

ETIOLOGY OF PORCINE RESPIRATORY DISEASE COMPLEX ON FARMS OF KHARKIV AND POLTAVA REGIONS

Voitenko R. Severyn R. V. (ORCID ID 0000-0003-4990-2489), **Hontar A. M.** (ORCID ID 0000-0003-0504-8663), **Haragulya G. I.*** (ORCID ID 0000-0003-4990-2489), **Basko S. O.** (ORCID ID 0000-0001-8314-2490)

State University of Biotechnology, Kharkiv (Ukraine); e-mail: vetvir.galina@gmail.com*

Abstract. *The paper reviews the study of the etiology of porcine respiratory disease complex (PRDC). Multiple respiratory infections in pigs are common worldwide and cause great economic losses in pig farming. The paper studied the epizootic situation on pig farms in Poltava and Kharkiv regions in Ukraine in 2019–2023. The findings showed an increase in the frequency of respiratory diseases in pigs, from 11.4 % to 23.7 %. Laboratory tests confirmed the multiple infections of porcine respiratory diseases. The infections included two key viruses (porcine reproductive and respiratory syndrome and porcine circovirus type 2 and from 4 to 8 types of bacteria, depending on the year of study. During the research period, the array of bacterial pathogens changed. The numbers of isolation of Mycoplasma and Pasteurella dropped by 7.2 and 6.3 times, respectively, and Escherichia coli and Actinobacillus increased by 17.7 and 8.0 times, respectively. During the study of antibiotic susceptibility, Streptococcus suis isolates showed the maximum susceptibility to antibiotics, while Pasteurella multocida isolates were the most resistant.*

Keywords: porcine respiratory disease complex, multiple infections of pigs, etiology.

Introduction. Porcine Respiratory Disease Complex (PRDC) has been the most important concern for swine producers for several decades. Porcine Respiratory Disease Complex is characterized as a condition clinically manifested by respiratory diseases that have a multifactorial nature and are resistant to treatment.

There are a lot of comprehensive scientific studies of PRDC. The scientists constantly point to its multifactorial etiology that includes infectious and non-infectious factors. Non-infectious factors include sanitary conditions in swine housing areas (ambient air temperature, relative humidity, ammonia and dust concentrations, stocking density, quality of flooring and ventilation), methods of herds formation (weaning age, methods of group formation for fattening), veterinary care (preventive vaccinations, treatment methods, monitoring of the infectious diseases), and the influence of climatic conditions on the spread of respiratory diseases agents (Wilson et al., 1986; Maes et al., 1999; Oba et al., 2020; Severyn, 2021; Pirolo et al., 2021; Pessoa et al., 2022).

Multiple pathogens promote the development of PRDC. Viral and bacterial pathogens play a special role in the development and course of PRDC. The clinical outcome and necropsy findings may differ depending on the involvement of the different pathogens. The complex nature of the PRDC impedes the diagnostic and preventive measures on affected farms (Eddicks, 2021).

The early publications on the study of multiple infections primarily focused on issues related to the interaction of bacteria that caused atrophic rhinitis and pneumonia, particularly mycoplasmas, bordetellas, streptococci, and pasteurellas (Wilson M. R., 1986). The isolation of porcine reproductive and respiratory syndrome virus (PRRSV) and porcine circovirus type 2 (PCV2) as the main immunosuppressive viruses, as well as the spread of African swine fever virus, opened up new avenues and methods for PRDC researching (Assavacheep, 2022).

We have reviewed literature of the last decade that focused on the study of PRDC in different countries around the world. The authors from the US, Canada, multiple Brazil (Choi et al., 2003; Arenales et al., 2022), European countries (Maes et al., 1999; Hansen et al., 2010; Pepovich et al., 2016; Eddicks et al., 2021; Vangroenweghe and Oliver, 2021; Petri et al., 2023), Africa (Oba et al., 2020) and Asia (Cheong et al., 2017; Qin et al., 2018; Zhu et al., 2021; Singh, 2022) devoted their efforts to isolate and identification of PRDC pathogens. The authors from Ukraine have also researched the PRDC spread issue (Prokhoriatova and Kolchyk, 2015; Masiuk et al., 2016; Sytiuk et al., 2016; Furda, 2018; Kovalenko and Kovalenko, 2021; Severyn et al., 2021).

Scientists highlighted the collective nature of PRDC, and the composition of the multiple pathogens can vary both quantitatively (from 2 to 5-6 or more microorganisms) and qualitatively (combinations of viruses and

bacteria or viruses and bacteria alone). Primary infections are most often viruses that cause damage to the mucous membranes of the respiratory tract that gives way to secondary bacterial infection development.

The majority of researchers consider the dominant combination of porcine reproductive and respiratory syndrome virus (PRRSV), porcine circovirus type 2 (PCV2), Swine Influenza virus (SIV), and less frequently Aujeszky's disease virus (PHV, PRHV), and sometimes classical swine fever virus (CSFV) mostly contribute to PRDC development. The key collective bacteria include *Actinobacillus pleuropneumonia*, *Streptococcus suis*, *Pasteurella multocida*, *Bordetella bronchiseptica*, *Haemophilus parasuis* i *Mycoplasma hyopneumoniae*.

Some researchers insist on the need to investigate other groups of pathogens that can influence the development and severity of PRDC. They include protozoa, pathogenic fungi, and helminths (Oba et al., 2020; Saade et al., 2020).

Certain studies are concentrated on the normal microbiota of the pig respiratory tract to understand its influence on PRDC development. A comprehensive DNA microarray technology allowed us to analyze more than 8,000 species of microorganisms. The outcomes confirm the importance of microbial diversity as a factor in preventing the inception of disease. Some researchers have found that the microbial structure of the upper respiratory tract undergoes noticeable evolution after birth and stabilizes before the weaning period. Less diversity and an imbalanced microbial composition increase the risk of respiratory diseases (Pirolo et al., 2021).

The group of scientists conducted a study of the composition of the microbiome in clinically healthy pigs in Eastern China. Molecular methods confirmed PCV2 pathogen in 59.9% of cases, and 27.2%, 52.3%, 33.2%, and 0.4% of PRRSV, *S. suis*, *H. parasuis*, and *A. pleuropneumonia*, respectively. The samples showed collective pathogens infection. Scientists are confident that mixed infections are common among cases of PRDC and may pose a greater threat to population health compared to single-pathogen infections (Zhu et al., 2021).

Collective pathogens causing respiratory diseases in pigs significantly vary between farms, production sites, regions, and countries, making it a challenge to generalize the PRDC diagnoses, treatment, and control. The interactions that occur at the cells and molecular level during infection of pigs with two or more respiratory pathogens are quite diverse and complex.

It should be noted that over the past decade in scientific literature about the isolation of PRDC pathogens, the findings were on multiple infections. We reviewed data from 20 scientific publications on the isolation of various bacterial and viral common pathogens associated with PRDC. Furthermore, 16 publications described the etiology of bacterial-viral interactions, while two articles were exclusively dedicated to viral infections (Qin et al., 2018; Singh et al., 2022) or bacterial (Pepovich et al., 2016; Petri et al., 2023) multiple infections.

According to various authors, during the laboratory diagnosis of respiratory diseases in pigs, usually, 2 or more microorganisms were identified with varying frequencies. In international literature, the part of multiple infections varies significantly: (6.2-35.4) % (Zhu, 2021), 42.3 % (Arenales, 2022), and even 88.2 % (Choi, 2003). Frequency of virus isolation depended on the type: PRRSV was mentioned as associate in 13 publications (65%), circovirus type 2 – in 8 (40%), different strains of influenza – in 8 (40%), Aujeszky's disease virus was isolated three times (15%). There were single cases of isolation of Porcine Rotavirus and Porcine Cytomegalovirus (5% each).

In cases of porcine respiratory pathology there were more bacteria isolated and identified. Scientists managed to isolate from 1-2 to 10 or more pathogenic (or opportunistic pathogenic) bacteria during the samples' examination. The most commonly isolated were Mycoplasmas: 55% of scientific publications mentioned them, Pasteurella were mentioned less frequently (35%), as well as Actinobacilli (30%), Streptococci (25%), and Haemophili (20%). The least were microorganisms from the Enterobacteriaceae family (5-10%).

According to some authors, the frequency of isolation of specific microorganisms varies widely. The quantity of isolation of individual viruses and bacteria is presented in Table 1.

Table 1

Literature analysis of the frequency of isolation of individual microorganisms in PRDC

Microorganism	Frequency of isolation, %		Source
	min	max	
Viruses types			
PRRSV	27.2	35.4-100	Choi et al., 2003; Zhao et al., 2020; Zhu et al., 2021
Influenza different strains	22.2	59.9	Choi et al., 2003; Zhu et al., 2021
Swine circovirus	7.1	18.6	Choi et al., 2003; Arenales et al., 2022;
Aujeszky's disease virus	12.0	90.0	Maes et al., 1999
Bacteria			
<i>Mycoplasma hyopneumoniae</i>	7.0-27.0	88	Maes et al., 1999; Choi et al., 2003; Arenales et al., 2022
<i>Pasteurella multocida</i>	31.6	34.0	Choi et al., 2003; Arenales et al., 2022
<i>Actinobacillus pleuropneumoniae</i>	0.4-7.7	18.3	Choi et al., 2003; Zhu et al., 2021; Arenales et al., 2022
<i>Haemophilus parasuis</i>	22.0	33.2-35.2	Choi et al., 2003; Zhu et al., 2021; Arenales et al., 2022
<i>Streptococcus suis</i>	13.5	52.3	Zhu et al., 2021; Arenales et al., 2022
<i>Bordetella bronchiseptica</i>	0	8.0	Choi et al., 2003
<i>Salmonella</i> spp.	0	18.6	Arenales et al., 2022
Opportunistic pathogenic microorganisms of the <i>Enterobacteriaceae</i> family.	0	100	Zhao et al., 2020

The role of each pathogen is still not fully investigated, but scientists are confident that collectively bacteria and viruses act synergistically, causing more severe respiratory diseases than those caused by an individual pathogen. It was found that infections caused by viruses make the course of the disease more complex compared to mono-infection. The additional agent can also disturb the targeted isolation of a known virus through interference, where a virus competitively oppresses the replication of other viruses. More than that, a virus can activate the replication of another virus and boost cell death, thereby increasing the severity of the disease (Kumar et al., 2018).

Sunaga F. et al. (2020) developed a system for 17 types of microorganisms' detection in the respiratory tracts of pigs using PCR. According to the research of pigs' lung samples with respiratory disease signs, 12 pathogens were identified (5 viruses and 7 bacteria).

Choi Y. K. (2003) et al. stated that more than 88% of respiratory diseases in pigs out of 2872 analyzed cases had two or more pathogens. The most common cause for PRDC was porcine reproductive and respiratory syndrome virus (PRRSV) or Swine influenza virus (SIV) combined with other bacterial agents such as *Pasteurella multocida*, *M. hyopneumoniae*, and *A. pleuropneumoniae*. The authors think that the introduction of new SIV subtypes (H3N2 and H1N2) to the US swine population has resulted in greater complications in porcine respiratory diseases.

Vangroenweghe F. A. C. J. et al. (2021) studied 22,266 pigs in 974 sow farms for 5 years. The trachea-bronchial swab (TBS) PCR testing was used to confirm different pathogens of PRDC. Samples from weaned piglets had the following dominant pathogens: influenza A virus, European strain of porcine reproductive and respiratory syndrome virus (PRRSV), and *M. hyopneumoniae*; in growing pigs, the main pathogens identified were *M. hyopneumoniae*, porcine circovirus type 2, and PRRSV.

For 15 months a total of 156 samples from pigs were analyzed by histopathology, bacterial isolation, PCR, and

immunohistochemistry. Multiple infections were common in 42.3% of samples with three types of viruses and 6 types of bacteria found (Arenales et al., 2022).

Zhao G. et al. (2020) studied the presence of enterobacteria involved in secondary respiratory infections in pigs. They managed to isolate approximately 13 types of bacteria from various organs of pigs. The enterobacteria were in 100% of samples from pigs infected with PRRSV. In the group with multiple infections involving more than 3 pathogens, the most common bacteria were *Escherichia coli*, followed by *Morganella*, *Proteus*, *Shigella*, *Salmonella*, *Klebsiella*, and *Aeromonas*. Most of the isolated enterobacteria were opportunistic pathogens. Therefore, for effective treatment of PRRSV-infected pigs, timely antimicrobial agents and antibiotic susceptibility of bacteria should be taken into account.

Our attention has drawn several latest domestic researches on the PRDC etiology, PRRSV and circovirus type 2 were considered the key primary pathogens with immunosuppressive qualities.

The publication of Prokhoriatova and Kolchyk (2015) reviewed data from laboratory research of samples from pigs with Respiratory Syndrome (RS), conducted in 2011–2014 in pig farms in 14 regions of Ukraine. The findings were the following: over the course of four years, 5 types of viruses (or their antibodies) were isolated, with PRRSV and porcine circovirus being the dominant ones. The key pathogens in 2011–2012 were *Mycoplasma*, *Pasteurella*, and *Fusobacterium* genera. In 2013–2014, new conditionally pathogenic microorganisms were detected, and they took a significant share in multiple infections: *Naumannella* spp., *Sphaerotilus* spp., *Leptotrichia* spp., *Leptotrix* spp. Researchers connect the increase in the share of conditionally pathogenic bacteria in the etiological structure of infectious diseases with PRDC in 2013–2014 with a weak immune status of pigs due to viruses such as Swine Fever (vaccine strain), PCV-2, PRRSV, PPV, that damage immune cells, and increased technological stress.

Serological studies of homegrown pigs for the presence of antibodies of the porcine reproductive and respiratory syndrome virus in most regions of Ukraine from 2013 to 2015 were presented by a group of authors (Sytiuk et al., 2016). The percentage of samples with positive results ranged from 6.16% in the western to 10.13% in the southern and 22.83% in the eastern and northern regions of Ukraine. The results showed an increase in the percentage of positive samples during the specified period, which allowed us to conclude that the PRRSV was circulating in most regions of Ukraine.

The studies conducted between 2013 and 2017 (Masiuk et al., 2016; Furda, 2018) confirmed the circulation of porcine reproductive and respiratory syndrome viruses and circovirus infections in pig populations throughout the entire study period. Calculations carried out in the study allowed for the prediction of further spread of both viruses, the authors thought that under similar conditions the circovirus infection would spread nearly twice as fast as the porcine reproductive and respiratory syndrome virus.

Kovalenko and Kovalenko did the study of the etiological structure of respiratory pathology in pigs on farms in Sumy and Chernihiv regions in 2021. In the structure of infectious pathology respiratory diseases accounted for up to 21.3% of infectious pathologies and were registered in pigs throughout the entire technological cycle, but with varying frequencies: in suckling piglets, the disease incidence was the lowest - (0.3–1.2) %, in the growers group, it increased to (31–46) % and in finishing group – 57.6%, respectively.

The key identified pathogens were PRRSV and circovirus, *Mycoplasma*, *Streptococcus*, *Pasteurella*, *Bordetella*, *Haemophilus*, *Actinobacillus*, *Salmonella*, and *Escherichia* genera bacteria. The study of the main bacteria sensitivity to antibiotics showed that the number of resistant strains among *Pasteurella*, *Streptococci*, *Bordetella*, and *Escherichia coli* increased.

The objective of our study was to investigate the etiological structure of pathogens of PRDC in individual farms in the Poltava and Kharkiv regions. This study is a continuation of previous research (Severyn et al., 2021), that dealt with PRDC multifactorial development in Poltava region farms.

Methods and materials. The study was conducted in the farms of the Ukrainian Agricultural Limited Liability Company Peremoha, Ukrainian Limited Liability Company Vovnyansky bekon in the Poltava region, and Ukrainian Agricultural Limited Liability Company Mria in the Kharkiv region. Epidemiology statistics of infectious diseases in pigs were provided by the Anti-Epizootic Department of the Main Directorate of the State Service of Ukraine for Food Safety and Consumer Protection in Poltava and Kharkiv regions. Some phases of the research were conducted in the Immunological, Bacteriological, and Pathomorphological Departments of the Poltava Regional Laboratory of the State Service of Ukraine for Food Safety and Consumer Protection. A comprehensive approach was used, which took into account the epizootiological, clinical, and laboratory data. Clinical examination and necropsy of dead and slaughtered animals of different ages were conducted to take the samples for laboratory testing.

Bacteriological studies of samples from sows and pigs of three age groups were conducted to analyze the etiological structure of respiratory pathology: newborn, from 2 to 4 months, and weaned piglets. Samples were taken from affected areas of the lungs at the border of healthy tissue, lymph nodes (mediastinum, submandibular, pharyngeal, mesenteric), heart blood, spleen, liver with the gallbladder, kidneys, and the tubular bone; exudate from the thoracic and abdominal cavities. Cultures from samples were inoculated on meat-peptone broth, meat-peptone agar, blood agar, Endo, and Pliskirev media. Special differential diagnostic media were also used. The cultures were incubated at a temperature of 37°C in a thermostat for 24 hours after the growth of microorganisms was observed. Morphological, staining, cultural-biochemical, and serological properties were studied in the isolated pure cultures. The isolated microorganisms were identified using commonly accepted microbiological methods. The susceptibility of the isolated cultures to antibacterial drugs was determined with the disc diffusion method according to "The Use of Discs for Antibiotic Sensitivity Testing Manual".

Results The study of the epizootic situation in pig farming in Poltava and Kharkiv regions used data from the Anti-Epizootic Department of the Main Directorate of the State Service of Ukraine for Food Safety and Consumer Protection. In recent years, the regions have been relatively stable regarding the epizootic situation concerning classical infections such as classical Swine Fever, Diamond Skin Disease, and Aujeszky's disease.

Analyzing the multiple infections structure in pigs for 2019–2023, it was found that gastrointestinal diseases totaled 34.0%, including colibacillosis – 17.7% and salmonellosis – 16.3%. Therefore, in two farms in the Poltava region, the diagnosis of dysentery was recorded in 4.3% of animals, and colibacillosis and salmonellosis were diagnosed in 10.2% of cases.

We observed a trend of respiratory diseases increasing in pig farms in the Kharkiv and Poltava regions (see Fig. 1).

The average share of respiratory diseases totaled 17.3% in the structure of infectious diseases. The research showed a trend of respiratory infections increasing from 11.4% to 23.7%.

There were 23.7% cases of respiratory diseases recorded in 2023, the most of the diseases had multiple infections nature. Viral infections in pigs caused respiratory disorders in 39.7% of all incidents, while bacterial multiple infections were recorded in 13.2%. The frequency of some viruses' isolation varied significantly. Thus, circovirus was isolated in 20.4% of incidents, Swine respiratory and reproductive syndrome virus in 19.3%, Porcine parvovirus in 7.1%, and Aujeszky's disease virus in 1.2% cases. The results identify two main viral agents of respiratory diseases – circovirus and porcine reproductive and respiratory syndrome virus.

Table 2 demonstrates key microorganisms and multiple infections isolated from pigs with respiratory diseases. The isolated microorganisms show that the structure of pathogens changed over time, the multiple infections included types of 1–3 viruses and types of 4–8 bacteria.

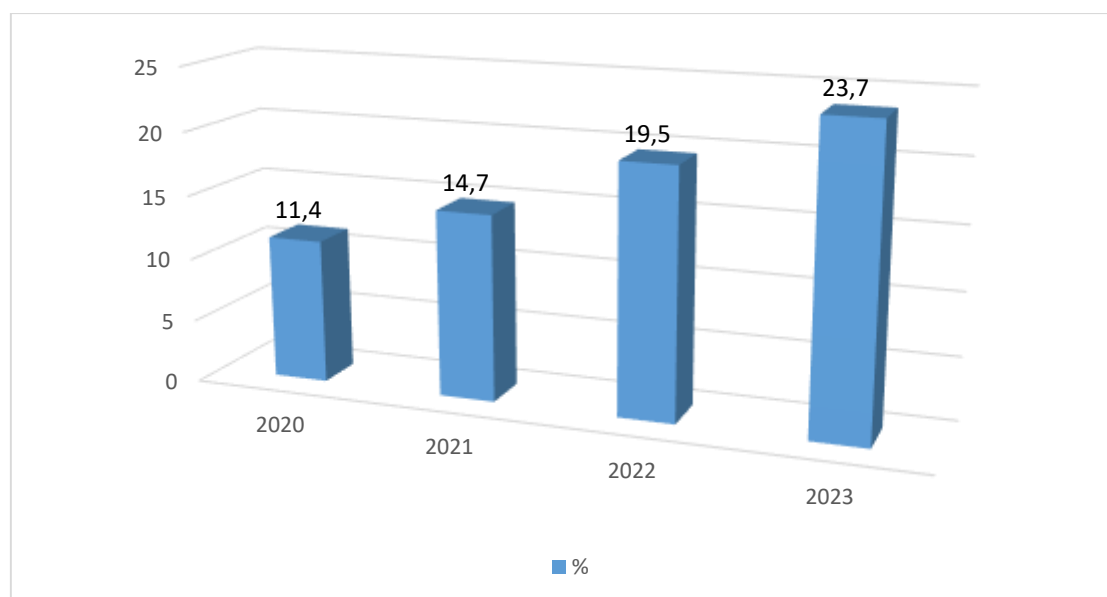


Figure 1. The Table shows the percentage of respiratory diseases in the structure of infectious diseases in pigs in Poltava and Kharkiv regions (TOV Vovnyansky bekon, STOV Peremoha, STOV Mria) for 2020–2023:

The study of blood serum samples from sows and piglets in the mentioned farms in 2019–2023 with the ELISA, identified the Porcine respiratory and reproductive syndrome virus and circovirus type 2, this shows the infection and host condition of the animals. As both viruses cause immunodeficiency, they may trigger the primary mechanism of respiratory organ damage, after which pathogenic and conditionally pathogenic bacteria complicate the course of the disease.

As for bacteria, *Pasteurella*, *Mycoplasma*, and *Escherichia coli* were isolated every year. In the past two years, *Haemophilus* and *Actinobacillus* appeared in the group of pathogens. This shows a wide range of bacteria in the pathogens and requires not only isolation but also the determination of their sensitivity to antibacterial drugs to choose the most effective ones.

Figure 2 shows the frequency of isolation of the key bacteria. As Figure 2 shows, the composition of bacterial infections changed significantly over the 5 years of the study. Only the frequency of *Salmonella* isolation remained nearly unchanged, ranging from 15.3% to 16.3%. The frequency of six agents dropped considerably, while two agents' frequency increased for four years. Thus, the frequency of *Mycoplasma* isolation dropped 7.2 times, *Pasteurella* – 6.3, and the latest study showed no staphylococci, streptococci, pseudomonads, and proteus isolation at all. At the same time, the frequency of *Escherichia coli* and *Actinobacillus* isolation increased: by 17.7 and 8.0 times respectively. The results indicate a change in the most of bacteria involved in multiple infections of respiratory diseases in pigs.

Laboratory analysis included the antibiotic susceptibility of the isolated bacteria to the most commonly used antimicrobial agents. The results of these tests with the samples of pathogens from the organs of deceased piglets that were more often isolated are shown in Table 3.

Table 2

Key respiratory pathogens in pigs on Poltava and Kharkiv regions farms (2019–2022)

Year	Microorganisms	
	Viruses	Bacteria
2019	PRRS	<i>E. coli</i> , <i>Proteus</i> spp., <i>Staphylococcus</i> spp., <i>Pasteurella multocida</i> серотипів A and D, E; <i>Salmonella</i> spp., <i>Streptococcus</i> spp., <i>Pseudomonas aeruginosa</i> , <i>Mycoplasma</i> spp.
2020	PRRS, circovirus, Aujeszky's disease	<i>Pasteurella multocida</i> серотипи A and D, <i>E. coli</i> , <i>Mycoplasma hyopneumoniae</i> , <i>Actinobacillus pleuropneumoniae</i>
2021	PRRS, circovirus, Porcine parvovirus	<i>Pasteurella multocida</i> серотипів A and D, <i>Mycoplasma hyopneumoniae</i> , <i>Haemophilus parasuis</i>
2022	PRRS, circovirus, Porcine parvovirus	<i>Mycoplasma hyopneumoniae</i> , <i>Pasteurella multocida</i> серотипу D, <i>Salmonella</i> spp, <i>E. coli</i>
2023	PRRS	<i>Mycoplasma hyopneumoniae</i> , <i>Pasteurella multocida</i> серотипів A and D, <i>Salmonella</i> spp., <i>E. coli</i> , <i>Actinobacillus pleuropneumoniae</i> , <i>Haemophilus parasuis</i>

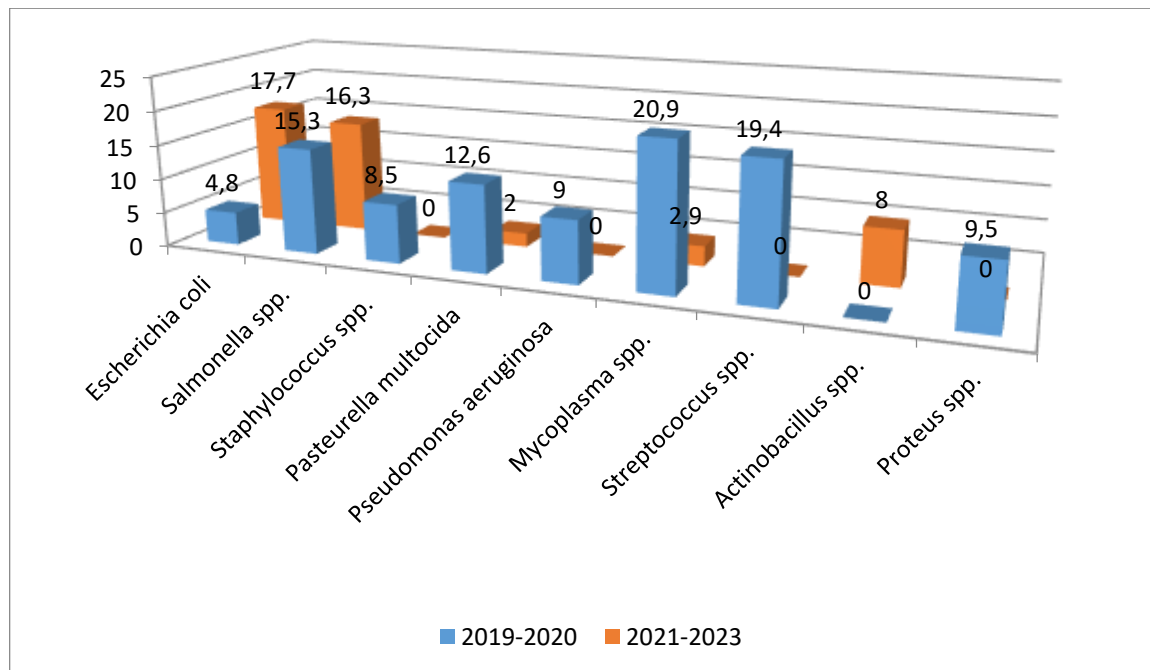


Figure 2. Frequency of isolated multiple infections pathogens in porcine respiratory diseases in two regions of Ukraine in 2019–2023, %

Table 3

The relative susceptibility of bacterial pathogens to antibiotics

Pathogen	Number of antibiotics	Bacteria susceptibility character		
		susceptible	intermediate	resistant
<i>Streptococcus suis</i>	13	11	-	2
<i>Escherichia coli</i>	11	7	-	4
<i>Pasteurella multocida</i>	21	10	6	5

Table 3 shows that *Streptococcus suis* has the highest antibiotic susceptibility (up to 85% of the drugs). Cefazolin, doxycycline, enrofloxacin, tetracycline, and oxytetracycline were the most effective antibiotics. Streptococci were resistant to tylosin and trimethoprim. *Escherichia coli* isolates had lower susceptibility – 64 %. Ciprofloxacin, doxycycline, and enrofloxacin showed the highest efficacy. Isolates of *Escherichia coli* were resistant to tylosin, trimethoprim, colistin, and oxytetracycline. Isolates *Pasteurella multocida* was the most resistant sensitivity to 48 % of drugs only). *Pasteurella* isolates showed the highest susceptibility to amoxicillin, enrofloxacin, florfenicol, and danofloxacin, and the lowest sensitivity was to oxytetracycline, colistin, and spectinomycin.

As the pathogens were different groups of bacteria, their susceptibility was determined to various antibiotics, of which only five were broad-spectrum and were used to study all types of bacteria. Table 4 shows the comparative susceptibility of pathogens to these antibiotics.

As Table 4 shows *Streptococcus suis* and *Escherichia coli* had similar susceptibility: Susceptible to 4 antibiotics and resistant to one. Susceptibility of *Pasteurella multocida* was different: susceptible to amoxicillin and enrofloxacin, intermediate to trimethoprim and ciprofloxacin, and resistant to doxycycline. Therefore, when choosing an antibiotic for treating animals from multiple infections involving bacteria, it is necessary to consider all microorganisms' susceptibility to antibiotics. This approach is the most efficient in treating multiple infections.

Table 4

Comparative susceptibility of *Streptococcus suis*, *Pasteurella multocida* and *Escherichia coli* to antibiotics

Antibiotics	Bacteria type and their susceptibility, mm		
	<i>Streptococcus suis</i>	<i>Escherichia coli</i>	<i>Pasteurella multocida</i>
Amoxicillin	22	20	25
Doxycycline	35	32	12
Enrofloxacin	35	32	24
Trimethoprim/Sulphate	0	0	16
Ciprofloxacin	26	34	18

Researchers from different countries state the frequency of multiple infections respiratory infections in pigs ranges from 6.2% to 88%. According to our studies, during 5 years, the share of respiratory infections increased from 11.4% to 23.7%, and laboratory testing confirmed the diseases with multiple infections. The study of pathogens shows that the quantity and species composition vary significantly in different countries, their regions, and even in different farms. However, PRRSV, PCV2, and influenza were the most common viral pathogens. Our study confirmed the role of the two viruses, while we did not manage to isolate the influenza virus.

In cases of multiple respiratory infections in pigs, researchers most frequently isolated Mycoplasmas, Pasteurellas, Actinobacilli, Streptococci, and Haemophilus, while Enterobacteria were less commonly identified. Our research has confirmed the multiple infections and respiratory diseases in pigs involved in Pasteurellas, Mycoplasmas, and *Escherichia coli*. The antibiotic susceptibility testing showed significant variation in different bacterial species and the selection of resistant strains of microorganisms. Our research confirmed the fact stated by various authors – the share of multidrug-resistant strains of *Pasteurella*, *Streptococcus*, and *Escherichia coli* can reach 40–80%.

Conclusions

The study of the epizootic situation in pig farms in Poltava and Kharkiv regions in 2019–2023, showed an increase in the frequency of respiratory diseases from 11.4% to 23.7%.

The study confirmed multiple infections in porcine respiratory diseases. The multiple infections involved two key viruses (PRRSV and PCV2) and a number of bacteria, ranging from 4 to 8.

During the research period, the variety of bacterial pathogens changed: The frequency of *Mycoplasma* and *Pasteurella* isolation decreased 7.2 and 6.3 times, respectively. *Staphylococci*, *Streptococci*, *Pseudomonads*, and *Proteus* were not isolated during the last year. The isolation of *Escherichia coli* and *Actinobacillus* increased by 17.7 and 8.0 times, respectively.

Streptococcus suis showed the maximum susceptibility (85 %): effective antibiotics were cefazolin, doxycycline, enrofloxacin, tetracycline, and oxytetracycline. Isolated *Escherichia coli* showed susceptibility of up to 64 % to the following antibiotics: ciprofloxacin, doxycycline, and enrofloxacin. The isolates *Pasteurella multocida* were the most resistant, up to 48 %, to antibiotics, including amoxicillin, enrofloxacin, florfenicol, and danofloxacin.

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ЕТИОЛОГІЯ РЕСПІРАТОРНИХ ХВОРОБ СВИНЕЙ ФЕРМЕРСЬКИХ ГОСПОДАРСТВ ХАРКІВСЬКОЇ І ПОЛТАВСЬКОЇ ОБЛАСТЕЙ

Войтенко Р. В., Северин Р. В., Гонтарь А. М., Гарагуля Г. І., Баско С. О.

Державний біотехнологічний університет, Харків (Україна);

e-mail:vetvir.galina@gmail.com*

Резюме Стаття присвячена вивченню етіології комплексу респіраторних захворювань свиней (PRDC). Асоційовані респіраторні інфекції свиней поширені в усьому світі. Вони причиною великих економічних збитків у свинарстві. Нами вивчено епізоотичну ситуацію у фермерських господарствах з вирощування свиней у Полтавській та Харківській областях за період 2019-2023 рр. Встановлено підвищення частоти виникнення респіраторних хвороб свиней з 11,4 % до 23,7 %. Лабораторні дослідження підтвердили асоційований перебіг респіраторних хвороб свиней. До складу асоціацій збудників входили два основних види вірусів (вірус респіраторного і репродуктивного синдрому свиней і цирковірус свиней II типу) та у різні роки від 4 до 8 видів патогенних бактерій. За період досліджень змінився спектр бактеріальних патогенів. Частота виділення мікоплазм і пастерел знизилася у 7,2 та 6,3 рази відповідно, а частота виділення кишкової палички та актинобацилюсів збільшилася відповідно у 17,7 і 8,0 разів. За даними вивчення антибіотикочутливості найбільш чутливими до протимікробних препаратів виявилися ізоляти *Streptococcus suis*, а найвищу резистентність продемонстрували ізоляти *Pasteurella multocida*.

Ключові слова: комплекс респіраторних хвороб свиней, асоційовані інфекції свиней, етіологія.

DOI: 10.31073/onehealthjournal2023-IV-02