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International Journal of Zoology and Animal Biology
ISSN: 2639-216X

Nosocomial Infection in Veterinary Medicine: A Rare Event or Neglected by Veterinarians?

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Review Article

Volume 6 Issue 1

Received Date: December 24, 2022

Published Date: January 11, 2023

DOI: 10.23880/izab-16000432

Abstract

In humans, nosocomial infections (HI), also known as healthcare-associated infections (HAIs), are those acquired by patient during hospital stay. They are unrelated to the reason for which the patient was hospitalized, and may manifest, mostly due to bacteria, during or after hospitalization. The environment has a strong connection with cases of nosocomial infection in human medicine, however, in veterinary medicine, there is still not much information regarding this connection, since there is no effective data on these infections. The main multidrug-resistant microorganisms involved in nosocomial infections in humans are: Methicillin-resistant *Staphylococcus* (MRS), Vancomycin-resistant *Enterococcus* (VRE), Gram-negative bacteria (*Enterobacteriaceae* family, *Pseudomonas aeruginosa* and *Acinetobacter baumanii*) that produce extended-spectrum beta-lactamase (ESBL) and those producing carbapenemases. As previously mentioned, bacteria are the main microorganisms involved in cases of nosocomial infections, which may come from the patient himself (endogenous contamination) after an immunological decline or come from the environment or cross-contamination (other animals or via health professionals). Generally, the bacteria involved in nosocomial infections are multi-resistant to antimicrobials, especially those most used in hospitals, which makes treatment and patient improvement even more difficult. Despite research related to antimicrobial resistance, the reality of the clinical routine of animals does not seem to be in line with the world reality. There are few studies in veterinary medicine regarding nosocomial infections (some extremely punctual), In the other hand, these infections are already a reality in veterinary hospitals, mainly of small animals, and, unfortunately, they are most of the time neglected due to the difficulty of their traceability or even by the lack of knowledge.

Keywords: Veterinary Medicine; Nosocomial Infection; MRS; VRE; ESBL

Abbreviations: HI: Nosocomial Infections; HAIs: Healthcare-Associated Infections; MRS: Methicillin-resistant Staphylococcus; VRE: Vancomycin-Resistant Enterococcus; ESBL: Extended-Spectrum Beta-Lactamase; MRSA; Methicillin-Resistant *Staphylococcus aureus*; PCS: Positive Coagulase; SCN: Negative Coagulase; SIG: *Staphylococcus* Intermedius Group; CoPS: Coagulase Positive *Staphylococcus*; KPC: Klebsiella Pneumoniae Carbapenemases.

Introduction

Nosocomial Infection

In humans, nosocomial infections (HI), also known as healthcare-associated infections (HAIs), are those acquired by patient during hospital stay. They are unrelated to the reason for which the patient was hospitalized, and may manifest, mostly due to bacteria, during or after hospitalization [1,2].

In veterinary medicine, there are still few studies related to nosocomial infections [3]. However, some important studies have contributed to assist this subject, such as the study by Ruple-Czerniak, et al. [4] which evaluated five school veterinary hospitals. Of the 1535 dogs and 416 cats treated in 12 weeks, 28.3% (16.3% dogs and 12% cats) had at least one case of nosocomial infection. Benedict KM, et al. [5] using a questionnaire carried out in 38 veterinary hospitals (European and North American), showed that 82% (31) reported the occurrence of at least one outbreak of nosocomial infection in the last five years preceding the interview.

In human hospitals, it is estimated that tens of thousands of people die each year of nosocomial infections [6]. The annual cost related to these infections ranges from 28 to 45 billion dollars, not including indirect costs such as community care, lost productivity and lost wages [7]. In veterinary medicine, treatment costs, indemnities due to owner dissatisfaction, loss of business and outbreaks of nosocomial infections are increasingly drawing the attention of veterinarians around the world [8,9].

Actions like the conscious use of antimicrobials, choosing the correct route of administration and monitoring the resistance profile through the antibiogram technique, must be taken to combat multidrug-resistant microorganisms and avoid the impact on public health [10].

The main factors that contribute to nosocomial infections, both in human medicine and in veterinary medicine are: the increased intensive care, a longer hospitalization, the surgical procedures, the use of intravascular devices and probes, the use of antimicrobials and the use of immunosuppressive drugs [8,11,12]. However, an aggravating factor in veterinary medicine that compromise the paciente hygiene is the act of licking wounds and the low concern with the control of nosocomial infections [3].

The pathogens responsible for nosocomial infections in animals could come from other patients, veterinarians, employees and/or the hospital environment [2]. These pathogens have a great zoonotic potencial, which points to the need for control strategies [13].

The environment has a strong connection with cases of nosocomial infection in human medicine, however, in veterinary medicine, there is still not much information regarding this connection, since there is no effective data on these infections [9]. In Brazil, Sfaciotte, et al. [14] isolated methicillin-resistant *Staphylococcus* (MRS), vancomycin-resistant *Enterococcus* (VRE), Gram-negative extended-spectrum beta-lactamase (ESBL) and carbapenemase-producing bacteria in a school veterinary hospital. Despite the authors not having made the connection with cases of nosocomial infections, this result could represents a risk factor for hospitalized animals and people circulating in that environment.

Some critical contamination points in a hospital are: doorknobs, light switches, computers, cell phones, cage doors, stethoscopes, thermometers, gags and, mainly, the hands of doctors and employees, which, when hygiene and disinfection fails, increase the chances of hospital infections [8,14-16].

As previously mentioned, bacteria are the main microorganisms involved in cases of nosocomial infections, which may come from the patient himself (endogenous contamination) after an immunological decline, or come from the environment or cross-contamination (other animals or via health professionals). Generally, the bacteria involved in nosocomial infections are multi-resistant to antimicrobials, especially those most used in hospitals, which makes treatment and patient improvement even more difficult [3].

As there is not much knowledge about the main microorganisms that cause nosocomial infections in animals, the great concern is with those that affect humans, since they have a great zoonotic potential. Another major concern is that they are commonly found in healthy animals/humans (*Staphylococcus, Enterococcus* and *Enterobacteriaceae*) as well as in the environment (*Pseudomonas aeruginosa* and *Acinetobacter baumanii*) [17].

The main multidrug-resistant microorganisms involved in nosocomial infections in humans are: Methicillin-resistant *Staphylococcus* (MRS), Vancomycin-resistant *Enterococcus* (VRE), Gram-negative bacteria (*Enterobacteriaceae* family, *Pseudomonas aeruginosa* and *Acinetobacter baumanii*) that produce extended-spectrum beta-lactamase (ESBL) and those producing carbapenemases [18].

Vancomycin Resistant *Enterococcus* (VRE)

The microorganisms belonging to the genus *Enterococcus* are Gram positive cocci, catalase negative, facultative anaerobes and they are being considered part of the normal intestinal microbiota of humans and animals [19]. More

than 40 different species have already been described, with *E. faecalis, E. faecium, E. cecorum, E. hirae* and *E. gallinarum* being the most prevalent ones found in animals.

Enterococci are considered commensal microorganisms with worldwide spread [20], and for a long time they were considered harmless microorganisms, however, recently, they have been considered emerging and of great importance in the health area, mainly with the increasing incidence of nosocomial infections [20-24].

Currently, *Enterococci* are considered important opportunistic pathogens capable of causing infections in animals and humans [20,25]. They are the third most prevalent pathogen in nosocomial infections [26].

Vancomycin is one of the main antimicrobials used in the treatment of *Enterococcus* infections, however, at the end of the 1980s, in Europe, the indiscriminate use of the glycopeptide avoparcin (analogous to vancomycin) as a growth promoter for production animals, led to the emergence of resistant strains, called vancomycin-resistant *Enterococcus* (VRE) [27,28]. Since then, VRE has already been isolated in the environment, in domestic and production animals, food of animal origin, fish, free-living animals, water, hospitals, among others [29-36].

The first VRE isolates from clinical samples were identified in England and France in 1988, being an isolate of E. faecium [37]. With the appearance of VRE strains in the hospital environment, the treatment of these microorganisms was limited, making them one of the most important multidrug-resistant bacteria in the world [26]. The only antimicrobials used in some situations for the treatment of VRE are: quinupristin/dalfopristin, linezolid, tigecycline and daptomycin. Meantime, resistance to these antimicrobials has already been described [38,39].

In veterinary medicine, especially in small animals, there is not much data regarding VRE. Sfaciotte, et al. [14] divided a veterinary hospital in Brazil into 39 locations, and in 10 of them, there was the presence of VRE identified as *Enterococcus faecalis* and with the presence of the vanA gene. So far, nine different variations in the vancomycin resistance gene of Enterococci have been found, with the vanA, vanB and vanC genes being the most commonly found [40,41].

The impact on public health caused by the transfer of the plasmid vanA gene between strains of Enterococcus isolated from humans and those isolated from animals is still unknown [42]. In addiction, it is already known that the transfer of this gene happens to microorganisms of different genera, since the vanA gene has been identified in strains of methicillin-resistant Staphylococcus aureus (MRSA) [43].

Methicillin Resistant *Staphylococcus* (MRS)

Staphylococci are Gram positive, catalase positive bacteria and comprise more than 40 different species. They are divided into two main groups: positive coagulase (PCS), mainly *S. aureus* and *S. pseudintermedius*; and negative coagulase (SCN), *S. epidermidis* and *S.* [44]. They are considered part of the normal microbiota of the skin and mucous membranes of animals and humans, and are commonly associated with opportunistic infections [45].

Staphylococcus pseudintermedius belongs to the "*Staphylococcus intermedius* group" (SIG group) and is an opportunistic pathogen, being considered the main pathogen isolated from dogs and cats [46,47]. The SIG group (*S. pseudintermedius, S. intermedius* and *S. delphini*) can only be differentiated by molecular techniques, however, when it is not possible to use these techniques, all dog and cat isolates can be classified as *S. pseudintermedius* [46,48].

The two main mechanisms of antimicrobial resistance in *Staphylococcus* are associated with resistance to the beta-lactam class, the first mechanism being an enzymatic inactivation encoded by the blaZ gene, usually plasmid, which confers resistance to penicillins [49]; and the second by the production of additional penicillin-binding protein (PBP2a or PBP2'), a low-affinity penicillin-binding protein encoded by the mecA and mecC genes [50], conferring resistance to all antimicrobials of the beta-lactam class [51], with the exception of fifth-generation cephalosporins (ceftaroline and ceftobiprole).

The blaZ gene has already been identified in *Staphylococcus* isolates of canine and feline origin [52], including strains of *S. pseudintermedius* methicillin resistant (MRSP) and methicillin sensitive strains (MRSS) [53,54], leading to an increase in resistance to penicillin and ampicillin mainly [55].

The mecC gene was recently identified, and, so far, there are few positive isolates for this gene. However, as it has already been isolated in different animal species and in humans in contact with animals, it is believed that mecC is of animal origin [56-58]. Phenotypically, the mecC gene is characterized by being resistant to cefoxitin, but sensitive to oxacillin, while the mecA gene is resistant to both antimicrobials [57,59].

Methicillin resistance is the most important antimicrobial resistance mechanism identified in *Staphylococcus*, which is characterized by the presence of mecA and mecC genes carried in a mobile "genetic island" called "*Staphylococcal Cassette Chromosome mec*" (SCCmec) [60]. The SCCmec elements are capable of harboring insertion sequences,

plasmids and transposons, conferring resistance to other classes of antimicrobials [61].

In total, 13 different types of SCCmec and their variations have already been identified in S. aureus and S. pseudintermedius [62]. Several studies have already identified the mecA gene as part of the SCCmec elements of animal origin [63-65].

The first phenotypic strain of MRSP was isolated from healthy dogs and dogs with pyoderma in France in the late 1980s [66]. The first identification of the mecA gene in dogs occurred in the United States in 1999 [67] and, later, in 2005, in Europe [68]. Since then, MRSP isolates have been reported worldwide in veterinary clinics and hospitals, being recognized as a pathogen of great importance due to multidrug resistance and the difficulty in treating infections [43,48,], in particular in cases of nosocomial infections [53,55].

Initially, *Staphylococcus pseudintermedius* was susceptible to most antimicrobials. However, from the year 2006, MRSP emerged as a pathogen resistant to almost all classes of antimicrobials used in dogs, making antibiotic therapy difficult in small animals [69,70].

In addition to being isolated in animals with some type of infection, MRSP have already been isolated in healthy dogs and cats, mainly in isolates from the nostrils, oral mucosa and skin [71,72], being found a prevalence of 1.5% to 10% [73,74].

The study conducted by Abusleme, et al. in a school veterinary hospital in Chile, a total of 45 strains of coagulase positive *Staphylococcus* (CoPS) were obtained, eight from veterinary professionals, three from hospital surfaces and eight from owners and 26 from dogs. Nine of the strains (20%) were methicillin resistant and all of them carried the mecA gene with high genetic diversity. The study also points out that veterinarians have a high risk of harboring methicillin-resistant CoPS (25% versus 2.5% of owners). In a study carried out in a school veterinary hospital in Brazil, MRS was isolated throughout the hospital environment, from those with large circulation of animals to those where there was no animals circulation, such as in bathrooms and restaurant [14].

These data are important because, despite being rare, human infections by MRSP have already been reported with suspected transmission from dogs [75]. Nasal colonizations by MRSP have also been described in veterinarians and dog owners who have already had MRSP infections [76-78], in addition to environmental contamination [79].

The treatment of MRSP isolates is a challenge in veterinary medicine, since the main antimicrobials used to treat these multiresistant microorganisms are vancomycin and linezolid, but their use is questionable due to the use of these antimicrobials in humans and the fact that they can lead to strains resistant to them [53].

Methicillin-resistant *Staphylococcus aureus* (MRSA) is the main problem of nosocomial infection in humans [63], but in dogs its prevalence is lower than MRSP, while in cats there are still doubts about which of the two is more prevalent [80]. Both healthy dogs and cats can be colonized by MRSA [81,82], but it is transient and can range from 0% to 3% in dogs and up to 4% in cats [83].

Other species of *Staphylococcus*, such as *S. schleiferi* and SCN, have also been described with the presence of the mecA gene, but it seems not to be relevant because they are less common in causing some type of infection. In a study carried out by Griffeth, et al. [84], a 2% prevalence of methicillin-resistant *S. schleiferi* (MRSS) was found in healthy dogs with skin inflammation, while Abraham, et al. [85] did not isolate MRSS in cats.

Extended Spectrum Beta-Lactamase (ESBL)

One of the main resistance mechanisms found in bacteria of the *Enterobacterales* order is the hydrolysis of the beta-lactam ring through enzymes, conferring resistance to antimicrobials of the beta-lactam class, including penicillins, cephalosporins and monobactams [86,87], but they do not hydrolyze cephamycins and carbapenems, in addition to being inactivated by beta-lactamase inhibitors (clavulanic acid, sulbactam and tazobactam) [88]. These enzymes are called extended-spectrum beta-lactamase (ESBL), being divided into three main families, TEM, SHV and CTX-M [89,90].

The genes that encode ESBL are located on conjugative plasmids or on integrons and can be transferred to other species of enterobacteria, further facilitating their propagation [91]. In recent decades, resistance to cephalosporins in much of the world has been considered a major public health threat [10,92,93], often being responsible for cases of nosocomial infections and even community infections [94].

The first enzyme conferring resistance to beta-lactams was of the TEM type, isolated in 1965 in Greece in a human patient called Temoneira, whose name gave rise to the TEM enzyme. This first enzyme, TEM-1, conferred resistance to penicillins and the first generation of cephalosporins, until in the 1980s, extended-spectrum variants of TEM-1 were identified [95].

The second enzyme identified was SHV (variable sulfhydryl), in 1979 [96], which, like TEM, other variants had already been discovered in the mid-80s, both having prominence in *Enterobacterales* resistant to the third generation of cephalosporins [97].

Currently, the most common ESBL is the CTX-M enzyme found mainly in *E. coli* strains [98]. It was identified for the first time by Matsumoto, et al. [99], in Japan, in the feces of a dog of laboratory. CTX-M are divided into five groups (1, 2, 8, 9 and 25), with CTX-M-15 (group 1) being one of the most frequently found in humans and animals [100]. It is being also associated with resistance to the class of fluoroquinolones and aminoglycosides [89]. However, in Brazil, a study showed a higher prevalence of CTX-M from groups 8 and 25 isolated from dogs and cats, showing that individual epidemiological studies are important to highlight the reality of each region [101].

Companion animals, mainly dogs and cats, are important sources of transmission of antimicrobial resistance genes due to their direct contact with humans. This fact represents a great risk to public health [102,103], even more after identifying several types of ESBL-producing microorganisms [93,100].

In veterinary medicine, the first clinical sample producing ESBL in companion animals was an *E. coli,* type SHV-12, isolated from a dog with urinary tract infection in Spain, in 1998 [104], followed by samples from dogs in Italy and Portugal [105,106]. Different variants of CTX-M have already been isolated in clinical samples from dogs, as well as the enzymes TEM [107] and SHV [108]. In Brazil, a study showed the presence of these three gene families within a school veterinary hospital [14] and in healthy and sick animals admitted to the same hospital.

One of the main studies in the detection of ESBL in small animals was carried out in Germany, where 2700 samples were analyzed. CTX-M (1, 2, 14 and 15), were detected in isolates of *E. coli, Salmonella enterica, Proteus mirabilis* and *Enterobacter cloaceae* from wounds, urinary, respiratory, abdominal and bone infections [107].

Most studies carried out with small animals to identify ESBL-producing microorganisms target *E. coli*, however, these enzymes have already been described in other *Enterobacterales*, such as: *Pantoea agglomerans*, *Morganella morganii, Providencia* sp . [109], *Citrobacter* sp., *Enterobacter* sp., *Klebsiella* sp., *Serratia marcescens*, as well as non-*Enterobacterales* bacteria, such as *Pseudomonas aeruginosa, Acinetobacter baumanii* and *Stenotrophomonas maltophilia* in animals.

Although several ESBL isolates have already been identified in small animals, the main studies are focused on production animals, since the transfer of resistance genes between food of animal origin and humans has already been widely described [110,111], but the prevalence, especially of CTX-M in small animals, is limited and requires further studies [112].

About nosocomial infection, ESBL are one of the main causes of this type of infection in humans, but the prevalence of this type of microorganism is still little known in veterinary medicine and the cases of nosocomial infections caused by them are even scarcer. In Brazil, Sfaciotte, et al. [101] collected rectal swabs from 106 animals (dogs and cats) admitted to a school veterinary hospital. 44.34% of which were colonized by ESBL-producing bacteria, showing the importance of disseminating these multiresistant microorganisms

Gram Negative Bacteria Producing Carbapenemases

Resistance to beta-lactams in Gram-negative bacilli has become an emerging problem worldwide in recent years, especially in cases of nosocomial infections, leading to increased patient mortality and increased hospitalization costs [113,114].

Carbapenems are antimicrobials of the beta-lactam class and are considered the last choice for treatments. They are used even in ESBL-producing microorganisms, and are often used to treat human nosocomial infections [115,116]. However, isolates resistant to carbapenems have already been reported, mainly microorganisms from the Enterobacterales order [117]. The mechanisms of resistance to these antimicrobials are associated with decreased membrane permeability, overexpression of beta-lactamase or expression of carbapenemases [118].

Several types of carbapenemases have already been described in *Enterobacterales* the most clinically important are: Klebsiella pneumoniae carbapenemases (KPC), zinc-dependent carbapenemases, also known as metallo-beta-lactamase (Verona integron – VIM, imipenemase – IMP, New Delhi – NDM), oxacilinases – 48 (OXA-48) [117,119] and a cephalosporinase associated with porin loss also leading to resistance to beta-lactams (AmpC) [120].

Beta-lactamases are classified according to several criteria, two of them are the most widespread criteria (1) according to Ambler RP, et al. [121] who classifies beta-lactamase according to their enzymatic molecular structure into 4 groups, where classes A, C and D are called serine-β-lactamase, which have the amino acid serine in the active

center of the enzyme; and class B, which are zinc-dependent and therefore called metallo-β-lactamase. (2) While the second criterion is according to the inhibition profile of the β-lactamases, known as the Bush group [122,123]. Bush, et al. [90] updated the classification scheme according to the two described criteria, which are represented in Table 1 & Figure 1.

Group Bush Jacob[1]	Class Melecular[2]	Representative Enzymes	Feature[3]	Substratos[4]	Inhibition by	
					Clavulanic acid	EDTA
1; 1e	C	CMY-2; CMY-37	AmpC	SCfs	Nao	Nao
2be	A	TE<-3, SHV-2, CTX-M-2, 14,15	ESBL	Oxiamino-Cfs e monobactans	Sim	Nao
2bre	A	TEM-50	IRT-ESBL	Oxiamino-Cfs e monobactans	Nao	Nao
2de; 2df	D	OXA-11, 115, OXA-23, 48	ESBL; Carbapenemases	Oxiamino-Cfs e carbapenemicos	Variable	Nao
2f	S	GES-2, KPC-2,3	Carbapenemases	Oxiamino-Cfs cefamicinas, monobactans e carbapenemicos	Variable	Nao
3a	B(MBL)	SPM-1, IMP-1, VIM-1, NDM-1	Carbapenemases	Oxiamino-Cfs cefamicinas, e carbapenemicos, e monobactans	Nao	Sim

[1]Bush and Jacob (2010); [2]Ambler (1980); [3]ESBL (extended Spectrum β-Lactamase); extended spectrum β-Lactamase; IRT; TEM inhibitor resistance; MBL (Metallo-β-Lactomase); [4]CFs: Cephalosporins Omiamino-Cfs; Broad-spectrum cephalosporins; [5]EDTA (from English, Ethylenediamine tereaacetic acid): Ethylenediamine tetraacetic acid.

Table 1: Classification of the main beta-lactamases in Gram negative bacteria.

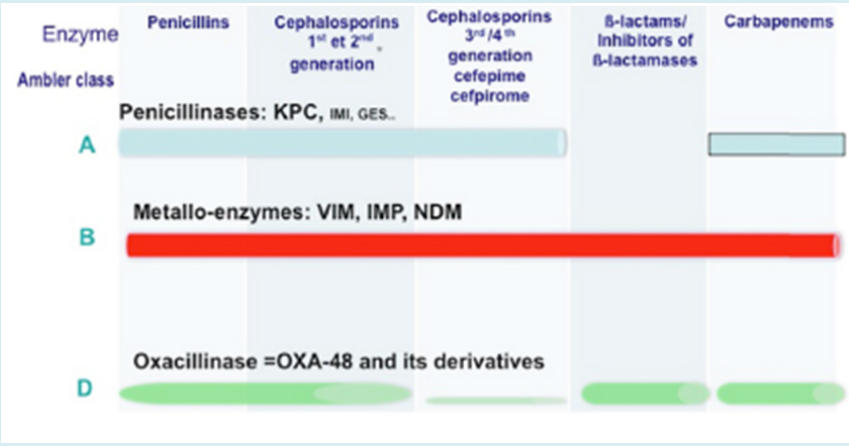

Figure 1: Spectrum of action of carbapenemases in *Enterobacterales*.

Despite name, the KPC enzyme is not restricted to *Klebsiella pneumoniae*, but to all enterobacteria, Pseudomonas aeruginosa and Acinetobacter baumanii, as it is normally found in plasmids and transposons, which facilitates its dissemination [122,124].

In 1996, the first KPC (KPC-1) located in a plasmid was identified, in North Carolina, USA [125]. After that, plasmid KPC began to be isolated in several countries around the world, such as: China and Taiwan [126], Brazil [127] and different countries in Europe [128-130].

The first NDM (metallo-β-lactamase) described was in a Swedish patient hospitalized with a urinary tract infection after a trip to New Delhi, India, in 2009. The microorganism was a *Klebsiella*. pneumoniae resistant to almost all antimicrobials, except for tigecycline and colistin [131]. British authors determined that the large reservoir of these carbapenemases is located in India, Pakistan, Bangladesh and Sri-Lanka, through a study where they isolated NDM from bacteria found in water consumed by the population and in rainwater [132].

In addition to being isolated in cases of nosocomial infections, NDM have already been identified in community samples, mainly in E. coli, in cases of urinary infection and diarrhea, which makes it increasingly difficult to control this multidrug resistance mechanism, since controlling these microorganisms in the hospital is possible, but in the community, it is almost impossible [133].

Carbapenemase OXA is derived from ESBL genes and is located in integrons, transposons and/or insertion sequences housed in plasmids [134]. The identification of OXA-48 is relatively recent, and like other carbapenemases, it has already been described in different bacterial genera of the *Enterobacterales* and responsible for several cases of nosocomial infection [135].

Although not considered a carbapenemase, microorganisms with the presence of the ampC enzyme are considered beta-lactamase hyperproducers, however, the presence of this enzyme confers resistance to carbapenems when associated with an efflux system or alteration in the permeability of the outer membrane [136]. The main ampC with resistance to carbapenems are CTM-Y and FOX [137].

The number of already identified enzymes responsible for conferring resistance to carbapenems is very large and there are several studies isolating these enzymes in cases of infections in humans. In the other hand, in veterinary medicine, these data are little known, with few reports in production animals, in small animals [138-154], and more recently in the veterinary hospital environment in Brazil [14].

Abraham, et al. [85], isolated specimens of *Salmonella* Typhimurium from four domestic cats, one sick and three healthy that were in an animal shelter [155-162]. The isolates harbored the blaIMP-4 gene. The genome sequencing revealed the acquisition of a multidrug-resistant plasmid that encoded resistance to nine antimicrobial classes, including carbapenems [163]. In Spain, Torralba-Gonzáles, et al. isolated a carbapenemase-producing *Klebsiella pneumoniae* by the blaVIM-1 gene in a dog rectal swab. As well as Franandes, et al. in Brazil, isolated a *Pseudomonas aeruginosa* ST233 with the blaVIM- gene 2 in a dog with otitis traced back to the dog's owner who had been hospitalized about a month before the animal's clinical signs manifested (this ST233 strain is internationally reported to be restricted to hospital settings) [164-170].

In a study carried out by Galarde López, et al. analyzing wastewater and treated wastewater from two hospitals in Mexico, 30 isolates were obtained, 26 (86.7%) of *Klebsiella pneumoniae* and 4 (13.3%) of of *Klebsiella oxytoca*, with 13 isolates carrying the blaKPC gene while one isolate was detected harboring both the blaKPC gene and the blaOXA-48 gene [171,s172].

Conclusion

The reality of nosocomial infections worldwide is a fact, with the costs associated with them and the number of deaths growing each year, mainly due to the indiscriminate and often wrong use of antimicrobials, a fact seen in the COVID-19 pandemic. However, in veterinary medicine these data are scarce, since research related to antimicrobial resistance is still punctual and often restricted to a few research groups around the world.

Despite research related to antimicrobial resistance, the reality of the clinical routine of animals does not seem to be in line with the world reality. There are few studies in veterinary medicine regarding nosocomial infections (some extremely punctual), In the other hand, these infections are already a reality in veterinary hospitals, mainly of small animals, and, unfortunately, they are most of the time neglected due to the difficulty of their traceability or even by the lack of knowledge.

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