Profile and antimicrobial sensitivity of bacteria in culture of patients with mechanical ventilation-associated pneumonia during the COVID-19 pandemic: An integrative review

https://doi.org/10.56238/sevened2024.001-014

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ABSTRACT

Respiratory failure caused by the COVID-19 virus in severe cases requires the use of mechanical ventilation. In this context, ventilator-associated pneumonia (VAP) is a nosocomial infection that develops frequently and is related to a worse prognosis. Gram-negative bacteria are commonly isolated in cultures of tracheal secretion. However, the abusive use of antibiotics during the pandemic may have contributed to the selection of resistant bacteria. OBJECTIVE: To identify the main bacterial etiologies and antimicrobial susceptibility profile in patients with VAP during the COVID-19 pandemic. METHODOLOGY: This is a descriptive research, with a qualitative approach, in the form of an integrative literature review. Between March 2020 and May 2022, we searched for publications on bacterial etiologies and antimicrobial susceptibility profile in cultures of patients with VAP in the Scopus, Cochrane Library, US National Library of Medicine (PubMed), and International Health Sciences Literature (Medline) databases. The results of the selected articles were shown in a table. RESULTS: In 14 studies, Gram-negative bacteria were more prevalent. Pseudomonas aeruginosa was identified in 12 studies; Klebsiella pneumoniae in 10 studies; Acinetobacter baumannii in eight; Staphylococcus aureus was isolated in six studies. There was an increase in antimicrobial resistance, especially to carbapenems. Pseudomonas aeruginosa strains were resistant to amikacin, colistin, cefepime, ceftazidime, piperacillin/tazobactam (PIP/TAZ); Klebsiella pneumoniae has demonstrated extensive resistance to extended-spectrum cephalosporins, fluoroquinolones, and aminoglycosides. CONCLUSION: Knowledge of the profile of the main bacterial etiologies, as well as antimicrobial resistance, is essential for the adoption of prophylactic measures and treatment for VAP.

Keywords: Ventilator-Associated Pneumonia, Etiology, Bacteria, Antibiogram.

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INTRODUCTION

COVID-19 is an infectious disease caused by severe acute respiratory syndrome-associated coronavirus 2 (SARS-CoV-2) (WANG et al., 2020). The pandemic unleashed by this new coronavirus has become the most significant in the recent history of humanity, with major impacts on the economy, public health, and the mental health of society as a whole (ALEXANDRINO, 2020). In this context, COVID-19 was classified as a pandemic by the WHO on March 11, 2020 (PAHO, 2020). In Brazil, the first cases were confirmed in February, leading to the implementation of a series of measures aimed at slowing the progression of infection cases (DIÁRIO OFICIAL DA UNIÃO, 2020).

SARS-CoV-2 is spread mainly by droplets, respiratory secretions, and direct contact with the infected patient (FAN et al., 2020). It is commonly a curable disease, but it can also be fatal, especially in high-risk groups, such as the elderly and those with chronic and/or pre-existing diseases (ARRUDA et al., 2020). In severe cases, it causes progressive respiratory failure (CAMPOS et al., 2020). In these clinical conditions, patients are referred to an Intensive Care Unit (ICU) for treatment with non-invasive or invasive ventilation. These intensive care procedures are recommended when there is deterioration in respiratory function, resulting in a decrease in the level of consciousness, increased respiratory rate, and the use of accessory muscles, which requires the use of supplemental oxygen (LIN et al., 2020).

In this scenario, ventilator-associated pneumonia (VAP) is one of the most prevalent infections, frequently developing in patients intubated for more than 48 hours (TEIXEIRA, 2021). This nosocomial infection is directly linked to the retention and aspiration of contaminated upper airway secretions, as well as the presence of resistant microorganisms on ICU surfaces and materials (NATIONAL HEALTH SURVEILLANCE AGENCY, 2017). Due to the severity of VAP, empirical treatment with broad-spectrum antibiotics is quickly initiated (LEAL et al., 2019).

According to studies, Gram-negative bacteria such as Klebisiella pneumoniae, *Acinetobacter baumannii*, and Pseudomonas aeruginosa, *and* Gram-positive bacteria such as Staphylococcus aureus, are the most commonly isolated microorganisms from tracheal cultures (CANZI et al., 2016; COAST; MOTTA; ALFRADIQUE, 2018; CAVALCANTE et al., 2020). However, due to the abusive use of antibiotics during the COVID-19 pandemic, species such as *Mycoplasma pneumoniae,* Haemophilus influenzae, *beta-lactamase-resistant* Klebsiella pneumoniae, *Enterobacter sp., Chlamydia sp., Enterococcus faecium*,   and *Serratia marscecens* they are also found in tracheal secretion culture (SILVA et al., 2021). Therefore, an adequate antimicrobial management program, as well as protocols for early detection of infections, based on the hospital bacterial profile, is essential to overcome this problem (MELO et al., 2019).

The indiscriminate use of antibiotics is considered the main factor for the development of bacterial resistance, often caused by the lack of knowledge of those who use them or by the difficulty of accessing health services, which leads the individual to self-medication (CANTÓN et al., 2020; HELLYER et al., 2020; LEAL et al., 2021). This situation is even more evident in the current scenario of the COVID-19 pandemic and, therefore, studies focusing on bacterial etiologies that presented microbial resistance to antibiotics are necessary.

The aim of this study is to conduct an integrative review in order to identify the main bacterial etiologies, as well as antibiotic sensitivity, of patients with ventilator-associated pneumonia (VAP) during the COVID-19 pandemic.

METHODOLOGY

This is a descriptive research, with a qualitative approach, in the form of an integrative literature review, whose objective is to synthesize knowledge from data from the theoretical and empirical literature, allowing a consistent construction of knowledge (PEREIRA et al., 2018; SOUZA et al., 2010).

The research was composed of five guiding stages: 1) Elaboration of the main guiding question of the research: "What is in the literature on bacterial etiologies and the profile of antimicrobial susceptibility in cultures of patients with VAP during the COVID-19 pandemic?"; 2) Search for studies related to the theme published in the years 2020 to 2022, in accordance with the inclusion and exclusion criteria; 3) Data collection; 4) Critical analysis of the selected articles and 5) Presentation and discussion of results.

The search for articles was carried out in a round of research in the following databases: Scopus, Cochrane Library, US National Library of Medicine (PubMed) and International Health Sciences Literature (Medline). Based on the guiding question of the research, the following descriptors were associated, according to the Health Sciences Descriptors (DeCS): "ventilator-associated pneumonia and bacteria and etiology or ventilator-associated pneumonia and antibiogram"

The search for publications related to the theme took place in the time interval between March 2020 and May 2022, and this period of publication of articles was established in view of the time elapsed between the beginning of the COVID-19 pandemic and the completion of this research.

Inclusion criteria were primary and original articles that addressed at least one of the specific objectives of the study, published in English or Portuguese during March 2020 to May 2022. Exclusion criteria were studies that were not available in full text, free of charge and that were duplicates.

The results of the selected articles were arranged in a systematic analysis instrument, made in the Microsoft Word 2019 program, containing year of publication, authors, objectives, and main results.

As this is a literature review and does not directly involve research with humans, this study did not require approval from the Research Ethics Committee. This work is based on the guidelines and regulatory standards established in resolutions No. 466/2012 and 580/2018 of the National Health Council of the Ministry of Health.

RESULTS

The descriptors and the association between them and the databases used can be seen in Table 1.

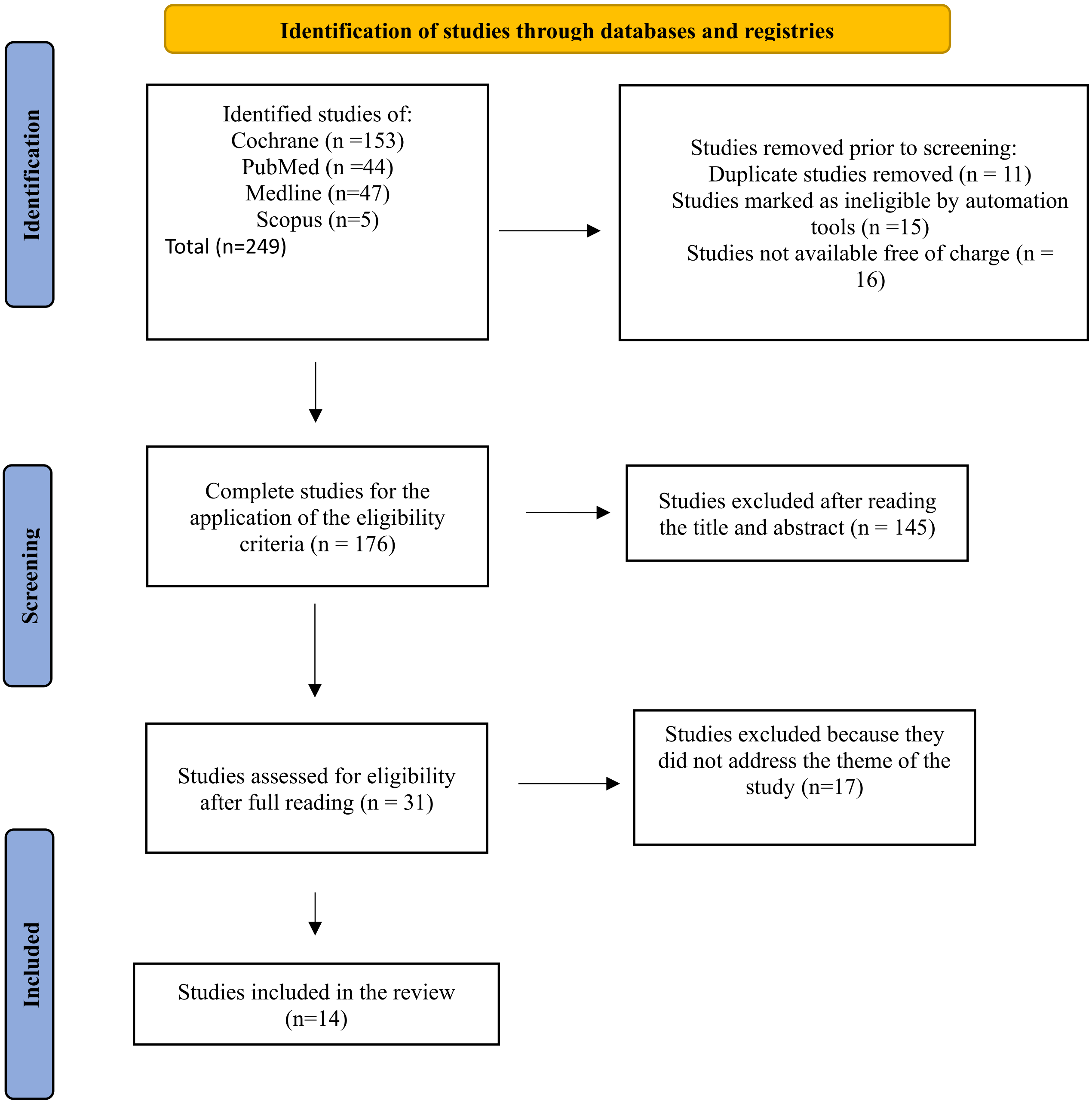
Table 1: Disposition of the number of articles according to the arrangements of the descriptors used in the database search.

Association of descriptors:	Cochrane Library	SCOPUS	MEDLINE	PUBMED
“Ventilator-Associated Pneumonia AND Bacteria AND Etiology OR Ventilator-Associated Pneumonia AND Antibiogram"	153	5	47	44
Total:	153	5	47	44

Source**:** Authors. Data were obtained from the COCHRANE LYBRARY, SCOPUS, MEDLINE and PUBMED databases.

The first stage of the research process resulted in a total of 249 articles. Of these, 11 duplicate articles were removed and 15 were not available due to an error in the online source of the study and 16 articles were not freely available. After reading the title and abstract, 145 articles were excluded because they did not address the theme of the study, then, after reading the full study, 17 articles were discarded because they did not meet the inclusion criteria. Figure 1 illustrates the schematization of the research process employed.

Figure 1 – Flow Diagram



FONTE: PAGE et al. (2021).

Through the methodology used in this research, 14 articles published between the years 2020 (n=3; 21%), 2021 (n=7; 50%) and 2022 (n=4; 28%) were selected. Of these, six (42%) are multicenter studies, while eight (57%) are monocenter. The data shown in Chart 1 allow the visualization of the main bacterial etiologies, as well as the antimicrobial susceptibility profile.

Table 1: Summary of articles published in this integrative review.

Author and year	**Type of production**	**Objectives**	**Main results**
MARJANOVIC et al., 2021	Randomized, multicenter, controlled, and open-label.	To identify whether continuous regulation of the tracheal cuff using a pneumatic device is preferable to intermittent regulation using a portable manometer in reducing the incidence of VAP in patients with severe trauma.	Greater colonization by Staphylococcus aureus (n=48 [44%]), *Haemophilus influenzae* (n=23 [21%]) and Escherichia coli (n=19 [17%]) was identified in early VAP and Staphylococcus aureus *(n=15 [28%]), Pseudomonas aeruginosa* (n=10 [19%]) *and Escherichia coli (n=9 [17 %]) in late VAP.*
YOSHIMURA et al., 2022	Multicenter, open-label, randomized non-inferiority clinical trial.	To compare the clinical response to Gram stain-guided restricted antibacterial therapy to broad-spectrum antibacterial therapy for patients with VAP.	*Staphylococcus aureus* (n = 103 [50.0%]) was the most frequently isolated bacterium from endotracheal aspirate, followed by *Klebsiella sp*. (34 [16.5%]) and *Haemophilus influenza* (20 [9.7%]).
TITOV et al., 2020	Randomized, controlled, double-blind phase 3 study	To evaluate the efficacy and safety of imipenem/cilastatin/relebactam in the treatment of hospital-acquired/ventilator-associated bacterial pneumonia (HABP/VABP).	The most frequent pathogens were *Klebsiella pneumoniae,* Pseudomonas aeruginosa, Acinetobacter calcoaceticus-baumannii *complex* and *Escherichia coli*. Regarding antimicrobial susceptibility, 79.7% of patients in the imipenem/cilastatin with relebactam (IMI/REL) group and 65.8% in the piperacillin/tazobactam (PIP/TAZ) group had all of these baseline pathogens susceptible to the respective drugs.
DAMAS et al., 2022	This is a prospective, multicenter, randomized, controlled, double-blind study.	To evaluate the potential benefit of the noble metal coating of endotracheal tubes for the prevention of VAP.	*Pseudomonas aeruginosa, Staphylococcus aureus, Klebsiella pneumoniae and Enterobacter cloacae* were the microorganisms most associated with VAP.
HABIB et al., 2020	Monocentric randomized clinical study.	To evaluate the role of probiotics in VAP prophylaxis in patients critically injured.	The bacterial species *Pseudomonas sp., Klebsiella sp.*, *Acinetobacter sp.* and *Streptococci sp.* There were more incidents.
AKBIYIK et al., 2021	Randomized controlled experimental study.	To investigate the effect of oropharyngeal aspiration on the incidence of VAP-associated pneumonia immediately prior to the patient's change of position.	*Acinetobacter baumannii* and *Pseudomonas aeruginosa* MDR (Multidrug-Resistant) were detected in 33.4% and 16.8%, respectively, of the cultures.
LI et al., 2021	This is a single-center, prospective, randomized, controlled study.	To explore the efficacy and safety of the rapid flow expulsion maneuver in the prevention of VAP compared to standard subglottic secretion drainage.	*Acinetobacter baumannii* (n=15 [62%]) and *Pseudomonas aeruginosa* (n=6 [25%]) were the most commonly detected pathogens.
KUMAR et al., 2021	Prospective, hospital-based cross-sectional study	To investigate the clinical-microbiological profile, antibiogram and production of metallo-β-lactamases (MBLs) in VAP infections with their subsequent outcome.	A higher frequency of *Acinetobacter baumannii, Pseudomonas aeruginosa, Klebsiella pneumoniae* and *Staphylococcus aureus* was observed in bacterial cultures. Among the Gram-negative bacteria, 144 (85%) were multidrug-resistant, 58% resistant to carbapenems. Regarding Gram-positive

			patients, 92% were *methicillin-resistant* Staphylococcus aureus (MRSA).
MAEBED et al., 2021	Observational and prospective incidence study	To identify the main pathogens causing VAP at the Beni-Suef University Hospital (BSU)	The most prevalent isolates were *Klebsiella pneumoniae*, *Acinetobacter baumannii* and *Moraxella sp*. Most of the K. *pneumoniae* isolates showed resistance to multiple drugs, while the Acinetobacter isolates showed pan-resistance patterns, including carbapenems, extended-spectrum cephalosporins, fluoroquinolones, and aminoglycosides.
BAIDYA et al., 2021	Laboratory-based cross-sectional study	To determine the biofilm produced by VAP-causing pathogens and their relationship to drug resistance.	Among the bacterial isolates, *Pseudomonas aeruginosa* (31%) was the most prevalent microorganism, followed by the *Acinetobacter calcoaceticus baumannii* complex (ACBC) totaling 16%. All cultures were susceptible to vancomycin, teicoplanin (gram-positive) and colistin (gram-negative). Finally, less than 50% of gram-negative isolates were sensitive to carbapenem.
GARDEN et al., 2022	This is a descriptive, retrospective and monocentric study.	To determine the bacterial agents isolated in tracheal aspirate cultures of patients in general Covid-19 intensive care, in addition to evaluating the bacterial resistance profiles to common antibiotics, comparing with the pre-pandemic period.	Pre-pandemic samples detected *Acinetobacter baumannii, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus*, and *Escherichia coli* more frequently. During the pandemic, they were *A. baumannii, K. pneumoniae, P. aeruginosa, and E. faecium.* In addition, *A. baumannii, K. pneumoniae, and P. aeruginosa* showed increased resistance to amikacin, meropenem, and colistin during the pandemic.
MOTSCH et al., 2020	Randomized, multicenter, controlled, double-blind, phase 3 trial.	To compare imipenem/cilastatin/relebactam (IMI/REL) with colistin-based therapy for severe gram-negative bacterial infections, not susceptible to imipenem.	The most frequent baseline pathogens *were Pseudomonas aeruginosa, Klebsiella pneumoniae*, and other *Enterobacteriaceae.*
DATA et al., 2022	This is a multicenter, open-label, randomized, controlled study.	To assess whether continuous cuff pressure control (CPC) is associated with reduced incidence of ventilator-associated respiratory infection compared to intermittent CPC.	The main etiologies isolated were *Pseudomonas aeruginosa*, *Klebsiella pneumoniae* and *Staphylococcus aureus*.
GYSIN et al., 2021	Single-center, prospective observational study.	To analyze the bacterial spectrum and antimicrobial susceptibility patterns of Gram-negative bacilli isolated from ICU-ventilated patients during the first wave of COVID-19 in Switzerland.	The Gram-negative pathogens isolated were *Pseudomonas aeruginosa*, *Enterobacter cloacae* and *Klebsiella pneumoniae*. A high proportion of P. *aeruginosa* isolates were resistant to the antibiotics cefepime, ceftazidime, meropenem and, especially, piperacillin/tazobactam. *Enterobacter cloacae* and *Klebsiella pneumoniae* were resistant to piperacillin/tazobactam, ceftriaxone and ceftazidime.

Source: Authors.

According to Chart 1, the most frequently detected microorganism was the Gram-negative bacterium *Pseudomonas aeruginosa*, with an incidence ranging from 16% to 31%. The presence of this pathogen was identified in 12 studies (85%), in addition, *Pseudomonas aeruginosa* was the main etiological agent of the samples collected from patients diagnosed with VAP (BAIDYA et al., 2021; DATA et al., 2022; GYSIN et al., 2021; HABIB et al., 2020 MOTSCH et al., 2020).

Ademais, outras bactérias Gram-negativas foram isoladas em culturas de secreção traqueal, como *Klebsiella pneumoniae*, identificada em 10 estudos (BAHÇE et al., 2022; DAMAS et al., 2022; DATA et al., 2022; GYSIN et al., 2021; HABIB et al., 2020; KUMAR et al., 2021; MAEBED et al., 2021; MOTSCH et al., 2020; TITOV et al., 2020; YOSHIMURA et al., 2022), *Acinetobacter baumannii* em oito (AKBIYIK et al., 2021; BAHÇE et al., 2022; BAIDYA et al., 2021; HABIB et al., 2020; KUMAR et al., 2021; LI et al., 2021; MAEBED et al., 2021; TITOV et al., 2020) e *Escherichia coli* em três (BAHÇE et al., 2022; MARJANOVIC et al., 2021; TITOV et al., 2020).

In four (28%) of the 14 scientific productions selected, *Acinetobacter baumannii* was the predominantly isolated organism (AKBIYIK et al., 2021; BAHÇE et al., 2022; KUMAR et al., 2021; LI et al., 2021).

Among the Gram-positive bacteria, *Staphylococcus aureus* was the most isolated. Six (42%) studies have identified this bacterium in tracheal secretion samples from patients with VAP and its incidence frequency ranged from 9% to 50% (BAHÇE et al., 2022; DAMAS et al., 2022; DATA et al., 2022; KUMAR et al., 2021; MARJANOVIC et al., 2021; YOSHIMURA et al., 2022). Other bacteria such as *Haemophilus influenzae*, *Enterobacter cloacae* and *Moraxella sp* were isolated less frequently than the others.

Regarding antimicrobial sensitivity, cultures of *Pseudomonas aeruginosa, Klebsiella pneumoniae, and Acinetobacter baumannii* have demonstrated resistance to carbapenems such as meropenem above 50% (BAIDYA et al., 2021; GYSIN et al., 2021; KUMAR et al., 2021). Furthermore, in two studies, isolated Gram-negative individuals were considered Multidrug Resistant (MDR) (KUMAR et al., 2021; MAEBED et al., 2021). Also, according to Gysin et al. 2021, the analysis of the antibiogram of *Pseudomonas aeruginosa* isolates found resistance to amikacin, colistin, cefepime, ceftazidime, piperacillin/tazobactam (PIP/TAZ), while those of *Klebsiella pneumoniae* showed patterns of extensive resistance to drugs, such as extended-spectrum cephalosporins, fluoroquinolones, and aminoglycosides. Among Staphylococcus aureus cultures, *92% were Methicillin-Resistant* Staphylococcus Aureus *(MRSA) (KUMAR et al., 2021).*

On the other hand, in the study by TITOV et al. (2020), 79% of the samples of *Pseudomonas aeruginosa, Klebsiella pneumoniae, Acinetobacter baumannii* , and *Escherichia coli* were susceptible to imipenem/colastatin, and 65% to piperacillin/tazobactam. The antimicrobial colistin was effective against *Pseudomonas aeruginosa* and *Acinetobacter baumannii* (BAIDYA et al., 2021).

DISCUSSION

The ICU environment is seen as an important source of outbreaks of multidrug-resistant microorganisms, with the excessive use of antibiotics as a risk factor, as well as the vulnerability of the hospitalized population, which increases the risk of infection (LONDE et al., 2017). In addition, the higher mortality rates in the case of ventilator-associated pneumonia (VAP) are linked to the presence of high-risk pathogens or situations in which initial antibiotic therapy is not adequate for the etiologic agent (COSTA et al., 2016).

In the present study, there was a predominance of colonization by Gram-negative bacteria. The main etiology associated with VAP was *Pseudomonas aeruginosa*, followed by *Klebsiella pneumoniae,* Acinetobacter baumannii *and* Escherichia coli, *as* well as the Gram-positive bacterium *Staphylococcus aureus*. In an investigational study on secondary bacterial infections in patients with COVID-19 on mechanical ventilation, the most isolated bacteria were *A. baumannii,* P. aeruginosa, *E. coli,* and *K. pneumoniae* (ZANCO, 2021). Another study conducted in a tertiary hospital in southern Brazil detected a higher incidence of *Acinetobacter baumannii* and *Klebsiella pneumonia* (TEJO et al., 2021). *Acinetobacter sp*. presents the highest risk of contamination in hospital environments, as it can often be found in valves and mechanical ventilation circuits, as well as in the oral cavity of ICU patients (ARAÚJO et al., 2018; EUGÊNIO et al., 2018). High-risk patients are more vulnerable to infection, especially those who use mechanical ventilation (MV), which is a probable explanation for its high prevalence in the samples of so many multicenter studies, such as those evaluated here (SÁ et al., 2021).

The distribution of etiologic agents varies among ICUs, depending on demographic variables, such as the patient population and the ICU model (DIAS et al., 2021). However, Gram-negative bacteria are often related to VAP (BATISTA et al., 2014). A cross-sectional study conducted at the Hospital de Clínicas of the Federal University of Uberlândia reported an increase in the prevalence of *Acinetobacter baumanii* and *Pseudomonas aeruginosa, in* addition to a decrease in Gram-positive bacteria, such as *Staphylococcus aureus* (MOREIRA et al., 2013). In another study conducted in 2017, the predominant bacterium was *Acinetobacter baumannii*, followed by *Klebsiella pneumoniae* and *Pseudomonas aeruginosa* (PHU; NADJM; DUY, 2017).

Furthermore, data from a study conducted in the Pediatric Intensive Care Unit of a tertiary hospital in northern India corroborate the bacterial profile identified in other studies. Among bacterial etiologies, *Acinetobacter baumannii* (47%) was the most common, followed by *Pseudomonas aeruginosa (28%) and* Klebsiella *(14%) (VIJAY et al., 2018*). The most isolated agent, in a retrospective observational study conducted between January 2010 and June 2015, was *Acinetobacter baumannii* susceptible to colistin, the other causative agents of VAP were *Pseudomonas aeruginosa* and *Klebsiella pneumoniae* (DJORDJEVIC et al., 2017).

Regarding the sensitivity of bacterial isolates to antimicrobials, colistin also demonstrates effectiveness against *Acinetobacter baumannii* strains. A study conducted at two coronavirus referral hospitals in Qom, Iran, showed that strains of A. *baumannii* were resistant to different classes of antibiotics except colistin (SHARIFIPOUR et al., 2020). However, seven studies, out of the 14 analysed here, identified Multidrug-Resistant (MDR) bacteria (AKBIYIK et al., 2021; BAIDYA et al., 2021; BAHÇE et al., 2022; GYSIN et al., 2021; KUMAR et al., 2021; MAEBED et al., 2021; TITOV et al., 2020).

Carbapenemic resistance was higher in the strains of *Pseudomonas aeruginosa*, *Klebsiella pneumoniae* and *Acinetobacter baumannii*, being above 50%. According to Castilho et al. (2017), in a study that evaluated 1,333 patients in five ICUs, most of the *A. baumannii* found were resistant to beta-lactam antimicrobials, specifically, cephalosporins and 3rd and 4th generation carbapenems, and 91.1% of the isolates were multidrug-resistant (MDR).

In addition, this study also identified resistance of *Pseudomonas aeruginosa* to amikacin, colistin, cefepime, ceftazidime, piperacillin/tazobactam (PIP/TAZ). This result is similar to that of a study carried out in the ICU of a teaching hospital, in which P. *aeruginosa* isolates showed greater resistance to beta-lactams: ceftriaxone (85%), piperacillin-tazobactam (55%), imipenem (40%) and meropenem (30%) (ALVARES et al., 2021). *P. aeruginosa* has a wide range of antibacterial drug resistance mechanisms at its disposal, such as multi-drug efflux pumps, changes in its outer membrane porins, and the expression of β-lactamases (HORCAJADA et al., 2019). The repercussion of inadequate therapy in these infections is significant, the World Health Organization reported in 2017 that carbapenem-resistant *P. aeruginosa* was listed in the "critical" group, requiring the urgent need for new antibiotics (TACCONELLI et al., 2018).

Based on the data, the cause of this scenario of widespread bacterial resistance is assumed to be the increased demand and use of antibiotics, especially during the COVID-19 pandemic (BATISTA et al., 2022). Despite the fact that only 15% of COVID-19 patients had a secondary bacterial infection, a study conducted at two hospitals in China found that 95% of these patients were using antimicrobial drugs (ZHOU et al., 2020).

It is noteworthy that some limitations of the study should be explained, such as the use of only four databases, in addition to the fact that the results of research comparing the clinical evolution or mortality caused by the strains in patients with VAP are not integrated into the study. In addition, not all of the analyzed diseases had etiological analysis as the main objective of the study. Therefore, based on the literature, Gram-negative microorganisms are the main etiologies associated with VAP, both before and during the COVID-19 pandemic. However, resistance to antibiotics has grown, especially carbapenems. The results of the study justify further exploration, since the time frame of this study is recent.

CONCLUSION

The COVID-19 pandemic still poses a challenge to physicians and the scientific community. Secondary bacterial infections can arise during or after COVID-19, which makes them inevitable. In this context, this study found greater bacterial colonization of patients with VAP by Gram-negative strains, especially *P. aeruginosa*, *Klebsiella pneumoniae* and *Acinetobacter baumannii*. *Staphylococcus aureus* representing Gram-positive microorganisms was present in smaller quantities.

No significant change in the microbiota involved in VAP cases was detected, however antimicrobial resistance increased considerably, especially to beta-lactam antimicrobials, such as carbapenems. Colistin showed good results in the fight against *A. baumannii* and *P. aeruginosa.*

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