <i>Amara convexiuscula</i> (Marsham, 1802)	–
22. <i>Amara consularis</i> (Duftschmid, 1812)	+
23. <i>Amara ingenua</i> (Duftschmid, 1812)	+
24. <i>Zabrus tenebrioides</i> (Goeze, 1777)	+
Scarabaeidae	
25. <i>Pentodon idiota</i> (Herbst, 1789)	+
26. <i>Anomala dubia</i> (Scopoli, 1763)	–
27. <i>Anomala errans</i> (Fabricius, 1775)	–
28. <i>Phyllopertha horticola</i> (Linnaeus, 1758)	–
29. <i>Anisoplia segetum</i> (Herbst, 1783)	+
30. <i>Anisoplia austriaca</i> (Herbst, 1783)	+
31. <i>Anisoplia deserticola</i> (Fischer von Waldheim, 1824)	–
32. <i>Melolontha melolontha</i> (Linnaeus, 1758)	
33. <i>Melolontha hippocastani</i> (Fabricius, 1801)	–
34. <i>Polyphylla fullo</i> (Linnaeus, 1758)	–
35. <i>Anoxia pilosa</i> (Fabricius, 1792)	+
36. <i>Rhizotrogus aestivus</i> (Olivier, 1789)	+
37. <i>Miltotrogus vernus</i> (Germar, 1823)	+
38. <i>Miltotrogus aeguinoctialis</i> (Herbst, 1790)	–
39. <i>Amphimallon solstitialis</i> (Linnaeus, 1758)	–
40. <i>Serica brunnea</i> (Linnaeus, 1758)	–
41. <i>Maladera holosericea</i> (Scopoli, 1772)	–
42. <i>Hoplia parvula</i> (Krynicky, 1832)	+
Elateridae	
43. <i>Selatosomus latus</i> (Fabricius, 1801)	+
44. <i>Selatosomus aeneus</i> (Linnaeus, 1758)	+
45. <i>Cidnopus aeruginosus</i> (Olivier, 1790)	–
46. <i>Athous jejunos</i> (Kiesenwetter, 1858)	+
47. <i>Melaotus brunnipes</i> (Germar, 1824)	–
48. <i>Agriotes lineatus</i> (Linnaeus, 1767)	+
49. <i>Agriotes obscurus</i> (Linnaeus, 1758)	+
50. <i>Agriotes sputator</i> (Linnaeus, 1758)	+
Alleculidae	
51. <i>Podonta daghestanica</i> (Reitter, 1885)	+
Tenebrionidae	
52. <i>Opatrum sabulosum</i> (Linnaeus, 1761)	+
53. <i>Opatrum riparium</i> (Gerhardt, 1896)	+
54. <i>Crypticus quisquilius</i> (Linnaeus, 1761)	+
55. <i>Oodescelis polita</i> (Sturm, 1807)	+
56. <i>Pedinus femoralis</i> (Linnaeus, 1767)	+
Chrysomelidae	
57. <i>Leptinotarsa decemlineata</i> (Say, 1824)	–
58. <i>Phyllotreta vittula</i> (Redtenbacher 1849)	+





Table 1. Continued

Order, family, insect species	Presence+/absence– of species
Curculionidae	
59. <i>Otiorrhynchus fullo</i> (Schrank, 1781)	–
60. <i>Otiorrhynchus ligustici</i> (Linnaeus, 1758)	+
61. <i>Otiorrhynchus raucus</i> (Fabricius, 1776)	–
62. <i>Otiorrhynchus singularis</i> (Linnaeus, 1767)	–
63. <i>Phyllobius maculicornis</i> (Germar, 1824)	–
64. <i>Phyllobius viridicollis</i> (Fabricius, 1792)	–
65. <i>Phyllobius urticae</i> (De Geer, 1775)	–
66. <i>Sciaphobus squalidus</i> (Gyllenhal, 1834)	–
67. <i>Brachysomus echinatus</i> (Bonsdorff, 1785)	–
68. <i>Cneorrhinus albinus</i> (Boheman, 1833)	–
69. <i>Sitona crinitus</i> (Herbst, 1795)	+
70. <i>Sitona cylindricollis</i> (Fahraeus, 1840)	+
71. <i>Sitona flavescens</i> (Marsham, 1802)	+
72. <i>Sitona griseus</i> (Fabricius, 1775)	+
73. <i>Sitona hispidulus</i> (Fabricius, 1776)	+
74. <i>Sitona humeralis</i> (Stephens, 1829)	+
75. <i>Sitona inops</i> (Gyllenhal, 1834)	+
76. <i>Sitona lineatus</i> (Linnaeus 1758)	+
77. <i>Sitona longulus</i> (Gyllenhal, 1834)	+
78. <i>Sitona puncticollis</i> (Stephens, 1831)	+
79. <i>Sitona sulcifrons</i> (Thunberg, 1798)	+
80. <i>Sitona tibialis</i> (Herbst, 1795)	–
81. <i>Tanymecus palliatus</i> (Fabricius, 1787)	+
82. <i>Chlorophanus viridis</i> (Linnaeus, 1758)	–
83. <i>Bothynoderes punctiventris</i> (Germar, 1794)	+
84. <i>Chromoderus fasciatus</i> (Müller, 1776)	–
85. <i>Cyphocleonus tigrinus</i> (Panzer, 1789)	–

Source: compiled by the authors based on Ya.P. Didukh (2017), A.A. Kuzemko *et al.* (2018), A.A. Minyailo *et al.* (2020)

The analysis determined that the biodiversity of geobiont insects in the biotopes of Kyiv Polissya amounted to 85 species and consisted of 5 orders, which included 12 families (Table 2). Ecological analysis of the entomofauna showed that the Coleoptera order had the largest number of families (8), which was 94.08% of the total. The orders Orthoptera, Homoptera, Dermaptera and Diptera – 1 family each, which was 4.68%. The most numerous in terms of species were the Curculionidae, Carabidae and Scarabaeidae families: 27, 18,

and 18 species, respectively. This is attributable to the fact that the larvae of these species have a habitat in the soil, where they spend a fairly significant period of their life cycle – from 1 to 4.5 years, until the emergence of the adult. The families Gryllotalpidae, Cixiidae, Alleculidae, Silphidae and Tipulidae each had 1 species. As a result of faunal studies conducted in biotopes disturbed by anthropogenic activity, 56 species of geobiont insects belonging to 11 families from 4 orders were collected, identified and systematised (Table 3).

Table 2. Taxonomic structure of biodiversity of insects-geobionts of biotopes of Kyiv Polissya according to analytical studies

No.	Order	Family	Species	
			quantity	(%)
1	Orthoptera	Gryllotalpidae	1	1.17
2	Dermaptera	Forficulidae	2	2.35
3	Homoptera	Cixiidae	1	1.17



Table 2. Continued

No.	Order	Family	Species	
			quantity	(%)
4	Coleoptera	Carabidae	18	21.17
		Scarabaeidae	18	21.17
		Elateridae	8	9.41
		Alleculidae	1	1.17
		Tenebrionidae	5	5.88
		Chrysomelidae	2	2.35
		Curculionidae	27	31.76
		Silphidae	1	1.17
5	Diptera	Tipulidae	1	1.17
Total	5	12	85	100

Source: developed by the authors based on Ya.P. Didukh (2017), A.A. Kuzemko *et al.* (2018), A.A. Minyailo *et al.* (2020)

Table 3. Taxonomic structure of biodiversity of geobiont insects of disturbed biotopes of Kyiv Polissya during faunal studies, 2022-2024

No.	Order	Family	Species	
			quantity	(%)
1	Coleoptera	Carabidae	17	30.35
		Scarabaeidae	8	14.28
		Elateridae	6	10.71
		Tenebrionidae	5	8.92
		Curculionidae	14	25.0
		Chrysomelidae	1	1.78
		Silphidae	1	1.78
		Alleculidae	1	1.78
2	Orthoptera	Gryllotalpidae	1	1.78
3	Dermatoptera	Forficulidae	1	1.78
4	Diptera	Tipulidae	1	1.78
Total	4	11	56	100

Source: compiled by the authors

The largest number of species (17) belongs to the family Carabidae, the family Curculionidae – 14 species, Scarabaeidae – 8, Elateridae – 6, Tenebrionidae – 5 species, and Silphidae, Alleculidae, Gryllotalpidae, Forficulidae, Tipulidae – had 1 species each. Thus, the soil entomofauna in 2022-2024 was represented mainly by the order Coleoptera (82.26%), in which the dominant species were the Carabidae family: *Pterostichus vernalis* (Panzer, 1795), *Harpalus distinguendus* (Duftschmid, 1812), *Broscus cephalotes* (Linnaeus, 1758), *Amara similata* (Gyllenhal, 1810), *Amara aenea* (De-Geer, 1774), *Amara familiaris* (Duftschmid, 1812), *Calathus erratus* (Sahlberg, 1827), *Bembidion*

properans (Stephens, 1828), *Harpalus luteicornis* (Duftschmid, 1812), which is 30.0% of the total, and Curculionidae: *Otiorrhynchus ligustici* (Linnaeus, 1758), *Sitona crinitus* (Herbst, 1795), *Sitona humeralis* (Stephens, 1829), *Sitona lineatus* (Linnaeus 1758), *Sitona longulus* (Gyllenhal, 1834), *Sitona puncticollis* (Stephens, 1831), which was 25.0%.

The most numerous families (Carabidae, Curculionidae, Scarabaeidae) of the Coleoptera order occupied 69.63% of the total in terms of species. A comparison of the taxonomic structure of the existing entomofauna of geobionts with the known science indicated a significant decrease in species biodiversity (Fig. 1).

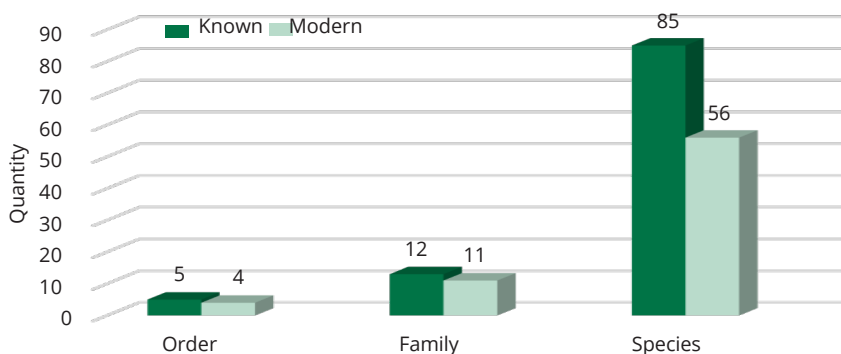


Figure 1. Comparative analysis of the results of the study of the known and current state of biodiversity of insect geobionts of biotopes of Kyiv Polissya by orders, families, and species

Source: compiled by the authors

Thus, the family Carabidae was represented by 17 compared to the known 18 species (a decrease of 1.05 times); Curculionidae – 14 against 27 (1.92 times); Scarabaeidae, respectively, – 8 against 18 (2.25 times); Elateridae – 6 against 8 (1.33 times); Tenebrionidae – 5 against 5; families Chrysomelidae and Forficulidae – 1 against 2 (2 times). Following the above analysis, the families Gryllotalpidae, Alleculidae, Tipulidae and Silphidae remained unchanged in species composition and were represented by one species per family.

Significant changes occurred in the taxonomic structure of the geobiont entomological complex. Thus, the number of orders decreased from 5 to 4, families from 12 to 11, and species from 85 to 56. The authors did not identify a significant part of the species (29), which will be the subject of further research and analysis. Analysis of the dynamics of the number of species of the entomological biodiversity of geobionts in biotopes disturbed by anthropogenic activity showed the following (Fig. 2).

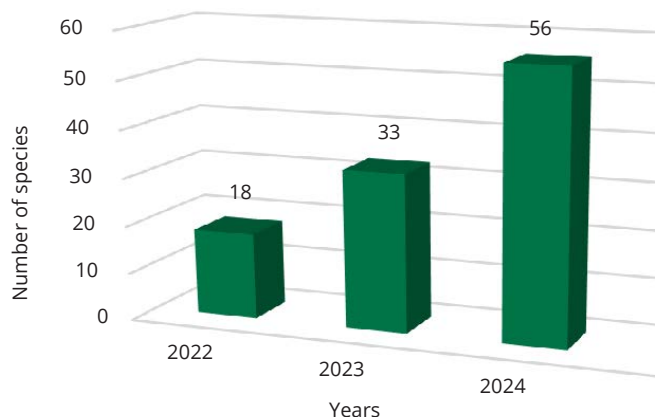


Figure 2. Dynamics of the number of geobiont insect species by year (biotopes of Kyiv Polissya disturbed due to anthropogenic activities)

Source: compiled by the authors

In 2022, the number of species was critically low – 18. It was caused by various reasons: stress and death of insects (adults, larvae, pupae, eggs) caused by flooding of biotopes with water, inaccessible places for surveys, etc. Studies in 2023 and

2024 showed an increase in the number of insect geobiont species at the level of 33-56, the result of which was the restoration of natural potential (migration to soil islands and settlement of flooded coastal areas) (see Fig. 2). In the spring and



summer, migratory activity and colonisation of disturbed biotopes by entomological biodiversity of the soil environment will increase.

Research on the ecological state of river basins according to O.O. Sydorenko (2011) ensured conservation and conservation of nature. At the same time, the ecosystem approach was based on ecological aspects and research methodology, which is primarily used to identify key factors that affect the life of the river basin and interact with the surrounding environment. I. Zagorodnik *et al.* (2023) noted that the study of diversity focused on the expressions: “rarity”, “threatened” and “extinction”, which in practice was manifested in the preservation of rare and endangered genetic, taxonomic and ecological units, while the greater part of living beings remained beyond the focus of the researcher.

S.R. Loarie *et al.* (2009) stated that populations of species were responding to global climate change by shifting their geographical ranges to regions with suitable climatic conditions or by remaining in their current locations and adapting phenotypically or genetically. Insects are responding to recent climate change in a variety of ways, including shifting their geographic ranges to cooler climates. The ability of a species to change its geographic range depended on its ability to disperse, and on physiological and behavioural adaptations that were able to keep pace with the rate of climate change. The survival of species may depend not only on their ability to adapt to changing climates but also on the extent to which the climate is stable. I. Zagorodnik (2012) noted that the extinction of species was an evolutionary process, which was an objective fact, as was their appearance. Extinction liberated a biological niche for new species. However, in every biotope, some species became extinct due to changes in the habitat and the activity of new species, including invasive ones.

A.A. Protasov (2002) concluded that due to structural and functional complexity, an ecosystem can hardly be fully assessed by only one criterion, which was biodiversity, or rather structural aspects. If biodiversity is in large quantities and abundance, which contributes to sustainable development, then the question of what should be the conditions for obtaining numerical biodiversity is relevant. The author further noted that

a model of changes in groups according to ecological indicators was proposed: a wide range of bioresources and their stability. Still, changes in biodiversity indicators were a reaction not only to environmental conditions. When biodiversity is at a minimum under stressful conditions, it is necessary to positively change these conditions (reduce anthropogenic pressure, reduce pollution, feed and water, etc.) and the biota will begin to increase. However, diversity did not grow monotonically, but, having reached a certain maximum, decreased, even under favourable conditions. Biodiversity was assessed not only by the environment that humans can influence (for example, by creating protected areas) but also by biotic interactions, which were difficult to influence.

In an analysis of biodiversity in a particular area of land or water, E. Morris *et al.* (2014) concluded that it all started with an assessment of species. Firstly, species present in a given area were identified with subsequent compilation of an annotated list. This was the simplest assessment of species diversity. The numerical indicator was “species richness”, the number of species. That indicator, although beneficial, was not very informative for characterising ecological groups, since it did not address the level of representation of each species.

E.M. Dillon *et al.* (2022) noted that the newest direction of biodiversity research was conservation paleobiology, which was currently being formed as a separate interdisciplinary branch of science. The need for such a direction was determined by modern (in the non-ontological sense) conservation biology studies and monitors biodiversity, which was under constant human pressure. Since the temperature state of the environment has changed over geological eras, the combination of the results of palaeontology, archaeology and conservation biology allowed authors to study the impact of stress factors on antiquity and choose promising new approaches to the preservation and restoration of biodiversity.

During the research of the current state of species diversity of geobiont insects in the biotopes of Kyiv Polissya, which were disturbed as a result of military actions, many questions regarding the future state and restoration of the natural floodplain of the Irpin River, as well as the restoration of the natural abundance of





entomological biodiversity and, in particular, the community of geobiont insects that were stressed, became relevant. Measures are needed to restore biodiversity and determine the possible timeframe for this process.

CONCLUSIONS

The analysis of literary sources established that the biodiversity of insect geobionts in the biotopes of Kyiv Polissya amounted to 85 species and consisted of 5 orders, which included 12 families. The ecological analysis of the entomofauna demonstrated that the order Coleoptera had the largest number of families (8), which was 94.08% of the total. The orders Orthoptera, Homoptera, Dermaptera and Diptera – 1 family each, which was 4.68%. The most numerous in terms of species were the families Curculionidae, Carabidae and Scarabaeidae: 27, 18, and 18 species, respectively. Faunistic studies (2022-2024) of the entomological biodiversity of geobionts of Kyiv Polissya in biotopes disturbed by anthropogenic activity identified 56 species that systematically belong to 11 families from 4 orders. The study determined that the soil entomofauna is represented mainly by the order of Coleoptera (82.26%), in which the dominant species are *Pterostichus vernalis* (Panzer, 1795), *Harpalus distinguendus* (Duftschmid, 1812), *Broscus cephalotes* (Linnaeus, 1758), *Amara similata* (Gyllenhal, 1810), *Amara aenea* (De Geer, 1774), *Amara familiaris* (Duftschmid, 1812), *Calathus erratus* (Sahlberg, 1827), *Bembidion properans* (Stephens, 1828), *Harpalus luteicornis* (Duftschmid, 1812), family Carabidae which is 30.0% of the total, and *Otiorrhynchus ligustici* (Linnaeus, 1758), *Sitona crinitus* (Herbst, 1795),

Sitona humeralis (Stephens, 1829), *Sitona lineatus* (Linnaeus 1758), *Sitona longulus* (Gyllenhal, 1834), *Sitona puncticollis* (Stephens, 1831) of the family Curculionidae, which is 25.0%.

The state of the known and modern entomofauna of geobionts was compared and, determining that significant changes have occurred in the taxonomic structure of the entomocomplex of geobionts: the number of orders decreased from 5 to 4, families from 12 to 11, species from 85 to 56. A significant part of the species (29) was not found. The current dynamics of the entomological biodiversity of geobionts of Kyiv Polissya were studied and analysed, which was positively reflected by the years: 2022 – 18 species, 2023 – 33 species, 2024 – 56 species.

The study determined the real state of the existing entomological biodiversity of geobionts in the biotopes of Kyiv Polissya was disturbed as a result of anthropogenic activity. Further research will be should be conducted as the studied biotopes that were subjected to negative human influence did not return to their previous state (until 2022). Furthermore, 4 years is a rather short period for the natural reproduction of biodiversity. Future research will address long-term monitoring of population dynamics, assessing trends in species adaptation to environmental changes, and developing conservation strategies for biodiversity preservation in affected biotopes.

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CONFLICT OF INTEREST

None.

REFERENCES

- [1] Barnosky, A.D., et al. (2012). Approaching a state shift in Earth's biosphere. *Journal of Nature*, 486, 52-58. doi: [10.1038/nature11018](https://doi.org/10.1038/nature11018).
- [2] Bocchi, F., Bokulich, A., Castillo Brache, L., Grand-Pierre, G., & Watkins, A. (2022). Are we in a sixth mass extinction? The challenges of answering and value of asking. *The British Journal for the Philosophy of Science*. doi: [org/10.1086/722107](https://doi.org/10.1086/722107).
- [3] Convention on Biological Diversity. (1992, June). Retrieved from https://zakon.rada.gov.ua/laws/show/995_030#Text.
- [4] Didukh, Ya.P. (2017). A classification scheme of shrub biotopes of Ukraine. *Ukrainian Botanical Journal*, 74(4), 347-354. doi: [10.15407/ukrbotj74.04.347](https://doi.org/10.15407/ukrbotj74.04.347).
- [5] Dillon, E.M., et al. (2022). What is conservation paleobiology? Tracking 20 years of research and development. *Frontiers in Ecology and Evolution*, 10. doi: [10.3389/fevo.2022.1031483](https://doi.org/10.3389/fevo.2022.1031483).



- [6] Hallman, T.A., & Robinson, W.D. (2020). Comparing multi- and single-scale species distribution and abundance models built with the boosted regression tree algorithm. *Landscape Ecology*, 35(5), 1161-1174. doi: [10.1007/s10980-020-01007-7](https://doi.org/10.1007/s10980-020-01007-7).
- [7] Hallmann, C.A., Ssymank, A., Sorg, M., de Kroon, H., & Jongejans, E. (2021). Insect biomass decline scaled to species diversity: General patterns derived from a hoverfly community. *Proceedings of the National Academy of Sciences of the U.S.A.*, 118(2). doi: [10.1073/pnas.2002554117](https://doi.org/10.1073/pnas.2002554117).
- [8] Kawahara, A.Y., Reeves, L.E., Barber, J.R., & Black, S.H. (2021). Eight simple actions that individuals can take to save insects from global declines. *Proceedings of the National Academy of Sciences of the U.S.A.*, 118(2), article number e2002547117. doi: [10.1073/pnas.2002547117](https://doi.org/10.1073/pnas.2002547117).
- [9] Klyachenko, O.L., Lisovsky, M.M., & Kvasko, O.Yu. (2022). *Fundamentals of biodiversity*. Kyiv: National University of Life and Environmental Sciences of Ukraine.
- [10] Kuzemko, A.A., Didukh, Ya.P., Onyshchenko, V.A., & Sheffer, Ya. (2018). *National catalogue of biotopes of Ukraine*. Kyiv: FOP Klymenko Yu.Ya.
- [11] Lisovoy, M.P., Bublyk, L.I., Vasechko, G.I., & Vasyliiev, V.P. (1999). *Handbook on plant protection*. Kyiv: Urojai.
- [12] Loarie, S.R., Duffy, P.B., Hamilton, H., Asner, G.P., Field, C.B., & Ackerly, D.D. (2009). The velocity of climate change. *Nature*, 462(7276), 1052-1055. doi: [10.1038/nature08649](https://doi.org/10.1038/nature08649)
- [13] Lopez-Vaamonde, C., Kirichenko, N., & Ohshima, I. (2021). Collecting, rearing, and preserving leaf-mining insects. In *Measuring arthropod biodiversity* (pp. 439-466). Cham: Springer. doi:[10.1007/978-3-030-53226-0_17](https://doi.org/10.1007/978-3-030-53226-0_17).
- [14] McLellan, R., Iyengar, L., Jeffries, B. & Oerlemans, N. (2020). *Living planet report 2020: people and places, species and spaces*. Gland: WWF.
- [15] Minyailo, A.A., Minyailo, N.V., & Chaika, V.M. (2020). Main environmental factors identification of disappearance of biota species in Ukraine. *Scientific Reports of the National University of Life and Environmental Sciences of Ukraine*, 16(3), 38-48. doi: [10.31548/dopovidi2020.03.004](https://doi.org/10.31548/dopovidi2020.03.004).
- [16] Morris, E., et al. (2014). Choosing and using diversity indices: Insights for ecological applications from the German biodiversity exploratories. *Ecology and Evolution*, 4(18), 3514-3524. doi: [10.1002/ece3.1155](https://doi.org/10.1002/ece3.1155).
- [17] Pivtoraiko, V., Kabanets, V., & Vlasenko, V. (2022). Diversity of the entomocomplex of the grass stand of a hemp field in the North-Eastern forest-steppe of Ukraine. *Scientific Horizons*, 25(4), 18-29. doi: [10.48077/scihor.25\(4\).2022.18-29](https://doi.org/10.48077/scihor.25(4).2022.18-29).
- [18] Protasov A.A. (2002). *Biodiversity and its assessment. Conceptual diversification*. Kyiv: Institute of Hydrobiology of the National Academy of Sciences of Ukraine.
- [19] Seibold, S., et al. (2019). Arthropod decline in grasslands and forests is associated with landscape-level drivers. *Nature*, 574, 671-674. doi:[10.1038/s41586-019-1684-3](https://doi.org/10.1038/s41586-019-1684-3).
- [20] Sozinov, O.O. (2005). *Agrobiodiversity of Ukraine: Theory, methodology, indicators, examples*. Kyiv: CJSC "Nichlava".
- [21] Sydorenko, O.O. (2011). *Flora of the floodplain of the Trubizh and Irpin rivers, its systematic and biomorphological analysis*. *Land Reclamation and Water Management*, 99, 120-128.
- [22] Vagaliuk, L., Lisovsky, M., & Palamarchuk, S. (2024). *Biodiversity and its conservation*. Kyiv: National University of Life and Environmental Sciences of Ukraine.
- [23] Zagorodniuk, I. (Ed.). (2012). *Dynamics of biodiversity 2012*. Luhansk: Taras Shevchenko Luhansk University Press.
- [24] Zagorodniuk, I., Barkaszi, Z., Protasov, O., & Prydatko-Dolin, V. (2023). The biodiversity concept in crisis? Global tendencies and a view from Ukraine. *Geo&Bio*, 24, 183-213. doi: [10.53452/gb2413](https://doi.org/10.53452/gb2413).



Сучасний стан видового різноманіття комах-геобіонтів порушених біотопів Київського Полісся

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Анотація. Серед біорізноманіття ентомофауни значну роль відіграють ґрунтові комахи (геобіонти), які мешкають в ґрунті та підґрунті постійно або певний проміжок життєвого циклу. Збереження і раціональне використання природного біорізноманіття стає однією з пріоритетних задач для біологів, екологів, ентомологів. Метою дослідження було провести фауністичні дослідження ентомологічного біорізноманіття геобіонтів в порушених, внаслідок антропогенної діяльності, біотопах Київського Полісся. У результаті дослідження визначено сучасний стан ентомологічного біорізноманіття геобіонтів у порушених біотопах Київського Полісся, зокрема в межах населених пунктів Лютиж, Демидів, Козаровичі, Гута Межигірська та Гостомель, розташованих у заплаві річки Ірпінь (Вишгородський район, Київська область, Україна). Проаналізовано динаміку чисельності видів у період 2022-2024 років, встановлено їх систематичну приналежність та оцінено вплив антропогенних факторів на склад ентомофауни досліджуваних територій. Зурахуванням проблеми зниження рівня чисельності біорізноманіття в біоценозах актуальним і дієвим є проведення досліджень щодо реального стану та розповсюдження видів, а також створення списку наявного ентомологічного біорізноманіття. Для досліджень ентомологічного різноманіття використовували загальновідомі методи обліку ентомофауни. В результаті проведених досліджень і аналізу поточного стану складено список ентомологічного біорізноманіття геобіонтів в порушених, внаслідок антропогенної діяльності, біотопах та виявлено 56 видів комах-геобіонтів із 11 родин 4 рядів. Домінуючим за родинами і видами є ряд Coleoptera, до якого входять 53 види з 8 родин, що становить 94,6 % від загальної кількості дослідженого ентомологічного біорізноманіття. Проведені дослідження обліків ентомологічного біорізноманіття геобіонтів сприятимуть збереженню та відновленню природного біорізноманіття Київського Полісся України

Ключові слова: аналітичні дослідження; фауністичні дослідження; структура ентомофауни; ряд; родина; моніторинг



Influence of meteorological conditions on the yield and seed quality of differently ripened soybean varieties in the central Forest-Steppe

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Abstract. The relationship between meteorological conditions and crop yields is mainly aimed at explaining the impact of climate change on the environment. Fluctuations in air temperature and humidity affect the water balance and are the main factors for increasing or decreasing crop yields. Such hydrothermal variations can affect any region. Despite this, the purpose of the study was to establish the influence of meteorological conditions such as temperature, precipitation, the sum of active temperatures, and the Selyaninov hydrothermal coefficient (HTC) on the yield and quality of seeds of different varieties of differently ripened soybeans *Glycine max* (L.) Merrill of foreign selection in the conditions of the central Forest-Steppe. The study used general scientific and special research methods, in particular, field, laboratory, and statistical. The highest yield on average over the years of research was observed in the standard Mentor variety (2.45 t/ha), which was slightly higher than the Cordoba variety (< 1%). The deviation of the target for the Moravia variety from the standard variety was 7.4%. According to the results, the lowest yield variability was found in the standard Mentor variety (2.57%), the Cordoba variety was also characterised by low variability (5.99%), while in the Moravia variety, this indicator was with an average variability of 17.62%. During the three-year research period, the protein content

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in soybean seeds ranged from 38.75% to 40.31%. All soybean varieties had low trait variability (< 3%). The analysis of the relationship between the yield and quality of seeds of soybean varieties of foreign selection and the main factors of climatic conditions formed in the central Forest-Steppe region was carried out. Correlation analysis showed the degree of influence of various meteorological conditions on the productivity of the soybean varieties under study, which facilitates a more purposeful and balanced approach to the choice of varieties in specific climatic conditions. The results of the conducted studies can be applied in the implementation of measures for a reasonable choice of soybean varieties to ensure consistently high yields during periods of possible adverse meteorological conditions

Keywords: *Glycine max* (L.) Merrill; productivity; sum of active temperatures; sum of precipitation; hydrothermal coefficient; correlation

INTRODUCTION

At the current stage of development of the agricultural industry, one of the main challenges for Ukraine's agricultural sector remains a significant increase and stabilisation of production of legumes, in particular soybeans. Ukraine is a key producer of soybeans in Europe and is one of the world's leading suppliers of this crop, occupying a significant share in the global market. The acreage under soybeans in Ukraine is constantly increasing, which indicates the importance of this crop. Ensuring stable yields of this crop in the context of global and local climate changes is an urgent scientific task.

Soybeans are highly sensitive to the presence of moisture, so its main growing areas in Ukraine are located in the zone with sufficient moisture supply – in the “soybean belt”, which includes the Forest-Steppe zone, Steppe areas with “forest-steppe” conditions and Southern Polissia regions with “forest-steppe” conditions. V.G. Didora *et al.* (2017) noted that the forest-steppe is the main area of soybean production, it is a significant area with suitable soils for growing soybeans, light, heat and water resources, and the duration of the growing season. Given this, the area under this crop should increase in these regions of the country. Despite the fact that most of the territory of Ukraine has favourable agroclimatic conditions for growing soybeans, even in relatively favourable areas, there is a periodic negative impact of extreme weather conditions on this crop.

Weather conditions make significant adjustments to the soybean yield. Drought in the leading regions of intensive soybean production worsens the prospects for its harvest. Temperature is a key climatic factor for growing soybeans. According to M.Y. Shevnikov (2010), due to

the wide diversity of varieties, soy demonstrates high adaptability to different growing conditions, and its distribution area covers territories from the equator to 52-54°N. During the growing season, most varieties require the sum of active air temperatures (above 10°C) from 1,600-2,000°C to 3,200°C. The requirements for active temperatures for different groups of varieties are as follows: for the earliest – maturing varieties – 1,600-1,900°C, for early-maturing varieties – 2,000-2,200°C, medium-maturing – 2,300-2,700°C, medium-late-maturing – 2,800-2,950°C and late-maturing – 3,000-3,200°C.

However, the impact of climate change on soybean quality is a serious problem. Researchers W. Zhu *et al.* (2024) found that factors such as temperature and precipitation caused by climate change have a direct and indirect impact on the growth, development, and quality of soybean. In addition, extreme weather events cause various types of damage to soybean plants, which further affects the quality indicators of seeds – the protein and oil content. Among extreme weather events, drought is the most common and strongly affects the development and yield of soybeans. According to F.A. Alsajri *et al.* (2020), S. Poudel *et al.* (2023), a drought at the beginning of the season can reduce the protein content, but at later stages of crop growth, on the contrary, it increases its content, in contrast to the oil content, which is negatively affected by a late seasonal drought.

An important measure to increase the yield and improve the quality of soybean products is the scientifically based selection of varieties for cultivation. O. Sydiakina & M. Ivaniv (2023) state that the variety is one of the resource-saving elements of cultivation technology, it accounts for up to

30-35% of crop growth, and in extreme weather years it is the variety that plays a crucial role in shaping crop productivity.

According to O.Y. Revtio & O.O. Zolin (2023), Ukraine has a fairly large assortment of soybeans of different ripeness groups: ultra-precocious, early-maturing, medium-early-maturing, medium-maturing, and medium-late-maturing. The State Register of Plant Varieties of Ukraine for 2022 includes 300 different varieties of soybeans, which are represented by breeding in more than 10 countries of the world. The largest share is made up of domestic varieties – 42.3% of the total number of soybean varieties, Canada – 24.7%, France – 16.5%, Austria – 5.1%, Serbia – 2.5%, and Poland – 1.8%. The share of varieties of foreign selection from other countries: Germany, USA, Romania, and Croatia as a whole are 7.1%.

In general, as stated by O.P. Tkachuk *et al.* (2022), for the conditions of the Ukrainian Steppe, mainly medium-ripened and late-ripened varieties are suitable, for the forest-steppe – early-ripened and medium-ripened, and in Polissia – ultra-early- and early-season varieties. In addition, H.M. Zabolotnyi *et al.* (2020) emphasised that when choosing a variety, it is necessary to consider nutritional properties – protein content, which, in turn, affects the cost of grown products. In conditions of intensive farming with extreme weather conditions, it is important to grow several varieties of different ripeness groups on farms.

Among environmental factors, the determining and most influential factors of agricultural productivity are weather and climate. According to conclusions of A.A. Zymaroyeva (2020), trends in climate change can significantly affect crop productivity, despite advances in cultivation technologies. Climate change is projected to be accompanied by an increase in global average temperatures, changes in precipitation patterns, and an increase in the frequency and intensity of extreme weather events, which will undoubtedly have an impact on crop yields.

Thus, obtaining stable yields of this crop in the context of global and local climate changes in Ukraine, in particular due to increased aridisation, is an urgent task. Its implementation is impossible without studying heterogeneous material, sampling the most adapted to arid conditions. Fluctuations in temperature and humidity affect the

water balance and are the main factors for increasing or decreasing the yield of agricultural crops, in particular soybeans. Such hydrothermal variations can affect any region of the country.

The purpose of the study was to identify the influence of agrometeorological conditions on the development of yields of various varieties of cultivated soybean *Glycine max* (L.) Merrill and the main indicators of the quality of seeds of this crop in the south-western part of the Forest-Steppe zone of Ukraine (on the example of the Vinnytsia Oblast).

MATERIALS AND METHODS

The research was conducted in the Forest-Steppe during 2019-2021 on the experimental field of the Institute of Agribiology LLC in Velykyi Mytnyk village, Khmilnyk district, Vinnytsia Oblast (Fig. 1).



Figure 1. Schematic map of the main cultivated areas of soybeans ("soybean belt") in Ukraine and the experiment site

Source: developed by the authors based on V. Petrychenko (2012)

Three soybean varieties *G. max* (L.) Merrill of foreign selection of different maturity groups were grown in experimental crops: Mentor (standard variety, st), Cordoba, and Moravia. Mentor variety: country of creation – France (Euralis Semans); year of registration – 2013; recommended growing area: Forest-Steppe, Polissia, Steppe; direction of use – grain; quality – medium oil; protein content, % – 39.6-40.7; oil content, % – 19.7-20.5; ripeness group – early ripening; yield: Steppe – 19.7 hwt/ha; Forest-Steppe – 22.5 hwt/ha; Polissia – 24.9 hwt/ha; drought resistance: 7.8-9.0 points; lodging resistance: 8.6-9.0 points; shedding resistance: 8.6-9.0 points; resistance to certain types of pests (diseases): peronosporosis – 9.0 points; ascochytosis – 9.0 points; bacteriosis – 9.0 points;

septoria – 9.0 points; fusarium – 9.0 points; growing season duration – 105-115 days.

Cordoba Variety: country of creation – Canada (Agreliant Genetix Inc.); year of registration – 2014; recommended area for cultivation: Forest-Steppe, Polissia, Steppe; direction of use – grain; quality – medium oil; protein content, % – 38.6-39.2; oil content, % – 20.9-22.3; ripeness group – medium early; yield: Steppe – 17.6 hwt/ha; Forest-Steppe – 23.7 hwt/ha; Polissia – 20.7 hwt/ha; drought resistance: 8.1 – resistance to shedding: 8.8-9.0 points; resistance to shedding: 8.5-9.0 points; resistance to certain types of pests (diseases): peronosporosis – 9.0 points; ascochitosis – 9.0 points; bacteriosis – 9.0 points; septoria – 9.0 points; fusarium – 9.0 points; growing season duration – 114-138 days.

Moravia variety: country of creation – Canada (Semenses Prograin Inc.); year of registration – 2011; recommended area for cultivation: Forest-Steppe, Polissia, Steppe (irrigation); direction of use – grain; quality – medium oil; protein content, % – 38-41; oil content, % – 20.5-22.0; ripeness group – medium-ripened; yield: Steppe – 17.6 hwt/ha; Forest-Steppe – 23.7 hwt/ha; Polissia – 20.7 hwt/ha; drought resistance – 8.1-9.0 points; resistance to lodging – 5.0 points; growing season duration – 122-135 days.

The total area of the experiment site was 150 m², accounting – 100 m². The repetition of the experiment was four-fold, the predecessor – fallow, and the method of placing variants in repetition was used by the method of randomised split plots. Agricultural techniques for conducting experiments were generally accepted for the growing area. Type of land – tilled soil. The soil is a typical low-humus, medium-loamy chernozem. When conducting the research, the authors were guided by the methodology of scientific research in agronomy regarding the specific features of research on leguminous crops according to V.G. Didora (2013). Regular phenological observations and biometric surveys were carried out throughout the growing season. The average yield was determined by the ratio of the weight of the harvested crop to the total area of the fields on which it was grown. The content of “crude protein” (protein) was determined by infrared spectroscopy according to DSTU 4117:2007 (2007).

To assess the impact of weather conditions on the yield and quality of soybean seeds, the following indicators were used: air temperature, precipitation, and Selyaninov hydrothermal coefficient (HTC) during the soybean growing season. The meteorological data were obtained from the Khmilnyk hydrometeorological station in Vinnytsia Oblast and recorded using a Bresser weather centre 5-in-1 weather station. HTC was defined as the ratio of the sum of precipitation (ΣR) in mm for a period with average daily air temperatures $> 10^{\circ}\text{C}$ (active growing period) to the sum of temperatures ($\Sigma t > 10^{\circ}\text{C}$) during the same time, reduced by 10 times using the following scale: $\text{HTC} < 0.4$ – very severe drought; HTC from 0.4 to 0.5 – severe drought; HTC from 0.6 to 0.7 – average drought; HTC from 0.8 to 0.9 – weak drought; HTC from 1.0 to 1.5 – sufficient moisture; $\text{HTC} > 1.5$ – excessive moisture. Mathematical and statistical processing of the obtained data was carried out using descriptive and variational statistics methods, using the data processing programmes “IBM SPSS Statistics (v. 23.0)” and “Microsoft Excel 2016”. The variability of a feature was considered insignificant if the coefficient of variation ($V, \%$) did not exceed 10%. If the value of this indicator was more than 10%, but less than 20%, the volatility was considered average. If $V > 20\%$, then the volatility was considered significant. The Pearson pair correlation coefficients were calculated (a certain number from -1 to +1, which characterises the tightness of the linear correlation between the dependent and independent random variables).

Experimental plant research, including the collection of plant material, complied with institutional, national or international guidelines and adhered to the standards of the Convention on Biological Diversity (1992).

RESULTS AND DISCUSSION

Weather conditions in the years of research differed in the temperature regime, the amount of precipitation, and the indicator of moisture content of the territory during the growing season (Table 1). The growing season of soybeans in 2019 was characterised by insufficient moisture supply (average drought) against the background of unseasonably high air temperature levels throughout the entire growing season. The hydrothermal coefficient (HTC) was 0.7; the sum of active temperatures above 10°C – $3,548^{\circ}\text{C}$ (Table 1).

Table 1. Weather conditions during the growing seasons of soybeans over the years of research (Velykyi Mytnyk, Khmilnyk district, Vinnytsia Oblast, 2019-2021)

Years of observations	Indicator of the growing season			
	Sum of active temperatures, °C ($\Sigma t > 10^{\circ}\text{C}$)	Amount of precipitation, mm (ΣR)	Average air temperature, °C (t_{avg})	HTC
2019	3,548	279.0	18.7	0.7
2020	2,525	252.6	19.0	1.0
2021	2,909	280.8	19.1	0.9

Note: HTC – Selyaninov hydrothermal coefficient

Source: compiled by the authors

In 2020, soybean growth and development took place under abnormal conditions, with a drought, a shortage of precipitation, and an increase in the duration of drought periods. The hydrothermal coefficient has reached 1.0, which indicates sufficient moisture content. The sum of active temperatures ($\Sigma t > 10^{\circ}\text{C}$) from germination to harvesting in the wax ripeness phase was 2,525°C, which is 1.4 times less compared to 2019 (Table 1).

In the third year of testing (2021), weather conditions in the first half of the growing season developed similarly to 2019. However, the presence of productive precipitation in April-May, high air temperature contributed to the development of a good vegetative mass. Flowering and bean development took place in conditions of mild drought. The hydrothermal coefficient (HTC) was 0.9. For the entire growing season from germination to soybean harvesting, the sum of active temperatures above 10°C was 2,909°C, which is 1.2 times less compared to 2019 and 1.1 times more than in 2020 (Table 1).

O.V. Shovkova (2022) noted that the yield indicator is a key element of the economic value

of an agricultural crop. It reflects the combined influence of all the factors that affect the plant during its growing season. Crop yield is always a consequence of the interaction between productivity and the ability to withstand adverse environmental conditions.

Considering the current meteorological conditions during the years of research, the average soybean yield in 2019 was 2.33 t/ha, in 2020 – 2.21, and in 2021 – 2.52 t/ha. The highest yield for all years of research was formed by Mentor st and Cordoba varieties, which were characterised by similar indicators – 2.45 and 2.43 t/ha, respectively (Table 2; Fig. 2). This indicator was lowest in the early-maturing Moravia variety – 2.28 t/ha. That is, the deviation of the yield of the Cordoba and Moravia varieties from the Mentor St standard variety is < 1% and 7.4%, respectively. The results showed the lowest yield variability in the Mentor St standard variety (2.57%) and Cordoba variety (5.99%), while in the Moravia variety this indicator was with an average variability of 17.62% (Table 2).

Table 2. Yield of soybean varieties (t/ha) over the years of research (2019-2021)

No.	Varieties	Yield, t/ha				Deviation, +/-		V, %
		2019	2020	2021	average	t/ha	%	
1	Mentor, st	2.49	2.39	2.47	2.45	–	–	2.57
2	Cordoba	2.43	2.28	2.58	2.43	-0.02	-0.8	5.99
3	Moravia	2.07	1.97	2.81	2.28	-0.17	-7.4	17.62

Note: V, % – coefficient of variation

Source: compiled by the authors

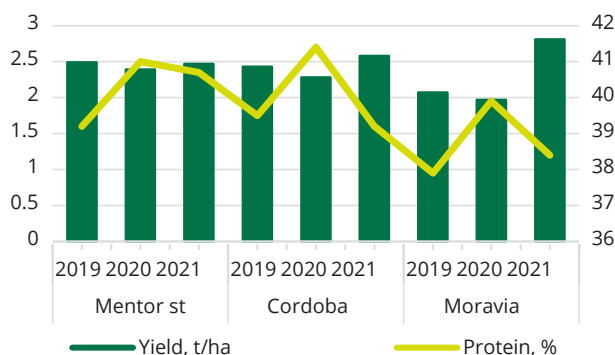


Figure 2. Yield (t/ha) and protein content (%) of soybean varieties depending on the year of research (Velykyi Mytnyk, Khmilnyk district, Vinnytsia Oblast, 2019-2021)

Source: compiled by the authors

According to L.V. Gubenko *et al.* (2019), the quality of products obtained in the process of growing agricultural crops is no less significant than the yield indicator. The main criterion that determines quality of soy seeds have a crude protein content. It is known that the commercial characteristics of soybean seeds are formed based on the combination of biological characteristics of the variety, agrotechnical practices, and soil and climatic conditions.

According to the results of biochemical analysis, it was found that the protein content in seeds of all soybean varieties averaged: in 2019 – 38.8%,

in 2020 – 40.7%, and in 2021 – 39.4%. The protein content in the seeds of soy varieties Mentor st, Cordoba, and Moravia in general over the years of research was on average in the range from 38.75% to 40.31% (Table 3; Fig. 2). The results showed a deviation of this indicator among all the varieties under study, compared with the Mentor st standard variety, the deviation in protein content ranged from -0.28% (Cordoba) to -1.56% (Moravia). Analysis of statistical parameters shows that during the study period, the coefficient of variation was not characterised by high variability of the trait, but was at a low level in all soybean varieties ($V < 3\%$) (Table 3).

Table 3. Protein content in soybean seeds (%) over the years of research (2019-2021)

No.	Varieties	Protein content, %				Deviation, +/-		V, %
		2019	2020	2021	average	% of protein content	%	
1	Mentor, st	39.2	41.0	40.7	40.31	–	–	2.40
2	Cordoba	39.5	41.4	39.2	40.03	-0.28	-0.69	2.97
3	Moravia	37.9	39.9	38.4	38.75	-1.56	-4.02	2.72

Note: Protein content in soybean seeds (%) over the years of research (2019-2021)

Source: compiled by the authors

The main indicators used in agrometeorology to assess weather conditions are air temperature, precipitation, the sum of active temperatures, and an integral indicator that simultaneously considers both of these indicators can be considered the Selyaninov hydrothermal coefficient (HTC) for displaying humidification conditions. It is well known that the limiting environmental

factor in Ukraine is, first of all, the hydrological conditions of existence of any living organisms, as a result of which special importance is attached to the assessment of moisture conditions. The correlation of yields and protein content in seeds of the studied soybean varieties of foreign selection with meteorological indicators for three years is presented in Table 4.

Table 4. Influence of meteorological conditions on yield and protein content in soybean seeds (correlation coefficients, r)

No.	Varieties	Indicator of the growing season			
		Sum of active temperatures, °C ($\sum t > 10^\circ\text{C}$)	Amount of precipitation, mm ($\sum R$)	Average air temperature, °C (t_{avg})	HTC
1	Mentor, st	+0.8 / -0.9 [#]	+0.9 / -0.5	-0.5 / +0.9	-0.8 / +0.9
2	Cordoba	+0.3 / -0.7	+0.8 / -0.9	+0.2 / +0.2	-0.3 / +0.7
3	Moravia	-0.03 / -0.9	+0.6 / -0.9	+0.6 / +0.5	+0.08 / +0.8

Note: # – parameter value separated by fractions is specified for yields / protein content; HTC – Selyaninov hydrothermal coefficient

Source: compiled by the authors

When evaluating the correlation coefficient between yield and weather conditions of the growing season for 2019–2021, a high correlation density was established in the Mentor st standard variety ($r = 0.9 \pm 0.8$), which showed a strong dependence of the obtained products on meteorological conditions (Table 4). There was also a strong direct relationship between the yield of the Cordoba variety and moisture availability ($r = 0.8$) during the growing season and a low degree of correlation with heat availability and moisture content. Correlation analysis between the yield and weather conditions of the growing season in the Moravia variety showed that the productivity of this variety did not correlate with the sum of active temperatures ($\sum t > 10^\circ\text{C}$) and HTC, but the average direct relationship between the yield from precipitation and temperature was established (Table 4).

According to the results of the analysis of the correlation coefficient between the seed quality (protein content) of soybean varieties and the weather conditions of the growing season of the three-year period (2019–2021), a high relationship was established in the Mentor st standard variety in terms of heat supply and moisture content ($r = 0.9 \pm 0.9$), and an average inverse correlation with precipitation ($r = -0.5$). A strong negative dependence of protein content on precipitation was recorded in the Cordoba variety ($r = -0.9$), and the correlation with other weather indicators was characterised by medium and low binding density. A qualitative assessment of the tightness of the correlation analysis between the protein content and the main weather indicators of the growing season in the Moravia variety showed a strong relationship between all the

studied indicators and a direct average sum of active temperatures ($\sum t > 10^\circ\text{C}$) (Table 4).

According to A.A. Korobko (2021), in Ukraine, the average soybean yield in 2019 was 2.40 t/ha, in 2020 it reached a lower level – 1.77 t/ha, and in 2021 – 2.23 t/ha. Analysis of available data in the State Register of Plant Varieties Suitable for Distribution in Ukraine (State Register ..., n.d.) and official descriptions of plant varieties and indicators of economic suitability, presented in the bulletins “Protection of rights to plant varieties”, placed in the information and reference system “Variety” (Information and reference system ..., 2024) showed that the yield of early-maturing soybean variety Mentor in various soil and climatic conditions of Ukraine is: Polissia – 2.49 t/ha, Forest-Steppe – 2.25 t/ha, and Steppe – 1.97 t/ha, and the protein content in seeds ranged from 39.6% to 40.7%. As for the mid-early soybean varieties – Cordoba and Moravia, the yield level of the Cordoba variety was on average: in Polissia – 2.07 t/ha, Forest-Steppe – 2.37 t/ha, and Steppe (irrigation) – 1.76 t/ha, and the protein content varied from 38.0% to 39.2%; in Moravia, these indicators on average reach 2.00 t/ha in terms of yield, and 41% in terms of protein content. With this in mind, for the Forest-Steppe zone, these varieties can be arranged in the following descending order relative to the yield level (t/ha): Cordoba > Mentor > Moravia; by protein content (%): Moravia > Mentor > Cordoba.

The results of three years of research in this paper are somewhat consistent, and in some ways differ from the above-mentioned data on the yield and quality (protein content) of seeds of these soybean varieties in the Forest-Steppe of Ukraine. It was found that in terms of yield, these varieties

are arranged in a similar way (Cordoba > Mentor > Moravia), but a radically different picture is observed regarding the protein content in seeds, their order of arrangement (descending) differs from above mentioned and has the following form: Mentor > Cordoba > Moravia.

Both Ukrainian and foreign researchers have conducted studies analysing the impact of climate change separately from other factors affecting soybean yields. However, it is worth noting that Ukrainian researchers paid less attention to the study of the impact of climatic conditions and weather data directly on the yield and, especially, the quality of soybeans compared to other priority crops, despite the fact that soybeans occupy a leading position in export and processing for food and feed needs (along with grain crops), and are also strategically important for ensuring food and economic security of the state.

In particular, the analysis of weather conditions of the Left-Bank Forest-Steppe (on the example of Poltava Oblast), L.G. Bilyavska (2010) showed that over the past 17 years, there has been a deterioration in humidification conditions, an increase in the average annual air temperature by 0.8-0.9°C, and there is also a pronounced downward trend in HTC indicators. As a result, the above-mentioned phenomena have a significant impact on the duration of seasons, there is a gradual increase in the heat supply of the growing season, and an increase in the number and intensity of stress factors. Under such conditions, fluctuations in the soybean yield occur in the range of 10-20%, and the impact of extreme weather conditions reaches the level of 30-60%. Therefore, the researcher notes that varieties intended for growing in the Forest-Steppe of Ukraine should be photoperiodically neutral, precocious, cold-resistant at different stages of organogenesis, and quickly release moisture during seed maturation. Ultimately, the researcher concluded that given the influence of environmental factors occurring in soybean production, it is necessary to introduce soybean varieties of regional selection adapted for certain soil and climatic zones.

V.S. Zuza *et al.* (2015) presented the results of studies on the yield of soybeans of the early-ripening Romantika variety of Ukrainian selection (growing season 90-100 days) in years with different levels of moisture supply (2009-2012) in the

conditions of the Left-Bank Forest-Steppe. It is shown that the level of soybean yield in some years of research was significantly influenced by the humidification regime during the critical period for yield development (from the third ten days of June to the third ten days of August inclusive). Research by A.A. Zymaroyeva (2020), which focused on establishing the contribution of agroecological factors, namely bioclimatic variables, soil indicators, and landscape diversity factors, to the variation of soybean yields in Polissia and Forest-Steppe of Ukraine (Vinnytsia, Volyn, Zhytomyr, Kyiv, Lviv, Rivne, Ternopil, Khmelnytskyi, Cherkasy, and Chernihiv oblasts) during 1991-2017, proved that the variation of the soybean yield growth rate by 9% depends on climatic conditions and soil variables. In addition, soil and climatic factors determined 51% variation in the minimum and 69% variation in the maximum yield of this crop.

According to the studies by Ukrainian researchers V. Polovyv *et al.* (2021), which were conducted during 1985-2018 at the stationary field of the Institute of Agriculture of Western Polissia of the National Academy of Sciences (Ukraine), clarified the trends of changes in temperature and humidity of the climate, which led to the restructuring of crops and the yield of some crops, in particular soybeans, in the north-western Forest-Steppe of Ukraine. The researchers have found that the heat supply of landscape agroecosystems has significantly improved: a rapid increase in the sum of effective temperatures has created favourable conditions for growing heat-loving crops such as soybeans, corn, and sunflower in the north-western Forest-Steppe. As these crops are rapidly expanding, the area structure and overall agricultural landscapes of the region are very similar to the southern Right-Bank Forest-Steppe.

A study conducted by A.V. Golodna *et al.* (2024) during 2021-2023, in the stationary experiment of the National Research Centre Institute of Agriculture of the National Academy of Sciences of Ukraine, which was geographically located in the Right-Bank Forest-Steppe, on the influence of weather conditions during the growing season of soybeans of the Ukrainian variety Muza on the yield level using correlation analysis, showed that there are different strengths and areas of the relationship between the yield of soybean seeds and weather conditions, both within decades and on



average for individual months of the growing season. It was found that the tightness of the connection ranged from weak to strong. When analysing the dependence of yields on individual weather factors, it was found that July had the most pronounced negative correlation with the average monthly air temperature, while May, June, and August had the highest correlation with precipitation. The greatest combined effect of average daily air temperature and precipitation was observed in the third ten days of June and August.

According to field research by M. Tsekhmeistruk *et al.* (2021), conducted in the period 2004–2020 at the V.Y. Yuriev Institute of Plant Production of the National Academy of Agrarian Sciences of Ukraine and subsequent correlation analysis between the impact of weather conditions on soybean yields, noted the negative impact of the average daily temperature in August when applying $N_{30}P_{30}K_{30}$ and 30 t/ha of manure before sowing soybeans. With a different mineral background of nutrition, the average daily temperature had little effect on the yield level. The amount of precipitation had a slightly greater impact, and the July precipitation had a positive effect on the crop on all mineral nutrition backgrounds. May precipitation had a positive effect only when growing soybeans under control (without fertilisers) and against the background of $N_{60}P_{60}K_{60} + 30$ t/ha of manure.

Analysing foreign statistics on the dynamics of growth of acreage and soybean yields, the United States of America is in the leading positions, along with Brazil, Argentina, China, and India, which together account for 48% of the world's land area (Sedibe *et al.*, 2023). Despite this, scientific research is actively conducted in these countries to investigate the impact of climate change and meteorological conditions (together with or without various agricultural activities) on soybean cultivation.

American researchers R.K. Sharma *et al.* (2022) using a fixed-effect model based on panel data to study the effects of climate variables such as maximum daily temperature, minimum temperature, and precipitation and soybean yields in the south-eastern region of the United States (Arkansas, Alabama, Florida, Louisiana, Mississippi, Georgia, Tennessee, North Carolina, South Carolina, Texas, and Virginia) from 1980 to 2020 showed significant variability in temperature and

precipitation over the past four decades. The maximum daily temperature, minimum temperature, and precipitation varied by: 0.50°C, 1.45°C, and 3.95 cm, respectively, during the soybean growing season. Moreover, the annual rate of change of the maximum daily temperature, minimum temperature and precipitation over the studied forty-year period increased by 0.012°C, 0.034°C, and 0.094 cm, respectively. Precipitation did not significantly affect soybean yields: an increase in precipitation by 1 cm reduced soybean yields by 0.40%. An increase in the minimum temperature by 1°C led to a decrease in soybean yield by 31.6%, and an increase in the maximum daily temperature by 1°C reduced soybean yield by 25.6%.

Research by American scientists F.A. Alsajri *et al.* (2020), which was aimed at studying the influence of temperature conditions (day/night temperatures: 21/13°C, 25/17°C, 29/21°C, 33/25°C, and 37/29°C) on the yield and quality of seeds of indeterminate (Asgrow AG5332, AG) and determinant (Progeny P5333RY, PR) of soybean varieties showed that the variety-temperature interaction was significant for seed yield, protein, oil and other quality parameters (palmitic, oleic, linolenic acids, raffinose and stachyose). Analysis of the quadratic functions of yield dependence on temperature showed that the optimal temperature for maximum yield was 26°C for AG and 23°C for PR. The temperature affected all indicators of seed quality in both varieties. The protein concentration in the seeds was slightly higher at two lower and higher temperatures than at 29/21°C. The oil concentration in the seeds increased with increasing temperature to 26°C for AG and 25°C for PR, and decreased at higher temperatures.

In a study by Argentine scientists E.O. Thomasz *et al.* (2024), using multiple partial regression, the correlation between soybean yields in various combinations of weather stations for the period 2001–2021 was estimated, which covered the entire soybean growing area in Argentina (an average of 17 million hectares). The results showed that there is a strong statistical relationship between precipitation and maximum temperature and overall soybean yield. However, precipitation did not have sufficient explanatory power at the local level due to the importance of other local agroclimatic variables, which explained an average of 72% of the yield variation in total



production. That is, precipitation as the only variable was statistically significant at the macro scale. When temperature was introduced into the model, the explanatory capacity increased to 91.3%.

Another study by Indian scientists R.S. Gadhav *et al.* (2023) conducted in 2019 in India (Parbhani) on the correlation between weather parameters and the yield of various soybean varieties (MAUS-71; MAUS-158 and JS-335) during the summer agricultural season (the so-called "harif") showed that temperature and some thermal indices have a significant impact on seed yield. The maximum temperature was positively associated with soybean seed yield at the stages: pre-emergence after sowing; from germination to branching; from branching to flowering; from flowering to pod formation; from pod formation to pod development containing full-size grain in the MAUS-158 variety, but negatively correlated at the stages – emergence; from pod formation to grain formation; from grain formation to bean development. The maximum temperature was positively associated with soybean seed yield in the stages from germination to branching, from branching to flowering; from flowering to pod formation; from pod formation to pod development containing full-size grain in relation to the MAUS-71 variety, while it was negatively correlated in the stages of emergence, from pod formation to grain formation, and from fully formed pod to maturation. The highest temperature was positively associated with soybean seed yield at the stages – from germination to branching, from branching to flowering, from flowering to pod formation, and from the end stage of pod formation to full maturation; and negatively correlated at the stages of emergence, from pod formation to grain formation, and from the fully formed pod to the beginning of maturation in the variety JS-335.

The correlation analysis carried out in this paper by the authors showed the degree of influence of the main meteorological conditions on the formation of yield and seed quality (protein content) of the studied differently ripened soybean varieties, which ripen at the sum of active temperatures above 10°C from 2000–2200°C to 2700°C, in the conditions of the central Forest-Steppe (Vinnytsia Oblast), which allows a more purposeful approach to the choice of varieties for specific climatic conditions. Mentor st (early-maturing) and

Cordoba (medium-early-maturing) varieties react approximately equally to growing conditions and climatic factors and have fairly similar patterns in yield development, but differ in its quality (protein content). However, this study has certain limitations that may be covered by future research areas. Among the most important is the inclusion of other agroclimatic variables, and various agricultural measures in the technology of growing soybeans in specific soil and climatic conditions.

CONCLUSIONS

Meteorological conditions that developed during the years of the study (2019–2021) in the south-western part of the Forest-Steppe zone of Ukraine (Vinnytsia Oblast) significantly varied in temperature conditions, indicators of moisture content of the territory, to a lesser extent – in the amount of precipitation during vegetation periods. In the soil and climatic conditions of the central Forest-Steppe, during the three-year research period, the deviation of the yield (in %) of soybean grain in experimental varieties from the standard variety (mentor) ranged from -0.8 (Cordoba) to -7.4 (Moravia). The lowest yield variability was recorded in the standard Mentor st variety (2.57%), while Cordoba and Moravia varieties were characterised by low (5.99%) and medium variability (17.62%), respectively. However, when compared with the standard Mentor st variety, the protein content deviation ranged from -0.69% (Cordoba) to -4.02% (Moravia) with low target trait variability in all varieties (< 3%).

In the conditions of the central Forest-Steppe, the yield of Mentor st and Cordoba varieties was significantly affected by the moisture availability of the growing season, the temperature regime had a strong degree of correlation only in the standard Mentor st variety, and vice versa – a low degree of correlation in terms of heat availability in the Cordoba variety. In the Moravia variety, the average indicators of moisture and heat supply during the growing season do not fully reflect their impact on yield, possibly because the direction of their influence varies greatly by the phases of crop development, which requires additional research.

A high correlation of protein content in the standard Mentor st variety was established in terms of heat supply and moisture content. A strong inverse dependence of protein content on

precipitation was recorded in the Cordoba variety, in contrast to other weather indicators of the growing season. The Moravia variety has a strong relationship between the protein content and all the weather indicators under study. Prospects for further research are to investigate the influence of meteorological conditions on the productivity of soybean varieties of foreign and Ukrainian regional

selection in the context of climate change using inoculation on different nutritional backgrounds.

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CONFLICT OF INTEREST

None.

REFERENCES

- [1] Alsajri, F.A., Wijewardana, C., Irby, J.T., Bellaloui, N., Krutz, L.J., Golden, B., Gao, W., & Reddy, K.R. (2020). Developing functional relationships between temperature and soybean yield and seed quality. *Agronomy Journal*, 112(1), 194-204. doi: 10.1002/agj2.20034.
- [2] Bilyavska, L.G. (2010). Adaptability of soybean varieties of Poltava selection in the conditions of climate change. *Scientific and Technical Bulletin of the Institute of Oilseeds Crops NAAS*, 15, 33-38.
- [3] Convention on Biological Diversity. (1992, June). Retrieved from https://zakon.rada.gov.ua/laws/show/995_030#Text.
- [4] Didora, V.G. (2013). Methods of agronomic research in agronomy. Kyiv: Center for Educational Literature.
- [5] Didora, V.G., Derebon, I.Y., & Savrasykh, L.D. (2017). Technological indicators of soybean quality depending on inoculation and fertilization in the conditions of Ukrainian Polissya. *Bulletin of Zhytomyr National Agroecological University*, 1(1), 57-63.
- [6] DSTU 4117:2007. (2007). *Grain and products of its processing. Determination of quality indicators by infrared spectroscopy*. Retrieved from https://online.budstandart.com/ua/catalog/doc-page?id_doc=85620.
- [7] Gadhav, R.S., Gade, S.A., & More, D. (2023). Correlation between weather parameters and different phenophases of soybean (*Glycine max.* [L.] Mirrll.) with seed yield. *The Pharma Innovation*, 12(12), 961-963.
- [8] Golodna, A.V., Hrytsiuk, Ya.V., Buslayeva, N.H., & Stolyar, O.O. (2024). The impact of fertilisation, seed treatment, and meteorological conditions on soybean yield in the Right-Bank Forest-Steppe. *Agriculture and Plant Sciences: Theory and Practice*, (2), 58-66. doi: 10.54651/agri.2024.02.07.
- [9] Gubenko, L.V., Holodna, A.V., & Remez, G.G. (2019). Influence of mineral fertilizers and bacterial preparations on the yield and quality of soybean seeds. *Scientific and Technical Bulletin of the Institute of Oilseeds Crops NAAS*, 27, 89-96. doi: 10.36710/ioc-2019-27-10.
- [10] Information and reference system "Sort" (2024). Retrieved from <http://sort.sops.gov.ua/search/search>.
- [11] Korobko, A.A. (2021). Dynamics of soybean production in Ukraine and the world. *Balanced Nature Management*, 4, 125-134. doi: 10.33730/2310-4678.4.2021.253098.
- [12] Petrychenko, V.F. (2012). Scientific bases of production and use of soybeans in animal husbandry. *Feeds and Feed Production*, 71, 3-11.
- [13] Polovyy, V., et al. (2021). The influence of climate changes on crop yields in Western Ukraine. *Ukrainian Journal of Ecology*, 11(1), 384-390. doi: 10.15421/2021_56.
- [14] Poudel, S., Vennam, R.R., Shrestha, A., Reddy, K.R., Wijewardane, N.K., Reddy, K.N., & Bheemanahalli, R. (2023). Resilience of soybean cultivars to drought stress during flowering and early-seed setting stages. *Scientific Reports*, 13, article number 1277. doi: 10.1038/s41598-023-28354-0.
- [15] Revtio, O.Y., & Zolin, O.O. (2023). Features of soybean cultivation under climate change (review). *Tavrian Scientific Bulletin*, 133, 105-112. doi: 10.32782/2226-0099.2023.133.15.
- [16] Sedibe, M.M., Mofokeng, A.M., & Masvoda, D.R. (2023). Soybean production, constraints, and future prospects in poorer countries: A review. In *Production and utilization of legumes – progress and prospects* (pp. 1-15). Rijeka: IntechOpen. doi: 10.5772/intechopen.109516.

- [17] Sharma, R.K., Kumar, S., Vatta, K., Dhillon, J., & Reddy, K.N. (2022). Impact of recent climate change on cotton and soybean yields in the southeastern United States. *Journal of Agriculture and Food Research*, 9, 1-9. doi: [10.1016/j.jafr.2022.100348](https://doi.org/10.1016/j.jafr.2022.100348).
- [18] Shevnikov, M.Y. (2010). [Efficiency of soybean cultivation in conditions of unstable moisture of the Forest-Steppe of Ukraine](#). *Bulletin of Poltava State Agrarian Academy*, 3, 19-23.
- [19] Shovkova, O.V. (2022). Productivity of soybean varieties of the early maturing group in the conditions of the left-bank forest-steppe of Ukraine. *Scientific Progress & Innovations*, 2(2), 113-118. doi: [10.31210/visnyk2022.02.13](https://doi.org/10.31210/visnyk2022.02.13).
- [20] State Register of Plant Varieties Suitable for Distribution in Ukraine (n.d.). Retrieved from <https://minagro.gov.ua/file-storage/revestr-sortiv-roslin>.
- [21] Sydiakina, O. & Ivaniv, M. (2023). Productivity of soybean varieties of different maturity groups depending on plant density under drip irrigation in the South of Ukraine. *Scientific Horizons*, 26(11), 100-110. doi: [10.48077/scihor11.2023.100](https://doi.org/10.48077/scihor11.2023.100).
- [22] Thomasz, E.O., Pérez-Franco, I., & García-García, A. (2024). Assessing the impact of climate change on soybean production in Argentina. *Climate Services*, 34, article number 100458. doi: [10.1016/j.cliser.2024.100458](https://doi.org/10.1016/j.cliser.2024.100458).
- [23] Tkachuk, O.P., Didur, I.M., & Pantsyreva, G.V. (2022). Ecological assessment of medium and medium late-ripening soybean varieties. *Agriculture and Forestry*, 1(24), 5-15. doi: [10.37128/2707-5826-2022-1-1](https://doi.org/10.37128/2707-5826-2022-1-1).
- [24] Tsekhmeistruk, M., Pankova, O., Kolomatska, V., Kobyzieva L., Artiimov, M., & Sirovitskiy, K. (2021). [Influence of weather and climatic conditions on soybean yield](#). *Ukrainian Journal of Ecology*, 11(4), 11-17.
- [25] Zabolotnyi, H.M., Mazur, V.A., Tsyhanska, O.I, Didur, I.M., Tsyhanskyi, V.I., & Pantsyreva, H.V. (2020). *Agribiological bases of soybean cultivation and ways to maximize its productivity*. Vinnytsia: Sole proprietor Korzun D.Y.
- [26] Zhu, W., Li, J., & Xie, T. (2024). Impact of climate change on soybean production: Research progress and response strategies. *Advances in Resources Research*, 4(3), 474-496. doi: [10.50908/arr.4.3_474](https://doi.org/10.50908/arr.4.3_474).
- [27] Zuza, V.S., Rozhkov, A.O., & Gutyansky, R.A. (2015). Soybean yield depending on the predecessor, meteorological conditions and herbicide efficiency. *Scientific Progress & Innovations*, 1-2, 22-24. doi: [10.31210/visnyk2015.1-2.02](https://doi.org/10.31210/visnyk2015.1-2.02).
- [28] Zymaroyeva, A.A. (2020). Ecological determinants of soybean yield. *Tavrian Scientific Bulletin*, 112, 69-76. doi: [10.32851/2226-0099.2020.112.9](https://doi.org/10.32851/2226-0099.2020.112.9).



Вплив метеорологічних умов на формування урожайності та якості насіння різностиглих сортів сої в умовах Центрального Лісостепу

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Анотація. Залежність між метеорологічними умовами та врожайністю сільськогосподарських культур спрямована переважно на пояснення впливу змін клімату на навколишнє середовище. Коливання температури та вологості повітря впливають на водний баланс і є головними чинниками підвищення або зниження врожайності сільськогосподарських культур. Такі гідротермічні варіації здатні вплинути на будь-який регіон. Зважаючи на це, метою досліджень було встановлення впливу метеорологічних умов таких як температура, опади, суми активних температур та гідротермічний коефіцієнт Селянінова (ГТК) на урожайність та якість насіння різностиглих сортів сої культурної *Glycine max* (L.) Merril зарубіжної селекції в умовах центрального Лісостепу. Використовували загальнонаукові та спеціальні методи досліджень, зокрема польовий, лабораторний і статистичний. Найбільша врожайність у середньому за роки досліджень відзначена у стандартному сорті Ментор (2,45 т/га), що незначно перевищує сорт Кордоба (< 1 %). Відхилення цільового показника в сорті Моравія від сорту стандарту було на рівні 7,4 %. За результатами досліджень виявлено найнижчу варіабельність урожайності у сорті стандарті Ментор (2,57 %), сорт Кордоба характеризувався також низькою мінливістю (5,99 %), тоді як у сорті Моравія цей показник був із середньою мінливістю – 17,62 %. За трирічний період досліджень вміст білка в насінні сортів сої знаходився у межах від 38,75 % до 40,31 %. Усі сорти сої мали низьку варіабельність ознаки (< 3 %). Проведено аналіз взаємозв'язку врожайності та якості насіння сортів сої зарубіжної селекції з основними факторами кліматичних умов, що формуються в регіоні центрального Лісостепу. Кореляційний аналіз показав ступінь впливу різних метеорологічних умов на формування продуктивності досліджуваних сортів сої, що дозволяє більш цілеспрямовано та виважено підходити до вибору сорту в конкретних кліматичних умовах. Результати проведених досліджень можуть бути застосовані при реалізації заходів щодо обґрунтованого вибору сортів сої для забезпечення стабільно високих врожаїв у періоди можливих несприятливих метеорологічних умов

Ключові слова: *Glycine max* (L.) Merril; продуктивність; сума активних температур; сума опадів; гідротермічний коефіцієнт; кореляційний зв'язок



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