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Antibiotic susceptibility of bacteria isolated from abscesses in cats

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The aim of this study was to identify opportunistic microorganisms in feline abscesses and determine their susceptibility to antibacterial drugs. Samples of biological material were cultured on appropriate nutrient media. Standard methods of microbiological practice were used to identify the isolated microorganisms. Pure cultures of microorganisms from abscesses were isolated on non-selective, selective, and differential nutrient media. Antibiotic susceptibility of the isolates was determined by disk-diffusion method on the Mueller-Hinton agar. We studied 17 samples of biological material from feline abscesses, from which 27 microorganisms were isolated: Enterobacteriaceae (8 isolates), *Pseudomonas* spp. (2 isolates), *Staphylococcus* spp. (7 isolates), *Enterococcus* spp. and *Streptococcus pneumoniae* (1 isolate each) and *Candida auris* (8 strains). One microorganism was isolated in 41.2% of cases, two pathogens in 52.9% of cases and three pathogens in 5.9% of cases. Multidrug resistance was determined in 73.7% of isolates. Only 26.3% of strains were susceptible to antibiotics (*Staphylococcus aureus*, *S. epidermidis*, *Streptococcus pneumoniae*, *Enterococcus* spp., *Proteus* spp.). *Staphylococcus aureus* was highly sensitive to nine out of ten antibiotics tested. The smallest were the zones of growth inhibition from the action of doxycycline and chloramphenicol against *S. epidermidis*. Isolates of gram-positive microorganisms were 100% susceptible to gentamicin and norfloxacin; to cefazolin 75%; to cefoperazone, kanamycin, amikacin 50%; to doxycycline, chloramphenicol and cefpirome 25%. Gram-negative *Proteus* spp. was resistant to norfloxacin. Regular antibiotic susceptibility testing will allow us to study antibiotic susceptibility profiles of isolates in animal wound infections and create a system for monitoring the spread of antibiotic resistance. The results obtained can also be used as a basis for developing a system for controlling and preventing the spread of antibiotic resistance.

Keywords: abscess; cats; opportunistic bacteria; bactericidal action; antimicrobial resistance.

Introduction

Bacterial infections associated with abscesses in cats are a significant concern in veterinary medicine. This issue is particularly critical given the increasing prevalence of antimicrobial resistance. Antimicrobial resistance poses a serious challenge to both veterinary and medical practice, threatening the successful treatment of infectious diseases. Veterinary practices, especially those involving companion animals, contribute significantly to this issue, as excessive and unwise use of antibiotics contributes to the development of resistant bacterial strains (Buranasinsup et al., 2023; Moon et al., 2023). This is especially true in the case of cat bite abscesses, where bacteria such as *Pasteurella multocida* are becoming resistant to traditional therapeutic strategies, making the treatment process more difficult (Westling et al., 2006; Meepoo et al., 2022).

The microbiota of abscesses in cats includes a variety of aerobic and anaerobic microorganisms, including Pasteurella multocida in 70% of bite cases (Westling et al., 2006). In addition, *Staphylococcus aureus*, streptococci and anaerobic bacteria such as *Bacteroides* and *Fusobacterium* are often present in these wounds, requiring a comprehensive approach to diagnosis and treatment (Scarpellini et al., 2023). The inherent complexity of the microbial composition of bite-related infections complicates treatment and requires consideration of all pathogens when selecting antibiotics (Marco-Fuertes et al., 2024).

It is important to note that abscesses and wounds caused by cat bites are closely related to the bacterial flora of the oral cavity of these animals, which facilitates cross-transmission of pathogens between animals and humans. Studies have shown that up to 50% of cat bite infections are associated with *Pasteurella multocida,* highlighting its high pathogenicity (Talan et al., 1999). The increasing resistance of abscess-related pathogens to antibiotics, including ampicillin and penicillin, necessitates the development of novel therapeutic strategies and increased regulation of antibiotic use in veterinary practice (Ludwig et al., 2016; Cobo-Angel et al., 2023). Veterinarians and pet owners must be aware of the risks associated with inappropriate antibiotic use, which also has implications for human health (Caneschi et al., 2023).

The categories of people at risk include veterinarians, livestock workers and pet owners. These groups are often exposed to resistant strains through contact with infected animals (Marco-Fuertes et al., 2023; Moon et al., 2023a). Pet owners may be at risk of infection through bites, scratches and contact with infected faeces (Marco-Fuertes et al., 2024).

The concept of One Health, which emphasises the interconnectedness of human, animal and environmental health, is an important aspect of the fight against antimicrobial resistance (Tóth et al., 2022; Osman et al., 2023). The extensive use of antibiotics in veterinary medicine contributes to the development of resistant bacteria which may spread to humans through contact with animals or contaminated environments (Li et al., 2021; Caneschi et al., 2023). It is therefore necessary to consider all aspects of health and develop multidisciplinary strategies to prevent the transmission of resistant bacteria from animals to humans in order to effectively combat antimicrobial resistance.

The aim of this study was to analyse the opportunistic pathogens of abscesses in cats and to assess their susceptibility to antibiotics.

Materials and methods

The study included 17 samples of biological material obtained from abscesses of cats of different age, sex and breed that had been treated at a veterinary clinic in Dnipro during 6 months in 2021. Samples were obtained following meticulous disinfection of the collection site. After making an incision at the point of greatest fluctuation, the material was collected from the walls of the abscesses using swabs packed in round-bottomed plastic tubes (12 × 150 mm) with Amies transport medium in individual packages (Microbiotech, Italy). The tubes were immediately sent for analysis to the Bacteriology Department of the Dnipro Regional Laboratory of the State Service of Ukraine on Food Safety and Consumer Protection. The laboratory used generally accepted methods of microbiological practice and guidelines approved by the institution to isolate microbial strains causing abscesses in animals.

Non-selective (beef extract agar, beef extract broth), selective and differential (mannitol salt agar, lactose agar, crystal violet agar, blood agar, Endo, Sabouraud, Bile Esculin Azide Agar, Streptococcus Selective Agar) nutrient media (HiMedia Laboratories Pvt. Ltd, India) were used for isolation of pure cultures. After enrichment in nutrient broth, streak plating was performed. For this, the Petri dish containing the nutrient medium was conditionally divided into sectors and each of the sectors was touched with a bacteriological loop in a zigzag motion. In this way, the last sector was used to grow isolated colonies. The inoculated Petri dishes were incubated in a TSO-80/1 thermostat (MICROmed, China, 2018) at 35 ± 1 °C for 24 hours.

Morphological and tinctorial properties of the isolated cultures were analysed by Gram staining method (1600×, microscope XS-3330, MICROmed, China, 2018). Species identification of isolates was confirmed using API 20 STREP, API 20 E, API 10 S, API Staph, API 20 NE diagnostic systems (Biomerieux, France).

According to the recommendations of the Clinical and Laboratory Standards Institute (CLSI), the susceptibility of the isolated bacterial cultures to the main groups of antibiotics was determined by the disc diffusion method. A suspension of daily bacterial cultures with sterile saline was brought to 0.5 McFarland standard turbidity, determined using a DEN-1 densitometer (Latvia, 2020), inoculated into Petri dishes with Mueller-Hinton Agar (HiMedia Laboratories Pvt. Ltd, India) within 15 min of preparation. The following antibiotic discs, available on the market, were used for the study: penicillin 10 µg, cefoperazone 75 µg, cefpirome 75 µg, cefazolin 30 µg, kanamycin 30 µg, gentamicin 10 µg, amikacin 30 µg, doxycycline 30 µg, norfloxacin 10 µg, chloramphenicol 30 µg (Farmaktiv LLC, Ukraine).

Antibiotic discs were applied to the inoculated agar with firm pressure. Incubation was performed in a thermostat TSO-80/1 (MICROmed, China, 2018) at a temperature of 35 ± 1 °C. Microbial susceptibility to antibiotics was assessed after 16–20 hours of incubation. Growth inhibition zone diameters were measured using TpsDig2 software and templates (Antibiotic Zone Scale-C, model PW297, India) (Zazharskyi et al., 2024). *Staphylococcus aureus* ATCC 25923, *Staphylococcus epidermidis* UNCSM-018, *Enterococcus faecalis* ATCC 29212, *Streptococcus pneumoniae* ATCC 49619 and *Proteus vulgaris* HX 19222 were used as control bacteria to determine antibiotic susceptibility. Data in the tables are presented as x ± SD (standard deviation). Differences were considered significant at $P < 0.05$. Samples were compared using analysis of variance (ANOVA) with Bonferroni correction.

Results

It was found that out of 17 samples of biological material from abscesses, one microorganism was isolated in 7 cases (41.2%), two microorganisms were isolated in 9 cases (52.9%) and three opportunistic microorganisms were isolated in 1 case (5.9%). A total of 27 isolates were identified, comprising *Klebsiella* spp. (n = 3), *Proteus* spp. (n = 3), *Escherichia coli* (n = 2), *Pseudomonas* spp. (n = 2), *Staphylococcus aureus* (n = 2), *S. epidermidis* (n = 2), *S. felis* (n = 1), *S. haemolyticus* (n = 1), *S. intermedius* (n = 1), *Enterococcus* spp. (n = 1), *Streptococcus pneumoniae* (n = 1). Other opportunistic microorganisms were *Candida auris* (n = 8, Table 1).

In total, 33.3% of cultures isolated from the abscess were represented by gram-positive bacteria, and 66.7% by gram-negative bacteria. However, only 5 isolated bacterial strains were susceptible to antibiotics: four were gram-positive (*Staphylococcus aureus*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Enterococcus* spp.) and one was gram-negative (*Proteus* spp., Table 2).

Table 1
Species spectrum of microorganisms in abscess material (n = 27)

Family	Microorganisms	Quantity of isolates	Proportion of total isolates, %
Saccharomycetaceae	*Candida auris*	8	29.6
Enterobacteriaceae	*Klebsiella* spp.	3	11.1
	Proteus spp.	3	11.1
	Escherichia coli	2	7.4
Pseudomonadaceae	*Pseudomonas* spp.	2	7.4
Staphylococcaceae	*Staphylococcus aureus*	2	7.4
	Staphylococcus epidermidis	2	7.4
	Staphylococcus felis	1	3.7
	Staphylococcus haemolyticus	1	3.7
	Staphylococcus intermedius	1	3.7
Enterococcaceae	*Enterococcus* spp.	1	3.7
Streptococcaceae	*Streptococcus pneumoniae*	1	3.7
Total		27	100

Table 2
Antibiotic susceptibility patterns of gram-positive and gram-negative bacteria (proportion of sensitive isolates, %)

Antibiotic	Gram-positive bacteria							Gram-negative bacteria			
	S. aureus	*S. epidermidis*	*S. felis*	*S. haemolyticus*	*S. intermedius*	*Enterococcus* spp.	*S. pneumoniae*	*Klebsiella* spp.	*Proteus* spp.	*Escherichia coli*	*Pseudomonas* spp.
Penicillin	50	50	0	0	0	0	100	0	33	0	0
Cefpirome	0	0	0	0	0	0	100	0	33	0	0
Cefoperazone	50	50	0	0	0	100	100	0	33	0	0
Cefazolin	50	50	0	0	0	100	100	0	33	0	0
Kanamycin	50	50	0	0	0	100	0	0	33	0	0
Gentamicin	50	50	0	0	0	100	0	0	33	0	0
Amikacin	50	50	0	0	0	100	0	0	33	0	0
Doxycycline	50	50	0	0	0	100	100	0	33	0	0
Norfloxacin	50	50	0	0	0	100	100	0	33	0	0
Chloramphenicol	50	50	0	0	0	100	100	0	33	0	0

Among the gram-positive bacteria, the isolated *Staphylococcus aureus* was sensitive to three out of four beta-lactam drugs: penicillin, cefoperazone, cefazolin (with inhibition zones measuring 34–38 mm), to aminoglycosides: kanamycin, gentamicin and amikacin – with inhibition zones measuring 20–27 mm, as well as to norfloxacin (27.0 ± 0.55 mm, $P < 0.05$), doxycycline (27.1 ± 0.58 mm) and chloramphenicol (28.0 ± 0.63 mm, $P < 0.05$). However, the isolated staphylococci were resistant to cefpirome (0.0 ± 0.0 mm), unlike the control (24.0 ± 0.63 mm, Table 3).

Staphylococcus epidermidis was found to be sensitive to cefazolin (zone of inhibition 34.0 ± 0.45 mm), penicillin (30.0 ± 0.63 mm), cefoperazone (23.0 ± 0.63 mm), amikacin (29.0 ± 1.10 mm, P < 0.05), gentamicin (23.0 ± 0.63 mm), norfloxacin (22.0 ± 0.32 mm, P < 0.05) and kanamycin (20.0 ± 0.89 mm, P < 0.05). *Staphylococcus epidermidis* was found to be moderately sensitive to chloramphenicol: with a zone of inhibition of 14.0 ± 0.71 mm (P < 0.05) and resistant to doxycycline (14.0 ± 0.77 mm, P < 0.05) and cefpirome (0.0 ± 0.0 mm, P < 0.05). Only chloramphenicol (with a zone of inhibition of 18.0 ± 0.26 mm, P < 0.05), norfloxacin (17.0 ± 0.26 mm), and penicillin (16.0 ± 0.63 mm, P < 0.05) were effective against the isolated *Enterococcus* species. However, *Enterococcus* spp. was resistant to cefpirome, cefoperazone, cefazolin, kanamycin, amikacin, doxycycline, and gentamicin (0–14 mm). The control bacterium exhibited markedly lower susceptibility to aminoglycosides, highlighting a contrasting resistance pattern.

Table 3
Zone of growth inhibition (mm, x ± SD, n = 5)

Antibiotic	*S. aureus* ATCC 25923	*S. aureus*	*S. epidermidis* UNCSM-018	*S. epidermidis*	*E. faecalis* ATCC 29212	*Enterococcus* spp.	*S. pneumoniae* ATCC 49619	*S. pneumoniae*	*P. vulgaris* HX 19222	*Proteus* spp.
Penicillin	37.0 ± 0.25	37.0 ± 0.55	30.0 ± 0.46	30.0 ± 0.63	18.2 ± 0.71	16.0 ± 0.63*	22.0 ± 0.75	12.0 ± 0.63*	20.4 ± 0.49	17.0 ± 0.89*
Cefpirome	24.0 ± 0.63	0.0 ± 0.00*	26.0 ± 0.23	0.0 ± 0.0*	0.0 ± 0.00	0.0 ± 0.00	25.4 ± 0.49	13.0 ± 0.55*	23.2 ± 0.98	17.0 ± 0.63*
Cefoperazone	29.4 ± 0.49	34.0 ± 0.89*	23.8 ± 0.75	23.0 ± 0.63	12.2 ± 0.75	11.0 ± 0.32	29.0 ± 0.89	13.0 ± 0.71*	29.2 ± 0.98	22.0 ± 0.63*
Cefazolin	35.0 ± 0.63	38.0 ± 0.63*	35.0 ± 0.89	34.0 ± 0.45	14.4 ± 0.55	14.0 ± 0.10	33.4 ± 0.89	37.0 ± 0.89*	25.2 ± 0.75	24.0 ± 0.55*
Kanamycin	20.4 ± 0.49	20.0 ± 0.63	22.0 ± 0.63	20.0 ± 0.89*	9.0 ± 0.70	11.0 ± 0.14*	12.2 ± 0.40	12.0 ± 0.32	22.4 ± 0.80	20.0 ± 0.84*
Gentamicin	27.2 ± 0.63	27.0 ± 0.89	22.4 ± 0.49	23.0 ± 0.63	8.2 ± 0.84	14.0 ± 0.71*	10.8 ± 0.75	12.0 ± 0.68*	24.6 ± 0.49	22.0 ± 0.89*
Amikacin	26.3 ± 0.60	27.0 ± 0.23	26.4 ± 0.49	29.0 ± 1.10*	9.8 ± 0.75	11.0 ± 0.44*	112 ± 0.75	12.0 ± 0.63	25.0 ± 0.57	19.0 ± 0.63*
Doxycycline	27.6 ± 0.49	27.1 ± 0.58	24.6 ± 0.49	14.0 ± 0.77*	17.0 ± 0.84	12.0 ± 0.26*	28.2 ± 0.40	22.0 ± 0.89*	21.8 ± 0.40	20.0 ± 0.71*
Norfloxacin	23,6 ± 0.49	27.0 ± 0.55*	24.6 ± 0.80	22.0 ± 0.32*	17.6 ± 0.49	17.0 ± 0.26	18.0 ± 0.63	17.0 ± 0.89	19.0 ± 0.63	14.0 ± 0.84*
Chloramphenicol	26.3 ± 0.40	28.0 ± 0.63*	20.6 ± 0.49	14.0 ± 0.71*	21.8 ± 0.40	18.0 ± 0.26*	24.2 ± 0.40	13.0 ± 0.63*	27.0 ± 0.89	31.0 ± 0.63*

Note: * – P < 0.05 compared to the control bacteria.

The most effective *in vitro* against *Streptococcus pneumoniae* was cefazolin (zone of inhibition 37.0 ± 0.89 mm, P < 0.05). This bacterial species was resistant to doxycycline (22.0 ± 0.89 mm, P < 0.05), norfloxacin (17.0 ± 0.89 mm), as well as penicillin, kanamycin, gentamicin, amikacin, cefpirome, cefoperazone, and chloramphenicol, with inhibition zones measuring ≤12–13 mm. The zones of growth inhibition of isolated *Streptococcus pneumoniae* in response to penicillin, cefpirome, cefoperazone, chloramphenicol, and gentamicin were significantly smaller compared to those observed for the control bacteria (P < 0.05).

Gram-negative *Proteus* spp. was most sensitive to chloramphenicol (an inhibition zone 31.0 ± 0.63 mm, P < 0.05), cefazolin (24.0 ± 0.55 mm, P < 0.05), cefoperazone (22.0 ± 0.63 mm, P < 0.05), to aminoglycosides such as gentamicin – 22.0 ± 0.89 mm (P < 0.05), kanamycin – 20.0 ± 0.84 mm (P < 0.05), amikacin – 19.0 ± 0.63 mm (P < 0.05) and doxycycline – 20.0 ± 0.71 mm (P < 0.05), cefpirome (17.0 ± 0.63 mm, P < 0.05) and penicillin (17.0 ± 0.89 mm, P < 0.05). *Proteus* spp. can be considered resistant to norfloxacin, with an inhibition zone of 14.0 ± 0.84 mm.

Complete resistance to all tested antimicrobial agents was observed in five gram-positive and nine gram-negative isolates. In addition, only 25% of the gram-positive isolates were sensitive to cefpirome.

Discussion

Antimicrobial resistance is a major threat to global health, affecting both human and veterinary medicine. The emergence of antimicrobial resistance is caused by mutations in microorganisms that make them resistant to antimicrobial drugs, leading to ineffective treatment, increased disease severity and mortality (Marco-Fuertes et al., 2023). The close interaction between companion animals and humans, particularly in the context of regular antibiotic use, increases the risk of transmission of resistant bacteria, although this direct route has received less attention than transmission via livestock (Tóth et al., 2022). Veterinary professionals play a pivotal role in implementing the One Health approach, focusing on antibiotic management, infection prevention and collaboration with human medicine to contain antimicrobial resistance (Caneschi et al., 2023; Mylostyvyi, 2023). Abscesses in cats are a common clinical problem, especially in outdoor and domestic animals, which are exposed to injuries from contact with sharp objects in 13.1% of cases and bites from other animals in 52.6% (Kulynych et al., 2021; Mylostyvyi et al., 2023). They most commonly occur after bites or fights, when bacteria from the oral cavity invade the underlying tissues and cause an inflammatory process (Lenart-Boroń et al., 2024).

Abscesses are usually localized on the head, neck, paws and tail, the most frequently injured areas (O'Neill et al., 2014; Mylostyvyi et al., 2022). The main pathogens found in abscesses are *Pasteurella multocida*, *Staphylococcus aureus* and anaerobic bacteria due to their presence in the oral cavity and on the skin of cats (Li et al., 2021). Lloret et al. (2013) indicate that *Pasteurella* spp. in cats are mainly concentrated in subcutaneous abscesses and pyothorax.

Risk factors for abscess formation include compromised immune status, suboptimal housing conditions, and insufficient vaccination protocols. Effective treatment of abscesses includes surgical drainage and antibiotic therapy (O'Neill et al., 2014), which helps to prevent complications and speed recovery.

Staphylococcus felis is considered to be commensal on the skin and mucosa of healthy cats and is capable of causing skin infections (Sips et al., 2023).

Our study found that 58.3% of isolates were gram-positive cocci. These data are consistent with the reports of Kožár et al. (2018) and Regmi et al. (2020), who stated that gram-positive bacteria are the cause of purulent wound infections in both humans and animals. Marco-Fuertes et al. (2024) isolated *Staphylococcus felis* in ≈50% of feline skin lesions. *Staphylococcus aureus*, *S. pseudintermedius* and *S. felis* have also been reported to cause superficial pyoderma in cats (Cavana et al., 2022). In addition to *Staphylococcus aureus* (34%), which was the most commonly isolated organism from wounds, *Klebsiella* spp. (13%), coagulase-negative *Staphylococcus* spp. (12%), and *Pseudomonas aeruginosa* (8%) were also reported (Mohammed et al., 2017). However, Kožár et al. (2018) argue that *Staphylococcus* spp. are not always isolated from the pus.

According to Trojan et al. (2016), the most common pathogen isolated from pus samples was *Escherichia coli* (51.2%), followed by *Staphylococcus aureus* (21%), *Klebsiella pneumoniae* (11.6%), *Pseudomonas aeruginosa* (5.8%), *Citrobacter* spp. (3.5%), *Acinetobacter baumannii* (2.3%), *Proteus mirabilis* (2.3%) and *Streptococcus* spp.

According to the results of our studies, the predominant isolates from biological material were *Klebsiella* spp., *Staphylococcus aureus*, *S. epidermidis* (>7%), *S. felis*, *S. haemolyticus*, *S. intermedius*, *Enterococcus* spp. and *Streptococcus pneumoniae* (3.7%), which is also confirmed by recent data from other researchers (Aleshina et al., 2024).

Enterococcus spp. are part of the normal intestinal and oral microbiota, but can cause secondary infections when they enter wounds and abscesses in cats (Osman et al., 2023). These bacteria are often resistant to antibiotics such as ampicillin and penicillin, highlighting the importance of an antibiogram to select appropriate therapy (Ludwig et al., 2016). Some strains, such as *Enterococcus faecalis* and *Enterococcus faecium*, can cause multidrug-resistant infections that require a special approach to treatment (Moon et al., 2023a).

Staphylococcus spp., particularly *S. aureus*, including methicillin-resistant strains (MRSA), are commonly found in infectious wounds in cats (Marco-Fuertes et al., 2024). Although many strains remain susceptible to penicillin and cephalosporins, the increase in resistance makes it necessary to monitor bacterial resistance and use antibiotic susceptibility testing to select the optimal therapy (Aleshina et al., 2024). *Staphylococcus epidermidis*, usually considered a commensal species, can also cause soft tissue infections when the skin barrier is compromised (Yudhanto et al., 2022).

Proteus spp. such as *P. mirabilis* are commonly found in infectious wounds in cats, especially when the skin barrier is impaired. These bacteria may be resistant to antibiotics, necessitating the use of alternative drugs such as fluoroquinolones (Lenart-Boroń et al., 2024).

Streptococcus spp. are also common pathogens in cats, especially in cases of trauma or bites. Most strains remain susceptible to penicillin, but susceptibility testing is necessary for optimal treatment selection (Aleshina et al., 2024). Although *S. pneumoniae* rarely causes skin infections in cats, its presence may be noted in the setting of comorbidities or injury (Kožár et al., 2018).

Enterococcus spp. and *Pseudomonas* spp. showed the highest levels of antimicrobial resistance in cats and were the leading pathogens of purulent infections in cats (Li et al., 2021). The emergence of amoxiclav-resistant *E. coli* strains has been reported (Rijal et al., 2017).

Awosile et al. (2018) point out the importance of identifying microorganisms in a variety of animal infections. Determining the antibiotic susceptibility of isolated bacteria will help clinicians choose antimicrobial agents. Their study revealed that 9% of bacterial isolates from cats were resistant to two or more classes of antimicrobial drugs. Similarly, Marco-Fuertes et al. (2024) reported that 30% of species exhibited multiple antibiotic resistance.

Normand et al. (2000) are concerned about the annual increase in the prevalence of animal pathogens with multiple antimicrobial resistance. In addition, the use of broad-spectrum antimicrobials in companion animals is increasingly leading to the emergence of microorganisms resistant to these agents in humans through close contact. Because of these problems, scientists around the world are developing new modern drugs with antimicrobial activity (Bilan et al., 2024; Kucherenko et al., 2024; Zazharskyi et al., 2024).

Conclusion

Abscesses in cats were caused by *Klebsiella* spp., *Proteus* spp., *Escherichia coli*, *Pseudomonas* spp., *Enterococcus* spp., *Streptococcus pneumoniae* and members of the genus *Staphylococcus*. The predominant isolates from biological material were gram-negative microorganisms (66.7%). Antibiotic susceptibility was demonstrated in 44.4% of gram-positive (*Staphylococcus aureus*, *S. epidermidis*, *Streptococcus pneumoniae*, *Enterococcus* spp.) and 10% of gram-negative (*Proteus* spp.) bacteria. The presence of bacteria with multiple antibiotic resistance was confirmed in both gram-negative and gram-positive isolates.

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