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RESEARCH ARTICLE

# Resistance profiles of bacterial pathogens isolated in a hospital institution in Montería - Córdoba, 2018

**Álvaro Bustos González[1], José Ortiz Girón[1], Nohra Diaz Cornejo[1], Olga Galván Garces[2], Luis Ruiz Garcés[1]***

**1** Faculty of Health Science, Medicine Program, University of Sinu, Monteria, Colombia
**2** Faculty of Education and Human Sciences, Bachelor´s Degree Program in Foreign Languages with an Emphasis in English, University of Cordoba

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* **Corresponding author**.

luiscarlosrg03@gmail.com

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## Abstract

**Objective:** To determine the resistance profiles of bacterial pathogens isolated in a hospital institution in Montería – Córdoba. **Methodology:** An observational study was carried out, during the months of January to December 2018; 344 samples were evaluated. Mention about the source of study samples. The identification and susceptibility of the bacteria were determined through the VITEK system. **Findings:** Among the Gram-negative bacteria identified were *Klebsiella pneumoniae, Pseudomonas aeruginosa, Escherichia coli, Acinetobacter baumannii* and *Serratia marcescens*, while Gram-positives were the *Staphylococcus epidermidis*, *S. aureus*, S. haemolyticus and *Enterococcus faecalis*. Gram-negative isolates such as *Klebsiella pneumoniae* showed resistance to piperacilina-tazobactam, ceftazidima, cefepima, doripenem, imipenem, meropenem, amikacina and ciprofloxacina, being sensitive to gentamicin. *P. aeruginosa, E. coli* and *A. baumannii* showed resistance to all antimicrobials, with the exception of colistin. S*. marcescens* only showed resistance to ceftazidime. *Enterobacter cloacae* showed resistance to most drugs, with the exception of amikacin and gentamicin. Among the Gram-positive isolates, *S. epidermidis* showed resistance to Trimethoprim / Sulfamethoxazole, erythromycin, nitrofurantoin, ciprofloxacin, and levofloxacin. *S. aureus* and *Staphylococcus haemolyticus* showed susceptibility to all antimicrobials, while *E. faecalis* and *Staphylococcus hominis* only showed resistance to erythromycin. **Conclusion:** A wide prevalence of antimicrobial resistance (mention the milieu) was observed in this investigation.

**Keywords:** Antibiotic; antimicrobial resistance; bacteria

## 1 Introduction

Antimicrobial drugs have saved millions of people from life-threatening bacterial infections. Nowadays the treatment of bacterial infections is becoming increasingly complicated[(1)]. Due to antimicrobial resistance (AMR), which is growing at an alarming rate, the situation may be exacerbated in developing countries as a result of abuse of antimicrobial use[(2)]. It is well-known that any use of antimicrobials, even appropriate and justified, contributes to the development of resistance, but

widespread unnecessary and excessive use makes it worse [3]. Overuse and misuse of antimicrobials are facilitated in many places by their availability over the counter and without prescription, but even where this is not the case prescribing practices vary hugely between (and often within) countries [3]. Globally, more than 50% of all drugs are improperly prescribed, dispensed or sold [4].

Bacterial infections caused by antimicrobial-resistant bacteria (AMR) are a growing threat throughout the world, being the leading cause of morbidity and mortality in developing countries, including Colombia [5]. As published by the World Health Organization in the United States, antimicrobial-resistant (AMR) microorganisms cause more than 2 billion infections and are associated with approximately 23,000 deaths each year, estimated at $35 billion annual health service expenditures, and the European Center for Disease Prevention and Control (ECDC) reported that AMR is associated with approximately 25,000 deaths per year, costing around €1.5 billion in additional health services and losses of productivity per year in Europe [6]. It is estimated that antibiotic-resistant bacterial infections could cause more than 10 million deaths in the year 2,050 if the problem of antibiotic resistance is not addressed from now on [7].

According to Anaya et al, 2020, the microorganisms that pose a threat to health not only in the US but throughout the world, due to increased resistance, are the carbapenem-resistant *Enterobacteriaceae*, methicillin-resistant *Staphylococcus aureus*, and bacteria producers of extended-spectrum $\beta$-lactamase (ESBL). According to a press release from the World Health Organization in February 2017, priority bacterial pathogens resistant to most antibiotics are *Acinetobacter baumannii* resistant to carbapenems, *Pseudomonas aeruginosa* resistant to carbapenems, *Enterobacteriaceae* resistant to carbapenems, producing ESBL; *Enterococcus faecium* resistant to vancomycin, *Staphylococcus aureus* resistant to methicillin and with intermediate sensitivity and resistance to vancomycin. These bacteria are spreading rapidly, not only in healthcare but also in the environment around the world through mobile genetic elements [8].

Antimicrobial resistance genes (ARGs) can be multiplied by proliferation of their bacterial hosts and transfer to phylogenetically unrelated bacteria through horizontal gene transfer (HGT) mediated by mobile genetic elements (MGE) such as integrons, transposons or plasmids [9]. The prevalence of antibiotic resistance genes in clinical and environmental settings has been recognized as one of the most serious threats to the health and well-being of humans and animals in the 21st century, with global implications [10].

When penicillin was introduced into clinical practice, the vast majority of *S. aureus* strains were susceptible, currently, they are less than 5-10%. When cefotaxime was introduced into the clinic in the early 1980s, all strains of *Escherichia coli* and *Klebsiella pneumoniae* were susceptible; today 13% and 16% respectively of the isolates in Spain are resistant. When fluoroquinolones were marketed in the mid-1980s, virtually all strains of *E. coli* were susceptible; today 34% are resistant in Spain [11]. The problem is aggravated by the scarce resources that pharmaceutical industries dedicate to research on antibiotics [12], which has resulted in few new ones and none with a different mechanism of action in recent years [12].

International epidemiological surveillance programs such as SENTRY, MYSTIC and TRUST have studied the behavior of specific pathogens in different clinical syndromes; a limited number of countries in Latin America have national programs for monitoring resistance, some of them being Argentina, Chile and Colombia [13].

The empirical use of antibiotics improperly in the treatment of bacterial infections can facilitate the development of resistance to antimicrobial agents, which poses a great challenge for clinicians and researchers, since data on prevalence and Antimicrobial sensitivity varies between care centers and cities. Hence, we sought to determine the main etiological agents and the frequency of resistance to antibiotics by isolated microorganisms in patients.

## 2 Materials and Method

### 2.1 Study design

An observational, prospective study was carried out in a clinic in the city of Montería - Córdoba, during the months of January to December 2018.

### 2.2 Sampling

During the study period, 344 samples from hospitalized patients with bacterial infections were evaluated. Informed consent was obtained from patients or close relatives prior to their inclusion in the study. All patients of both sexes, all age groups with suspected or proven infection were admitted [11].

The samples were collected by trained laboratory personnel at the request of the physician. The samples were inoculated in 50 ml of tryptone soy broth and incubated at 37°C [14]. Turbidity (sign of bacterial growth) was checked daily until day 14 to report no bacterial growth. The cloudy broth cultures were subcultured on MacConkey agar, blood agar, chocolate agar and mannitol salty agar, to later be incubated at 37°C for 24 to 48 hours [11,14,15].

Subsequently, the pure colonies were grown on nutrient agar and blood agar for their identification through the VITEK system, using the GNI + cards for Gram-negative bacilli and GPI for Gram-positive cocci. Prior to the inoculation of the cards, the Gram staining and oxidase, catalase and/or coagulase reaction were performed in all cases according to the

microorganism [16].

### 2.3 Susceptibility testing

The susceptibility of the bacterial isolates to different antimicrobials was determined through the VITEK system, for which three milliliters of sterile saline solution was transferred to a test tube, later an isolated colony was selected, mixed and the density determined through the McFarland scale, which should have been between 0.5 - 0.63 [16,17]. In the susceptibility studies, the GNS 113 and GPS 102 cards were used for Gram-negative bacilli and Gram-positive cocci, respectively [16]. The antimicrobials used were: piperacillin / tazobactam, ceftazidime, cefepime, doripenem, imipenem, meropenem, amikacin, gentamicin, ciprofloxacin, colistin, trimethoprim / sulfamethoxazole, erythromycin, nitrofurantoin, teplanofycin, and vancomampicinminicillin, vancomofloxacin, teicoplanin, minocycline, rifampin, and tetracillin.

## 3 Results

### 3.1 Distribution of positive samples

During the period from January to December 2018, a total of 344 patients were confirmed with bacterial infections, of which it was found that the frequency of isolation of Gram-negative bacteria 268 (78%) was higher than that of Gram-positive 76 (22%) bacteria (Figure 1).

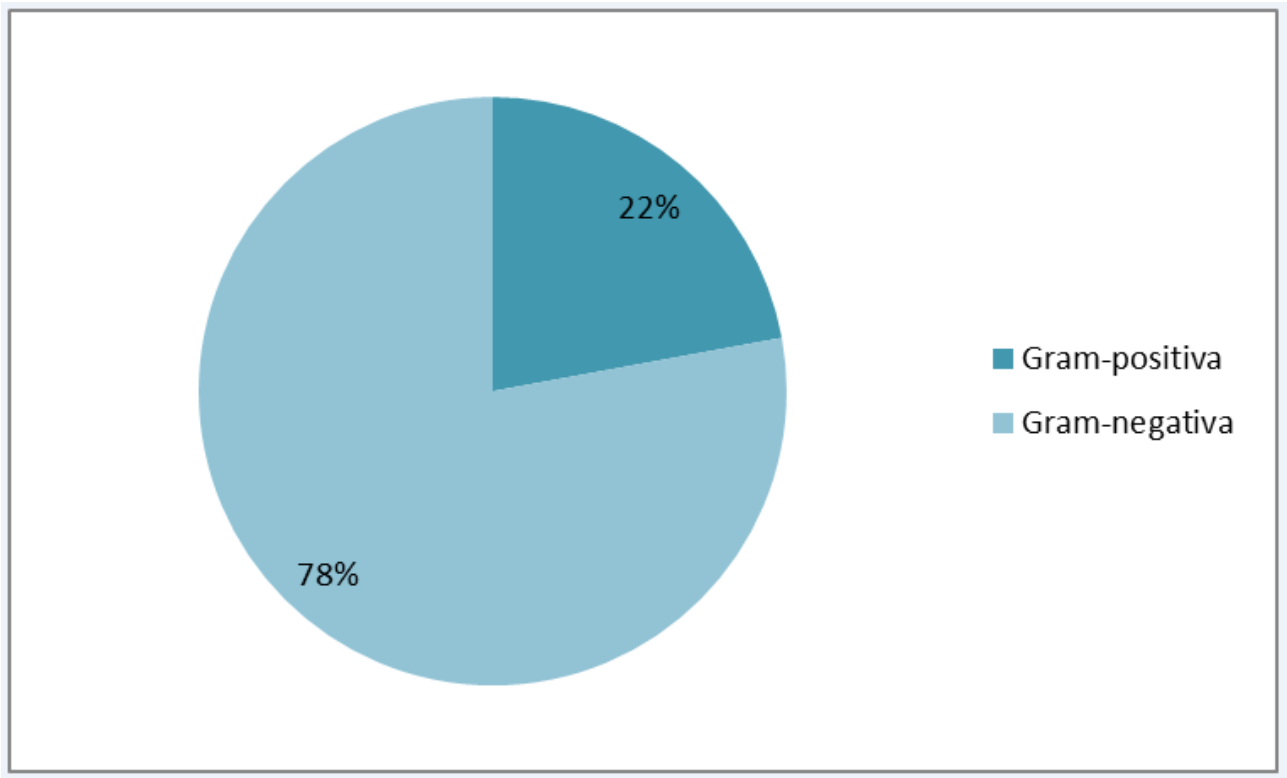


**Fig 1.** 3Distribution of positive culture samples from patients with suspected bacterial infections

### 3.2 Frequency of appearance of microorganisms

The Gram-negative bacteria identified were *Klebsiella pneumoniae* 68 (25.4%), *Pseudomonas aeruginosa* 65 (24.3%), *Escherichia coli* 64 (23.9%), *Acinetobacter baumannii* 33 (12.3%), *Serratia marcescens* 25 (9.3%) and *Enterobacter cloacae* 13 (4.9%) (Figure 2 ) Figure 1. Distribution of positive culture samples from patients with suspected bacterial infections.

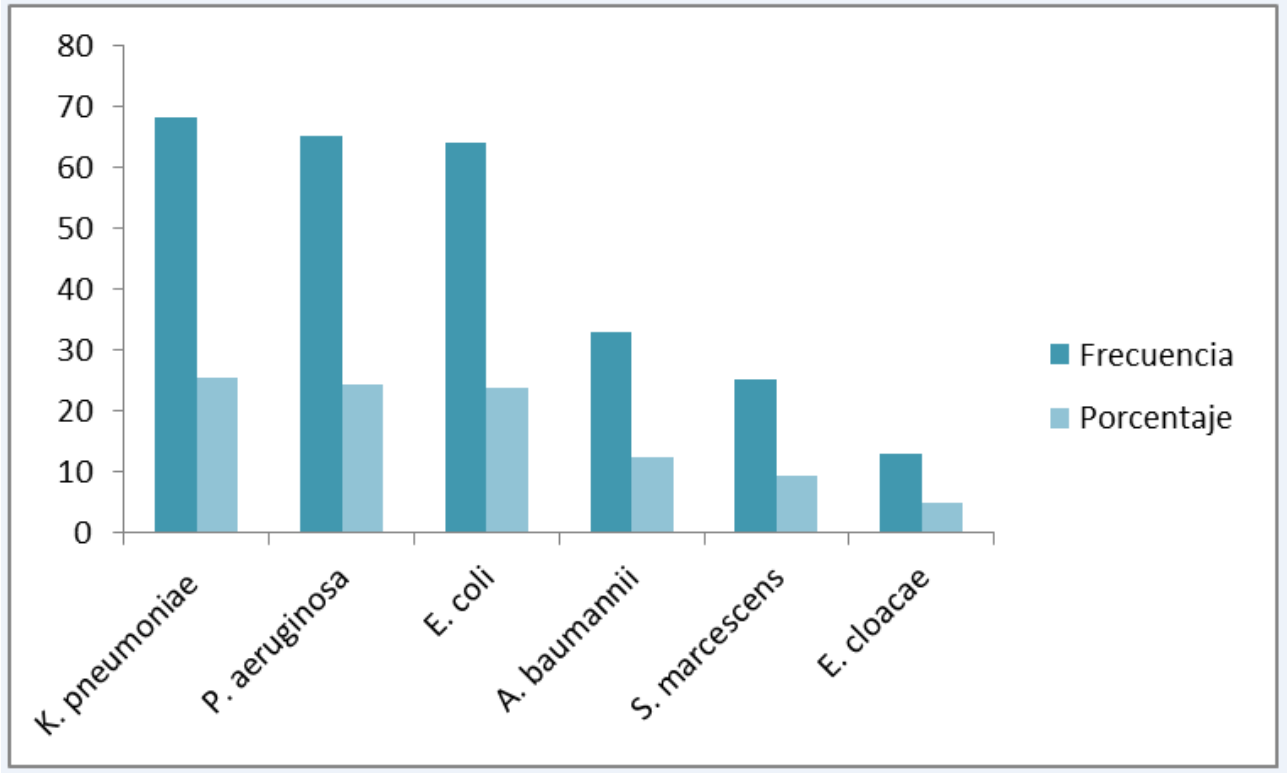


**Fig 2.** Frequency of appearance of Gram-negative microbial strains in bacterial infections

The most frequently identified Gram-positive bacteria were *Staphylococcus epidermidis* 21 (27.6%), *Staphylococcus aureus* 21 (27.6%), *Enterococcus faecalis* 17 (22.4%), *Staphylococcus haemolyticus* 10 (13.2%) and *Staphylococcus hominis* 7 (9.2) (Figure 3 ).

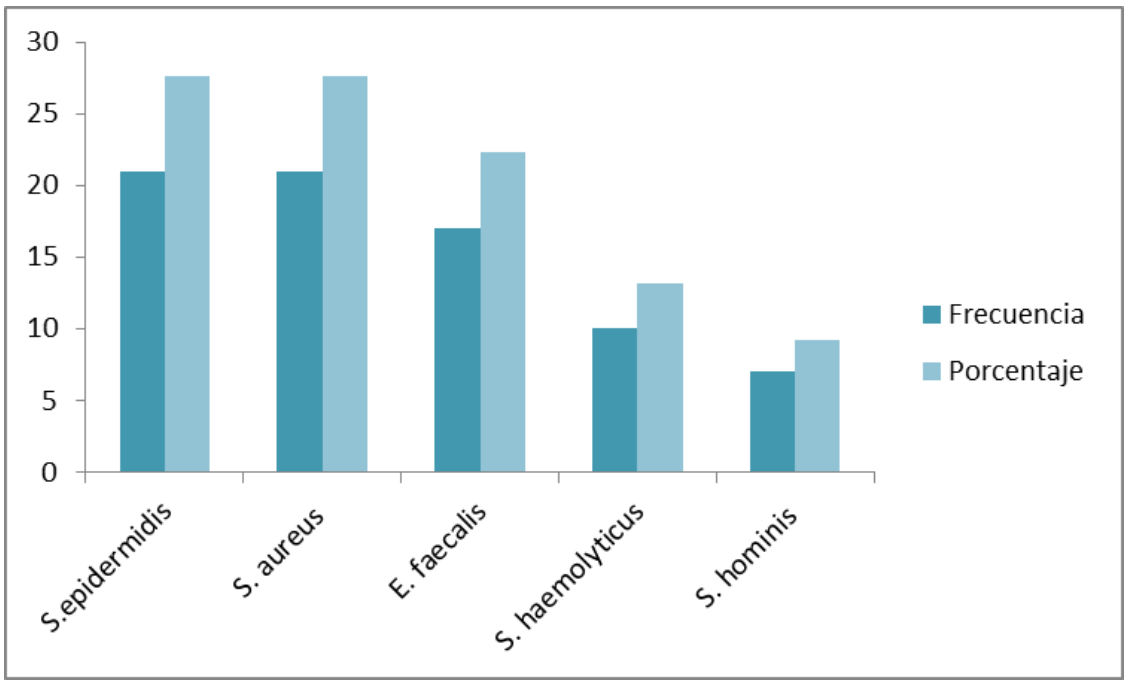


**Fig 3.** Frequency of appearance of Gram-positive microbial strains responsible for bacterial infections

### 3.3 Microorganisms isolated by type of samples

Table 1 shows the distribution of Gram-negative microorganisms isolated by cultured sample collection site: blood, urine, catheter, and respiratory secretions. *K. pneumoniae*, *P. aeruginosa*, and *A. baumanniise* most frequently isolated from respiratory secretions*; E. coli* had the highest number of isolates in urine, *while S. marcescens* and *E. cloacae* had a higher incidence in blood.

**Table 1.** Gram-negative bacilli isolated by type of samples

| Bacilos Gram-negative | TYPES OF SAMPLES | | | | |
|---|---|---|---|---|---|
| | Blood | Urine | Catheter | Respiratory secretions | Total |
| | N/(%) | N/(%) | N/(%) | N/(%) | N/(%) |
| *Klebsiella pneumonia* | 12 (4.8) | 12 (4.8) | 0 (0.0) | 22 (8.7) | 46 (18.3) |
| *Pseudomonas aeruginosa* | 16 (6.3) | 14 (5.6) | 0 (0.0) | 24 (9.5) | 54 (21.4) |
| *Escherichia coli* | 12 (4.8) | 24 (9.6) | 0 (0.0) | 6 (2.3) | 42 (16.7) |
| *Acinetobacter baumannii* | 18 (7.1) | 12 (4.8) | 0 (0.0) | 20 (7.8) | 50 (19.7) |
| *Serratia marcescens* | 14 (5.6) | 0 (0.0) | 6 (2.4) | 12 (4.7) | 32 (12.7) |
| *Enterobacter cloacae* | 12 (4.8) | 0 (0.0) | 6 (2.4) | 10 (4.0) | 28 (11.2) |
| Total | 84 (33.4) | 62 (24.8) | 12 (4.8) | 94 (37) | 252 (100) |

Table 2 shows the distribution of Gram-positive microorganisms isolated by cultured sample collection site: blood, urine, catheter, and respiratory secretions. *S. epidermidis, S. aureus, E. faecalis, S. haemolyticus*, and *S. hominis* were most frequently isolated from blood.

**Table 2.** Gram-positive cocci isolated by type of samples

| Cocos Gram-positive | TYPES OF SAMPLES | | | | |
|---|---|---|---|---|---|
| | Blood | Urine | Catheter | Respiratoy secretions | total |
| | N/(%) | N/(%) | N/(%) | N/(%) | N/(%) |
| *Staphylococcus epidermidis* | 10 (10.9) | 8 (8.7) | 4 (4.3) | 6 (6.5) | 28 (30.4) |
| *Staphylococcus aureus* | 10 (10.9) | 8 (8.7) | 0 (0.0) | 4 (4.3) | 22 (23.9) |
| *Enterococcus faecalis* | 10 (10.9) | 10 (109) | 0 (0.0) | 0 (0.0) | 20 (21.8) |
| *Staphylococcus haemolyticus* | 12 (13.0) | 0 (0.0) | 0 (0.0) | 0 (0.) | 12 (13.0) |
| *Staphylococcus hominis* | 10 (10.9) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 10 (10.9) |
| Total | 52 (56.6) | 26 (28.3) | 4 (4.3) | 10 (10.8) | 92 (100) |

### 3.4 Resistance of Gram-negative microorganisms to antimicrobial agents

The susceptibility and resistance of Gram-negative bacteria are shown in Table 3 . *K. pneumoniae* presented resistance to most of the antimicrobials used, with the exception of gentamicin. *P. aeruginosa* exhibited greater resistance to doripenem (53.8%), imipenem (41.5%) and meropenem (46.1%), being susceptible to colistin (100%). *E. coli* presented resistance to piperacillin-tazobactam (14.1%), ceftazidime (51.6%), cefepime (51.6%), doripenem (14.1%), imipenem (14.1%), meropenem (14.1%) and ciprofloxacin (65.6%), being susceptible to amikacin (65.6%), gentamicin (65.6%) and colistin (85.9%). *A. baumannii* showed resistance to all the drugs used. *S. marcescens* only showed resistance to ceftazidime (8.0%). *E. cloacae* presented a low percentage of resistance to most of the antimicrobials used, piperacillin-tazobactam (7.7%), ceftazidime (7.7%), cefepime (7.7%), doripenem (8.3%), imipenem (7.7%), meropenem (7.7%), ciprofloxacin (7.7%) and colistin (7.7%), being sensitive to amikacin (100%) and Gentamicin (100%).

### 3.5 Resistance of Gram-positive microorganisms to antimicrobial agents

The susceptibility and resistance of Gram-positive bacteria are shown in Table 4. Of all the antimicrobials used, *S. epidermidis* presented resistance to trimethoprim / sulfamethoxazole (14.3%), erythromycin (80.9%), nitrofurantoin (4.8%), ciprofloxacin (4.8%) and levofloxacin (9.1%). *S. aureus* (38.1%) and *E. faecalis* (35.3%) only showed resistance to erythromycin. *S. haemolyticus* was susceptible to all the antimicrobials used and *S. hominis* presented resistance to erythromycin (28.6%) and nitrofurantoin (28.6%).

**Table 3.** Antibiotic susceptibility pattern of Gram-negative bacteria

| | | PIP-TZ | CAZ | FEP | DPM | IPM | MEM | AMK | G | CIP | COL |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | N/(%) | N/(%) | N/(%) | N/(%) | N/(%) | N/(%) | N/(%) | N/(%) | N/(%) | N/(%) |
| *Klebsiella pneumoniae* (68) | S | 58(85,3) | 49(72) | 49(72) | 62(91,2) | 62(91,2) | 62(91,2) | 62(91,2) | 62(91,2) | 52(76,5) | |
| | I | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 6(8,8) | 10(14,7) | |
| | R | 10(14,7) | 19(28) | 19(28) | 6(8,8) | 6 (8,8) | 6 (8,8) | 6 (8,8) | 0 (0) | 6 (8,8) | |
| *Pseudomonas aeruginosa (65)* | S | 35(53,8) | 37(56,9) | 40(61,5) | 35(53,8) | 27(41,5) | 33(50,8) | 40(61,5) | 50(76,9) | 45(69,2) | 65(100) |
| | I | 10(15,4) | 9(13,8) | 10(15,4) | 0 (0) | 0 (0) | 2 (3,1) | 10(15,4) | 0 (0) | 0 (0) | 0 (0) |
| | R | 20(30,8) | 19(29.3) | 15(23,1) | 30(46,2) | 38(58,5) | 30(46,1) | 15(23,1) | 15(23,1) | 20(30,8) | 0 (0 |
| *Escherichia coli* -64 | S | 55(85,9) | 31(48.4) | 31(48.4) | 55(85,9) | 55(85,9) | 55(85,9) | 64 C | 64(100) | 22(34.4) | 55(85,9) |
| | I | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0(0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 9(14.1) |
| | R | 9 (14.1) | 33(51,6) | 33(51,6) | 9(14.1) | 9(14.1) | 9(14.1) | 0 (0) | 0 (0) | 42(65,6) | 0 (0) |
| *Acinetobacter baumannii (33)* | S | 13(39,4) | 9(27,3) | 12(36,4) | 12(36,4) | 12(36,4) | 12(36,4) | | 12(36,4) | 12(36,4) | 29(87,9) |
| | I | 0 (0) | 5(15,1) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | | 11(33,3) | 0 (0) | 0 (0) |
| | R | 20(60,6) | 19(57,6) | 21(63,6) | 21(63,6) | 21(63,6) | 21(63,6) | | 10(30,3) | 21(63,6) | 4(12,1) |
| *Serratia marcescens* (25) | S | | 18(72,0) | 25(100) | 25(100) | | 25(100) | 25(100) | 25(100) | 25(100) | |
| | I | | 5(20,0) | 0 (0) | 0 (0) | | 0 (0) | 0 (0) | 0 (0) | 0 (0) | |
| | R | | 2(8,0) | 0 (0) | 0 (0) | | 0 (0) | 0 (0) | 0 (0) | 0 (0) | |
| *Enterobacter cloacae (13)* | S | 11(84.6) | 9(69,3) | 12(92,3) | 12(92,3) | 12(92,3) | 12(92,3) | 13(100) | 12(92,3) | 9(69,3) | 9(69,3) |
| | I | 1(7.7) | 2(23.0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 1 (7,7) | 2(23.0) | 2(23.0) |
| | R | 1(7.7) | 1 (7.7) | 1(7,7) | 1(8,3) | 1(7,7) | 1(7,7) | 0 (0) | 0 (0) | 1(7.7) | 1(7.7) |

N:number of susceptible isolates.
Piperacillin-Tazobactam (PIP-TZ); ceftazidime(CAZ); Cefepime (FEP); Doripenem (DPM); Imipenem (IPM); Meropenem (MEM);AmiKacin (AMK); Gentamicin (G); Ciprofloxacin (CIP); Colistin (COL).

**Table 4.** Antibiotic susceptibility pattern of Gram-positive bacteria

| | | TMP/SMX | E | NIT | CIP | LFX | VAN | GEN | TEC | MINO | RIF | TET |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *Staphylococcus epidermidis* (21) | S | 18(85,7) | 1(4.8) | 18(85.7) | 16(76,2) | 18(85.7) | 21(100) | 21(100) | 21(100) | 21(100) | 21(100) | 21(100) |
| | I | 0 (0) | 3(14.3) | 2(9,5) | 4(19.0) | 2(9,5) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) |
| | R | 3(14,3) | 17(80.9) | 1(4,8) | 1(4.8) | 1(9,1) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) |
| *Staphylococcus aureus* (21) | S | 21(100) | 13(61.9) | 21(100) | 21(100) | 21(100) | 21(100) | 21(100) | 21(100) | 21(100) | 21(100) | 21(100) |
| | I | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) |
| | R | 0 (0) | 8(38.1) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) |
| *Enterococcus faecalis* (17) | S | 17(100) | 11(64.7) | 17(100) | 17(100) | 17(100) | 17(100) | 17(100) | 17(100) | 17(100) | 17(100) | 17(100) |
| | I | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) |
| | R | 0 (0) | 6(35.3) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) |
| *Staphylococcus haemolyticus*(10) | S | 10(100) | 10(100) | 10(100) | 8(80.0) | 8(80.0) | 10(100) | 10(100) | 10(100) | 10(100) | 10(100) | 10(100) |
| | I | 0 (0) | 0 (0) | 0 (0) | 2(20.0) | 2(80.0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) |
| | R | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) |
| *Staphylococcus hominis* (7) | S | 6(85.7) | 5(71.4) | 5(71.4) | 7(100) | 7(100) | 7(100) | 7(100) | 7(100) | 7(100) | 7(100) | 7(100) |
| | I | 1(14.3) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) |
| | R | 0 (0) | 2(28.6) | 2(28.6) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) |

N: number of sensitive isolates
Trimethoprim / Sulfamethoxazole (TMP / SMX); Erythromycin (E); Nitrofurantoin (NIT); Ciprofloxacin (CIP); Levofloxacin (Lfx); Vancomycin (VAN); Gentamicin (GEN); Teicoplanin (TEC); Minocycline (MINO); Rifampicin (RIF); Tetracillin.

## 4 Discussion

Providing effective medical care in developing countries like Colombia is challenged by the spread of antimicrobial-resistant pathogenic bacteria, so surveillance programs have become important in defining species distribution and resistance patterns of the pathogens that cause infections; this is the basis for adequate empirical therapy [18]. Bacterial infection caused by antibiotic-resistant bacteria is one of the main causes of morbidity and mortality throughout the world, which requires urgent and effective treatment to control infections; Mortality rates double from 30% to 60% when inadequate empirical treatment was administered to patients in the Intensive Care Unit (ICU) [19]. In this prospective study, information is provided on the distribution of bacterial isolates along with the pattern of susceptibility to antibiotics, crucial information in the effective management of cases caused by bacterial infections.

According to Biedenbach et al., 2004, the frequency of appearance of bacterial species that cause infections in different parts of the world is quite variable; they demonstrated that Gram-positive species were causal agents in 57% of infections in North American Medical Centers compared to fewer cases in Latin America and Europe (51%). However, Orsini et al., 2012 and Wisplinghoff et al., 2004, reported that in the United States of America there is a trend towards an increase in the incidence of Gram-negative organisms that cause infections. This variation in etiological agents from one country to another could be due to geographic locations and epidemiological differences in etiological agents; other factors may also be due to the nature of the patient population, limited sample size, and study period. In the present investigation, Gram-negative bacteria (78%) were the most frequent cause of infections (Figure 1 ); Similar results were reported in Colombia by De la Rosa et al., 2016, which carried out a prospective, multicenter study, carried out in ten hospitals in four cities between September 2007 and February 2008; Also, similar results have been reported in Mexico by Sánchez et al., 2010, and in Argentina by Saad et al., 2018.

Among the Gram-negative bacteria, those that were isolated with the highest frequency were *K. pneumoniae* (25.4%), *P. aeruginosa* (24.3%), and *E. coli* (23.9%), while the least frequent was *A. baumannii* (12.3%), *S. marcescens* (9.3%) and E. cloacae (Figure 2 ), these results are similar to those reported in Colombia by Briceño et al., 2010, they also coincide with the studies carried out by Sabzghabaee et al., 2012, who studied the antimicrobial resistance patterns of bacterial isolates from burn wounds at an Iranian university hospital. The reason for the high isolation rates of these Gram-negative bacteria may be due to the acquisition of an infection during the hospital stay, since they are recognized opportunistic pathogens that mainly affect hospitalized patients, by remaining on inanimate surfaces and between the hands. Of health personnel for long periods, which facilitates its dissemination in the hospital environment, continuously increasing the incidence of infections [20]. The results of the present study are consistent with others in which *K. pneumoniae* and *Pseudomonas* spp. were the most common bacterial organisms causing infections.

Gram-positive bacteria also pose a serious threat because their morbidity is constantly increasing worldwide [21,22]. In the present study, among Gram-positive bacteria, *S. epidermidis* (27.6%) and *S. aureus* (27.6%), were the most frequently isolated pathogens, followed by *E. faecalis* (22.4%), *S. haemolyticus* (13.2%) and *S. hominis* (9.2) (Figure 3 ). These bacterial species have been reported in national and international studies as the most frequent among nosocomial infections [23]; It was also reported earlier [24,25]. *S. epidermidis* was recognized as low-incidence pollutants until the 1970s; however, several studies have reported an increase in the incidence of infection by this bacterium, which is of growing concern due to the high distribution of methicillin resistance among isolates [23]. The possible reason for the high frequency is that these bacteria are part of the normal flora of the skin and intestine of healthy individuals; when the skin and soft tissues are injured, they move from their site of residence to other sterile sites. Furthermore, most of these bacteria are commonly found in the hospital setting, which could increase the proportion of wound, ear and urinary tract infection, and cross-contamination among admitted patients [26].

As published by the World Health Organization in the United States, antimicrobial-resistant (AMR) microorganisms cause more than 2 million infections and are associated with approximately 23,000 deaths each year, and the European Center for Disease Prevention and Control (ECDC) reported that AMR is associated with approximately 25,000 deaths per year [6]. In the present study, the antimicrobial resistance profile of Gram-negative bacteria showed a higher rate of resistance compared to Gram-positive bacteria, as has also been shown in other studies carried out in Ethiopia, Saudi Arabia and Libya [27,28]. *K. pneumoniae* was resistant to most of the antibiotics used in the present study, with the exception of gentamicin. According to Garbati and Godhair, 2013, the optimal treatment of *K. pneumoniae* is still unknown; Doctors have turned to the use of previously discarded antimicrobials such as colistin and tigecycline to treat these infections. A recent review [29], reported variable in vitro susceptibilities to tigecycline (98%), colistin (86%), amikacin (45%), and gentamicin (22%) among 60 patients. Pseudomonas aeruginosa presented high resistance to most of the drugs used, however, it showed high acolistin susceptibility. Comparing the results obtained with other studies carried out in Latin America (Argentina, Brazil, Chile, Costa Rica, Ecuador, Guatemala, Mexico, Panama, Peru and Venezuela), it was possible to observe a similarity in the results with resistance to imipenem (44.9%), meropenem (38.4%) and doripenen (49%) [30]. This may be due to empirical and inappropriate use as a first-line treatment. Which is an alarming sign for clinicians because it leaves a very limited choice of drugs such as colistin and tigecycline, which have serious side effects and toxicity [27]. Isolates of *A. baumannii* were resistant to most antibiotics, with the exception of colistin. According to [24], in Colombia

a five-fold increase in resistance was reported between 2001 and 2008. Worldwide, this bacterium has also shown high resistance to most antibiotics [31]. There are multiple studies that explore treatment alternatives for *A. baumannii* infection; Today, antibiotic therapies have been resumed that was ruled out due to high toxicity rates; Like colistin, these antibiotics have shown efficacy in the treatment of multi-resistant strains of this microorganism [32]. While the rates of multidrug resistance in isolates of *S. marcescens, E. coli, E. cloacae* were low, similar studies have been reported as those conducted by Hasani et al., 2019.

*S. epidermidis* and *S. haemolyticus* are frequent natural colonizers of moist body surfaces, such as the armpits, groin area, and perineal area; they have adapted to become nosocomial pathogens because they exhibit resistance to antibiotics and antiseptics, as well as their ability to produce biofilms. In the present work *S. epidermidis*, *S. hominis*, *E. faecalis* and *S. aureus* showed high resistance to erythromycin (Table 2 ). Similar results were published by Bouchami et al. in 2007, where they reported a high resistance of these bacteria to erythromycin (62% of isolates), oxacillin (51%), gentamicin (61%), lincomycin (60%), ofloxacin (60%) and rifampicin (51%). Bora et al, 2018, also reported resistance to several types of non-$\beta$-lactam antimicrobials, such as ciprofloxacin (58% –72%), gentamicin (26% -72%), and cotrimoxazole (46% -47%).

## 5 Conclusion

In the present study, it was established that Gram-negative bacteria were isolated more frequently from respiratory secretions than Gram-positive ones from blood. A high prevalence of antimicrobial resistance could also be established, particularly in Gram-negative bacteria. This high prevalence of antimicrobial resistance in the region may be due to the excessive use of antibiotics due to their easy availability. A prospective study is suggested.

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