

RESULTS OF AN ANALYSIS OF THE PREVALENCE OF BACTERIAL AGENTS IN ANIMALS, ANIMAL FEED, AND WATER

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Summary. This study aimed to conduct a retrospective analysis of bacteriological test results from 2019 to 2025 to determine the prevalence of colibacillosis, staphylococcosis, and streptococcosis in farm animals. The study also aimed to assess the level of bacterial contamination in drinking water and water of various origins using sanitary-microbiological indicators, and to evaluate the microbiological contamination of feed within the framework of state veterinary control. Research materials consisted of archived laboratory monitoring data from the State Service of Ukraine on Food Safety and Consumer Protection from 2019 to 2025. This data included results from bacteriological examinations of pathological material obtained from cattle, pigs, poultry, and companion animals. It also included microbiological assessment data from water and feed samples collected from farms in Kharkiv Region. The study employed retrospective epizootiological analysis methods, statistical generalization, comparative evaluation, and dynamic trend analysis. The results showed that *Escherichia coli* accounted for 41.0% of bacterial infections, followed by *Staphylococcus* spp. (31.0%) and *Streptococcus* spp. (17.0%). *Salmonella* spp. was detected in 5.0% of cases. Colibacillosis was most frequently recorded in poultry. A significant proportion of staphylococcosis isolates originated from companion animals. The detection rate of streptococcosis remained relatively low (2.9%) yet stable. Water testing revealed periodic deviations in indicator parameters, primarily at processing enterprises. The overall percentage of noncompliant feed samples was 3.4%, with enteropathogenic *E. coli* and other Enterobacteriaceae predominating. These results suggest the continuous circulation of opportunistic and pathogenic bacteria within the 'animal-feed-water-environment' system, emphasizing the importance of systematic microbiological monitoring and the responsible use of antimicrobial agents

Keywords: colibacillosis, staphylococcosis, streptococcosis, epizootiological analysis

Introduction. Colibacillosis is one of the most common bacterial infections in poultry, pig and cattle farming. It is caused by pathogenic strains of *Escherichia coli* that have a variety of virulence factors and the ability to develop antimicrobial resistance. In the context of intensive livestock production, the spread of these strains is of particular concern due to the resulting economic losses, reduced productivity and potential zoonotic risks (Ponomarenko et al., 2021; Ushkalov, 2023).

Recent international studies confirm an increase in the prevalence of multidrug-resistant *E. coli* isolates in production animals. In particular, Kathayat et al. (2022) demonstrated a high prevalence of APEC strains with multidrug resistance to β -lactams, tetracyclines, and fluoroquinolones in commercial poultry farming. Similarly, Lyimo (2026) emphasize the global trend of antimicrobial resistance gene accumulation in animal-origin pathogenic *E. coli* populations and their circulation within the 'animal-environment-human' system.

The problem of escherichiosis is also a pressing issue in Ukraine. A study by Eckenko et al. (2024) demonstrated the circulation of multidrug-resistant *E. coli* strains among wild and domestic waterfowl, confirming the existence of a natural reservoir of resistance. Additionally, fluoroquinolone-resistant *E. coli* isolates have been detected in animal and poultry feed produced in Ukraine (Kuryata et al., 2025), which poses a risk of spreading resistant strains on farms. Mastitis monitoring in cows across various regions of Ukraine revealed that *E. coli* is one of the etiological agents of udder

inflammation (Hadzevych et al., 2019; Chechet et al., 2023), highlighting its importance in cattle pathology.

The available data indicate the global and Ukrainian spread of antibiotic-resistant *E. coli* strains, underscoring the need for systematic microbiological monitoring and principles for the rational use of antimicrobials in animal husbandry.

Along with colibacillosis, staphylococcal infections are prevalent among both livestock and domestic animals and play a significant role in the spectrum of bacterial infections in animals (Paliy et al., 2023). Of particular concern is the circulation of methicillin-resistant strains of *Staphylococcus aureus* and *S. pseudintermedius*. A study by Thomson et al. (2022) confirmed the presence of resistant staphylococci in healthy dogs, cats, and humans, suggesting potential interspecies transmission. Similarly, Araújo et al. (2024) identified a high prevalence of multidrug-resistant *Staphylococcus* isolates from clinical samples of companion animals, including carriers of *mecA* gene. A systematic analysis of the prevalence of coagulase-negative staphylococci points to their role as reservoirs of antimicrobial resistance genes (Ocloo et al., 2022). In Ukraine, Shevchenko et al. (2023) confirmed the prevalence of staphylococci in dogs and cats, respectively, and Pasternak et al. (2023) confirmed it in cattle. These findings underscore the need to monitor antibiotic resistance in companion and livestock animals.

Streptococcal infections in farm animals, especially in swine, are also significant. *Streptococcus suis* is one of the

leading pathogens in pigs and has high economic and zoonotic significance. Molecular studies by Li et al. (2024) revealed substantial serotype diversity and the prevalence of resistance genes (*ermB* and *tetO*) among isolates. Costinar et al. (2024) also reported multidrug-resistant streptococcal strains on swine farms, complicating treatment. Xia et al. (2024) also confirmed the genomic variability of *S. suis* and its tendency to accumulate antimicrobial resistance genes. Ukrainian data indicate frequent detection of *Streptococcus* spp. in cow's milk in cases of subclinical mastitis (Pasternak et al., 2023; Hadzevych et al., 2019; Shkromada et al., 2019).

Thus, along with colibacillosis, staphylococcosis and streptococcosis pose significant problems for modern animal husbandry. These problems stem from the rise in antimicrobial resistance, the genetic variability of pathogens, and the potential for zoonotic transmission. This justifies the need for systematic microbiological monitoring and the rational use of antimicrobial drugs.

Currently, it is difficult to find a body of water that has not been affected by human-caused pollution. The deterioration of water quality in Ukraine's natural water bodies, particularly due to military operations and abnormally hot summers in recent years, is a serious problem. Most bodies of water receive inadequately treated effluents from industrial, food processing, and livestock enterprises, as well as domestic wastewater. This makes continuous water quality monitoring essential for protecting human and animal health, and maintaining ecological balance (Hadzevych et al., 2022; Savenko and Koba, 2022).

Anthropogenic pressure leads to the biological contamination of water bodies, particularly through the introduction of invasive alien microorganisms. Pathogenic bacteria of the Enterobacteriaceae family are of particular concern in this regard. The most important indicator of fecal contamination is the presence of *E. coli*, which enters the water from livestock farms, industrial facilities, and domestic sources. Their presence indicates organic contamination and an increased risk of intestinal infections in humans and animals. Systematic microbiological monitoring of water based on coliform counts is therefore essential for ensuring a safe water supply, assessing the sanitary condition of water bodies, and preventing negative impacts on aquatic ecosystems (Nazarenko et al., 2020; Zinchenko et al., 2024).

Review studies show that various microorganisms, including pathogenic strains of *Escherichia coli*, can contaminate feed during production, transportation, and storage (Olson et al., 2023; Bogach et al., 2024). Laboratory data confirm that feed for pigs, poultry, and other species often contains *E. coli* and *Salmonella* spp. with signs of antimicrobial resistance (Paredes et al., 2023), and may also serve as a source of bacterial contamination in the 'farm-to-table' chain (Kolchyk et al., 2022; Raspa et al., 2023). Of particular concern is the detection of multidrug-resistant *Bacillus* spp. in feed and food products (Haque et al., 2024). Bacterial

contamination, including both opportunistic and pathogenic flora, as well as molds and yeasts, has also been detected in farming systems and can negatively affect the productivity and safety of final livestock products (Orobchenko et al., 2023; Dančová, Gregová and Szabóová, 2024). These findings underscore the need for systematic microbiological monitoring of feed in livestock production.

Food safety encompasses a set of interrelated processes and requirements that are implemented at every stage of food production (Rodionova and Paliy, 2017). One of the key components of this system is controlling the quality and safety of animal feed. According to Kravtsova et al. (2022), achieving good animal health, high productivity, and the production of safe animal-derived products requires nutritious, high-quality, and safe feed (Mikhailchenko, Paliy and Pavlichenko, 2025). Feed quality directly affects animals' physiological condition, productivity levels, disease resistance, and herd survival (Kolchyk et al., 2020; Paliy et al., 2020; Kushnir et al., 2021).

Thus, ensuring the safety of food products and animal feed remains a top priority for establishing an effective food safety system in Ukraine.

The spread of antibiotic-resistant strains of *Escherichia coli*, *Staphylococcus* spp., and *Streptococcus* spp., as well as the bacterial and microbial contamination of water and animal feed, respectively, are particularly relevant in the context of intensive livestock farming and increasing anthropogenic pressure. Pathogens circulating within the 'animal-feed-water-environment' system contribute to the formation of reservoirs of antimicrobial resistance, increasing risks to animal and human health. This necessitates a systematic analysis of bacteriological monitoring results.

The relevance of this study lies in the need for a comprehensive assessment of the prevalence of colibacillosis, staphylococcosis, and streptococcosis in farm animals; the levels of bacterial contamination in drinking water and surface water bodies; and the microbiological contamination of feed under current production conditions. Conducting a retrospective analysis enables identification of trends in pathogen composition, isolation frequency, and the potential risk of resistant strain spread on farms.

The **aim** of the study is to conduct a retrospective analysis of the results of bacteriological studies from 2019 to 2025 regarding the prevalence of colibacillosis, staphylococcosis, and streptococcosis in farm animals, to determine the level of bacterial contamination in drinking water and surface water bodies based on the total coliform count, and to assess microbiological contamination of feed.

The study involves synthesizing and systematizing archived laboratory research data from 2019 to 2025. The goal is to establish the dynamics of pathogen spread, assess circulation trends, and justify the need for further systematic microbiological monitoring of agri-food products.

Materials and methods. To achieve the objective of the study, which was to conduct a retrospective analysis of the prevalence of colibacillosis, staphylococcosis, and streptococcosis in farm and domestic animals, as well as to assess bacterial contamination in drinking water, surface water, and animal feed based on bacteriological indicators, a comprehensive analysis of archival and current data from 2019 to 2025 was conducted.

The primary source of information was archival materials from laboratory studies conducted by the State Service of Ukraine for Food Safety and Consumer Protection. These materials included statistical reports, laboratory study logs, and the author's observations from 2023 to 2025. The analysis included data from bacteriological tests of pathological and biological materials from cattle, pigs, and poultry, as well as results from microbiological tests of feed and water in Kharkiv Region.

The materials were provided by the Kharkiv Regional State Laboratory of the State Service of Ukraine for Food Safety and Consumer Protection, as well as its interdistrict divisions.

We identified trends in the isolation of major pathogenic bacteria, such as *Escherichia coli*, *Staphylococcus* spp., and *Streptococcus* spp., in pathological and biological samples received by the laboratories between 2019 and 2025.

We calculated the ratio of the volume of materials tested to the number of positive pathogen isolation cases. We used indicators of frequency, relative distribution, and trends over the observation period.

We examined the distribution of bacterial infections according to animal species, disease location, and pathogen type. We identified major trends in changes to pathogen structures and in the spread of resistant strains.

We evaluated the spread of pathogens among farms and animal species. We identified potential reservoirs of antimicrobial resistance and zoonotic risks. To forecast trends in key indicators, we created trend lines and used comparative visualizations of results by year.

We systematized and integrated data from various sources, including official statistics and publications by domestic and foreign researchers.

Results and discussion. An analysis of bacteriological study results from 2019 to 2025 (Fig. 1) shows *Escherichia* bacteria, which cause colibacillosis in farm animals and poultry, were the most common pathogens, accounting for 41.0% of cases. Bacteria of the genus *Staphylococcus* also played a significant role, causing staphylococcal infections in farm animals, poultry, and companion animals and accounting for 31.0% of cases. Infections caused by *Streptococcus*, the causative agent of streptococcal diseases, were found in 17.0% of cases. Infections caused by *Salmonella*, the causative agent of salmonellosis in animals and poultry, were detected in 5.0% of cases.

Less common pathogens included bacteria of the genera *Borrelia*, *Pasteurella*, *Aeromonas*, and *Paenibacillus*, accounting for 2.22%, 1.48%, 1.48%, and 1.48%, respectively. Despite their low detection rate, these bacteria can be dangerous to animal health and cause serious infectious diseases under certain conditions.

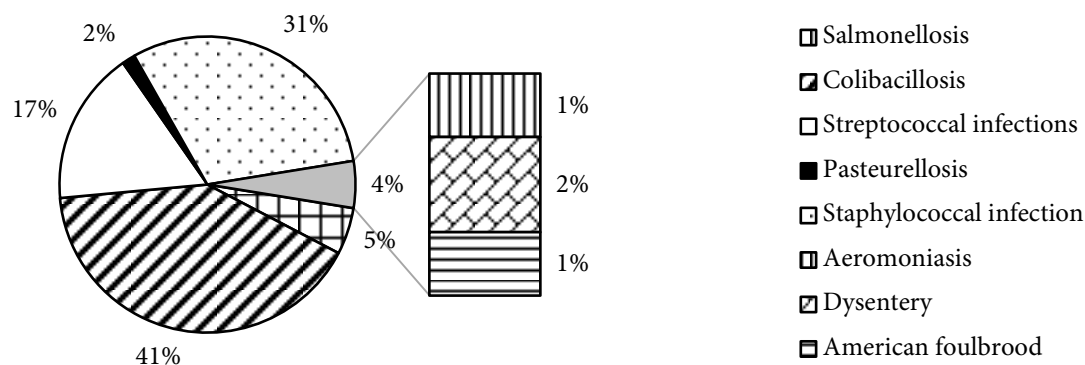


Figure 1. Prevalence of bacterial diseases in animals in Kharkiv Region for the period 2019–2025.

A total of 1,483 samples of pathological material were sent to the laboratory for bacteriological testing. Based on the results, a diagnosis of colibacillosis was confirmed in 66 cases. Of these cases, 44 were in poultry, indicating a high susceptibility of the poultry population to this infection. Nine cases of colibacillosis were confirmed in cattle, highlighting its significance as a livestock pathogen. Additionally, three cases of colibacillosis were detected in fur-bearing animals, showing that the pathogen can infect different species. The diagnosis was confirmed in 49 cases based on the results of laboratory tests of 570 samples of pathological and biological material, including carcasses, organs from farm animals

and poultry, conjunctival swabs, and ear swabs from domestic animals, sent to the state laboratories of the State Service of Ukraine for Food Safety and Consumer Protection in Kharkiv Region. Of these cases, 27 were from domestic animals, 17 were from poultry, six were from cattle, and one each was from small ruminants and fur-bearing animals. These results suggest that domestic animals and poultry are most commonly affected. Cases of infection in cattle, small ruminants, and fur-bearing animals are less common. This underscores the need for continuous monitoring and preventive measures across various animal categories (Fig. 2).

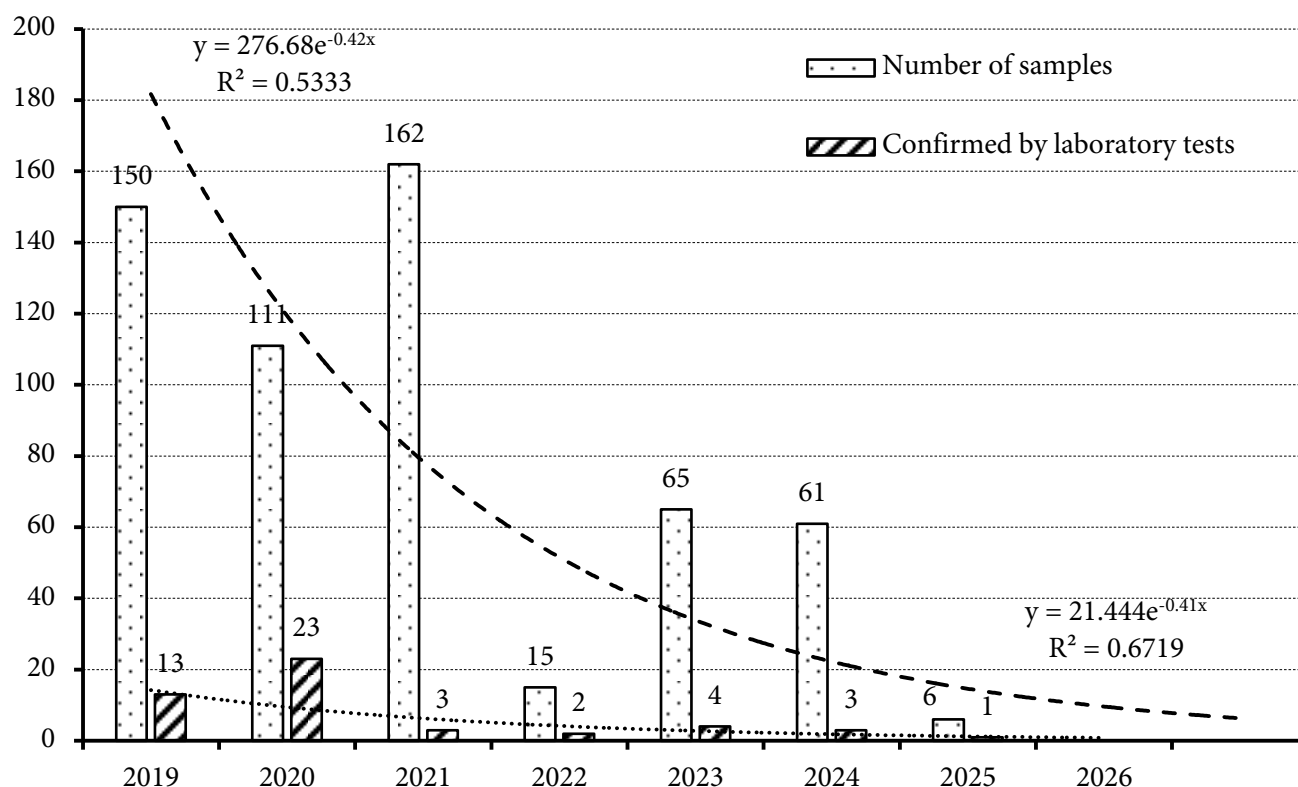


Figure 2. Analysis of test results for staphylococcal infection on pathological material from 2019 to 2025.

In addition, it is important to note the results of bacteriological testing of pathological material from birds that died from highly pathogenic avian influenza. In early 2025, an outbreak of highly pathogenic avian influenza was reported at a backyard farm in the Kharkiv region.

As a result of bacteriological testing, *E. coli* and *S. aureus* cultures, which are pathogenic to white mice, were isolated from bone marrow. The original cultures of these bacteria were re-isolated from the heart blood of the dead mice. Antibiotic susceptibility testing revealed multidrug resistance in the isolates: *S. aureus* was resistant to cephalosporins, macrolides, nitrofurans, and fluoroquinolones; *E. coli* was resistant to cephalosporins and macrolides.

Given the lack of antimicrobial use on farms where poultry deaths from highly pathogenic influenza were observed, the results indicate the presence of spontaneously developed multidrug-resistant strains in the natural environment.

During the period under review, 782 samples of pathological material were delivered to laboratories for bacteriological testing, from which the causative agent of streptococcosis was isolated in 23 cases. Specifically, 9 isolates were obtained from poultry, 8 from cattle, 4 from swine, and 2 from domestic animals (Fig. 3).

Although the overall detection rate of streptococcosis is low (2.9%), the stability in case reporting suggests that the pathogen is circulating among various animal species. Poultry and cattle remain the primary risk groups, necessitating enhanced clinical and bacteriological monitoring in these sectors specifically.

The decrease in the number of samples tested, coupled with an increasing proportion of positive results, suggests that diagnostic testing is focused on farms where infection is suspected.

The data support continued epizootic surveillance and improved preventive measures that consider the disease's species-specific characteristics.

Overall, the situation regarding streptococcal disease in the region is under control. However, given the possible upward trend in confirmed cases, it requires systematic monitoring.

During the review period, various types of water were tested for total bacterial contamination, coliform count, thermotolerant coliforms, *E. coli*, and enterococci. The statistical data on the results of the water testing are presented in Table 1.

An analysis of microbiological test results for water from various sources from 2019 to 2025 (Table 2) shows varying levels of bacterial contamination depending on the water source.

Water from livestock facilities was tested — 553 samples were analyzed for total bacterial contamination, of which 27 (4.9%) tested positive. A total of 533 samples were tested for coliform count, with 2 (0.38%) testing positive. Thermotolerant coliform bacteria, *E. coli*, and enterococci were not detected. *Salmonella* was tested in 14 samples — no positive results were found. Clostridia (11 samples) and *Pseudomonas* (13 samples) were also not isolated. The data indicate a relatively satisfactory sanitary and hygienic condition of the water in livestock facilities.

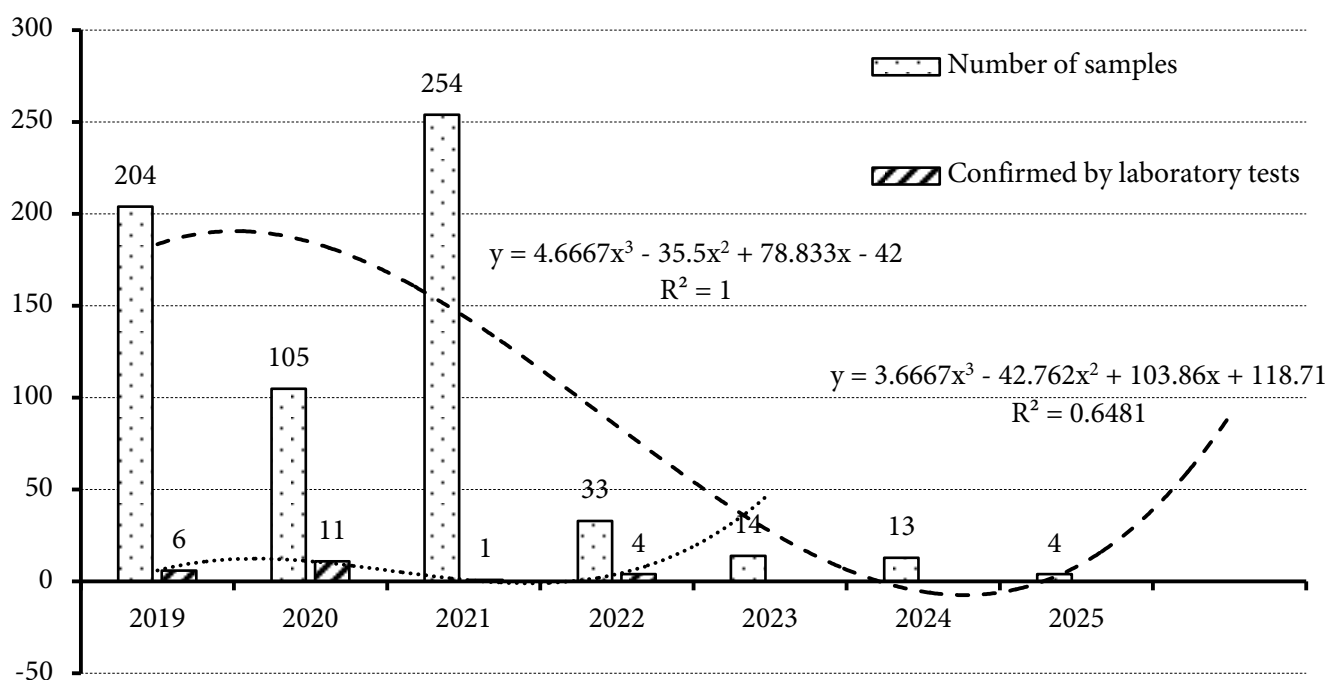


Figure 3. Analysis of test results for streptococcal infections in pathological materials from 2019 to 2025.

Table 1 — Water quality test results for the period from 2019 to 2025

Type of water	Total bacterial contamination		Coli-titer		Thermo-resistant coliform bacteria		<i>E. coli</i>		<i>Enterococcus</i>		<i>Salmonella</i>		Clostridia		<i>Pseudomonas</i>	
	Tested	Positive	Tested	Positive	Tested	Positive	Tested	Positive	Tested	Positive	Tested	Positive	Tested	Positive	Tested	Positive
Water from livestock facilities	553	27	533	2	0	0	35	0	0	0	14	0	11	0	13	0
Water from processing plants	557	39	1,199	52	81	12	473	13	0	0	45	0	24	0	24	
Surface water bodies	8	0	14	0	0	0	0	0	8	0	0	0	0	0	0	0
Wastewater	0	0	0	0	0	0	0	0	0	0	48	0	0	0	0	0

Table 2 — Results of animal feed testing from 2015 to 2025

Years	Number of samples			Number of tests			Noncompliance (positives)					
							samples			tests		
	exports	imports	domestic production	exports	imports	domestic production	exports	imports	domestic production	exports	imports	domestic production
2019	290	13	586	290	13	586	0	0	33	0	0	33
2020	3	0	401	15	0	763	0	0	0	0	0	0
2021	95	0	237	19	0	866	0	0	0	0	0	0
2022	29	1	92	71	2	401	1	0	14	1	0	14
2023	21	0	98	71	0	333	1	0	6	1	0	12
2024	29	0	49	106	0	195	0	0	12	0	0	17
2025	47	0	43	179	0	136	0	0	3	0	0	3
Total	514	14	1,506	578	15	3,280	2	0	68	2	0	79
	2034			3873			70			81		

Of the 557 water samples tested from processing plants, 39 (7.0%) exceeded the limit for total bacterial contamination. A total of 1,199 samples were tested for coliform count, of which 52 (4.3%) were positive. Thermotolerant coliform bacteria were detected in 12 of 81 samples (14.8%), and *E. coli* was detected in 13 of 473 samples (2.7%). *Salmonella* (45 samples) and clostridia (24 samples) were not detected. The presence of positive results for indicator microorganisms indicates periodic violations of sanitary standards and possible fecal contamination of process water.

No positive results were found in the 8 water samples tested for total bacterial contamination or in the 14 samples tested for coliform counts. Enterococci were tested in eight samples, but none were detected. Other parameters were not recorded. Overall, the water quality met regulatory requirements based on the tested parameters.

Wastewater was tested only for *Salmonella* (48 samples), and the pathogen was not isolated in any case.

The highest level of microbial contamination was found in water from processing plants. Positive results were recorded for total bacterial contamination, coliform count, heat-resistant coliform bacteria, and *E. coli*. Water from livestock facilities showed isolated deviations. No

pathogenic microflora was detected in surface water bodies or wastewater based on the tested parameters.

The results confirm the need for systematic microbiological monitoring of water, especially at processing facilities, to prevent the spread of opportunistic and pathogenic microorganisms.

Between 2019 and 2025, as part of state veterinary and departmental controls, 3,873 microbiological tests were conducted on 2,034 animal feed samples, revealing 81 noncompliances in 70 feed samples.

The overall noncompliance rate was 2.1% of the total tests and 3.4% of the total samples, indicating a relatively stable level of microbiological safety in animal feed throughout the study period. Table 1 presents a statistical analysis of the number of animal feed samples for various species that were collected from feed production facilities operated by market participants and subjected to microbiological testing.

The analysis of detected nonconformities revealed that enteropathogenic *Escherichia coli* (EPEC) was the most prevalent microbiological contaminant, accounting for approximately 45% of all nonconformities. Enterobacteria ranked second at 28.9%, indicating a significant proportion of indicator and potentially pathogenic microorganisms (Fig. 4).

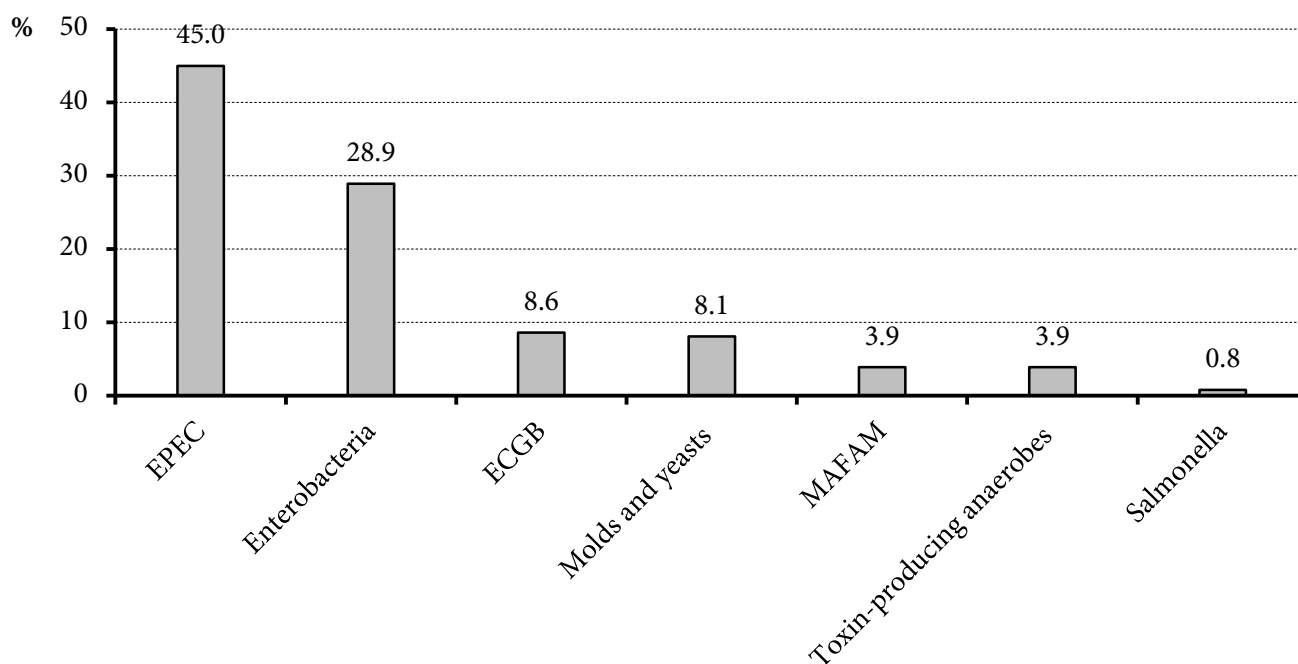


Figure 4. The most common agents of microbiological contamination in animal feed.

The proportion of *Escherichia coli* group bacteria (ECGB) was approximately 9–10%, confirming isolated cases of noncompliance with sanitary and hygienic requirements during feed production or storage. In addition to bacterial contamination, the presence of molds and yeasts (8.1%) was detected, which may be associated with noncompliance regarding humidity and temperature conditions during storage of raw materials and finished products. Noncompliance with MAFAM indicators and toxin-producing anaerobes accounted for

3.9% each, indicating isolated instances of exceeding the total microbial count and a potential risk of toxin accumulation. *Salmonella* spp. was detected in only one case, accounting for less than 1% of the total noncompliance and indicating a low level of circulation of this pathogen in the tested feed samples.

Conclusions. A retrospective analysis of the years 2019–2025 revealed that colibacillosis, staphylococcosis, and streptococcosis were the dominant bacterial infections in animals in the Kharkiv region. Colibacillosis

was particularly prevalent among poultry. Staphylococcal infections were more frequently reported in domestic animals and cattle, while the detection rate of streptococcosis remained stable, albeit low. Multidrug-resistant strains of *Escherichia coli* and *Staphylococcus aureus* were identified. Water testing revealed predominantly satisfactory sanitary conditions, with isolated deviations at processing plants. The level of

microbiological noncompliance in animal feed remained relatively low, though enteropathogenic bacteria were present. This study justifies the need for systematic microbiological monitoring and the timely implementation of preventive measures to reduce epizootic and zoonotic risks.

Declaration of competing interest. The author declare that he has no conflict of interest.

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Received 04.03.2026

Accepted 17.06.2026

Published 28.08.2026

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