ARTÍCULO ORIGINAL

Gac Méd Caracas 2024;132(4):1022-1036
DOI: 10.47307/GMC.2024.132.4.14

Resistance profile of pathogenic bacteria isolated in a hospital in the municipality of Monteria – Colombia, during the period 2020 – 2022

Perfil de resistencia de bacterias patógenas aisladas en un hospital del municipio de Montería – Colombia durante el período 2020 – 2022

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SUMMARY

Antibiotics are the most widely used drugs and play a fundamental role in treating infectious diseases worldwide. **General objective:** *To describe the resistance profiles of pathogenic bacteria isolated at the E.S.E Hospital San Jerónimo during the period 2020 – 2022 in Monteria, Colombia.* **Methodology:** *A descriptive, cross-sectional, retrospective study considered the patients' clinical histories.* **Results:** *A total of 3 050 samples were obtained. Staphylococcus aureus and Acinetobacter baumannii were isolated more frequently in blood samples; Klebsiella pneumonae was isolated more frequently in urine samples; while Pseudomonas aeruginosa and Enterobacter cloacae were isolated in bronchial samples and secretions. Gram-negative bacteria (78 %) were isolated more frequently than Gram-positive bacteria. The most frequently identified Gram-positive bacteria was Staphylococcus aureus; while in Gram-negative bacteria it was Escherichia coli. Antibiotics used to determine the sensitivity of Gram-positive and Gram-negative bacteria were amoxicillin/clavulanic acid, Ampicillin/Sulbactam, Ampicillin, Cefazolin, Ciprofloxacin, Daptomycin, Erythromycin, Gentamicin, Moxifloxacin, Rifampicin, Trimethoprim/sulfamethoxazole, Vancomycin, Amikacin, Colistin, Levofloxacin, Meropenem, Piperacillin-tazobactam and Tobramycin*. **Conclusion:** *The present investigation observed a high prevalence of antimicrobial resistance.*

Keywords: *Microbial sensitivity testing, antibacterials, bacteria, gram-positive cocci.*

RESUMEN

Los antibióticos son los fármacos más utilizados y juegan un papel fundamental en el tratamiento de enfermedades infecciosas en todo el mundo. **Objetivo general:** *Describir los perfiles de resistencia de bacterias patógenas aisladas en el E.S.E Hospital San Jerónimo durante el período 2020 – 2022, en Montería, Colombia.* **Metodología:** *Se llevó a cabo un estudio de tipo descriptivo, transversal, retrospectivo teniendo en cuenta las historias clínicas de los pacientes.* **Resultados:** *Se obtuvo un total de 3050 muestras, en las muestras de sangre se aisló con mayores frecuencias Staphylococcus aureus y Acinetobacter baumannii; en las de orina se aisló con mayores frecuencias Klebsiella pneumonae; mientras*

DOI: https://doi.org/10.47307/GMC.2024.132.4.14

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Recibido: 19 de septiembre 2024
Aceptado: 20 de octubre 2024

que en muestras bronquial y secreciones se aislaron Pseudomonas aeruginosa y Enterobacter cloacae. Las bacterias Gram-negativas (78 %), se aislaron con mayor frecuencia que las Gram-positivas. Las bacterias Gram positivas identificadas con mayor frecuencia fue Staphylococcus aureus; mientras que en las Gram-negativas fué Escherichia coli. Los antibióticos utilizados para determinar la sensibilidad de las bacterias Gram-positivas y Gram-negativas fueron amoxicilina/ácido clavulánico, Ampicilina/Sulbactam, Ampicilina, Cefazolina, Ciprofloxacina, Daptomicina, Eritromicina, Gentamicina, Moxifloxacina, Rifampicina, trimethoprim/sulfametoxazol, Vancomicina, Amikacina, Colistina, Levofloxacina, Meropenem, Piperacilina-tazobactam y Tobramicina. **Conclusión:** *En la presente investigación se observó una alta prevalencia de resistencia a los antimicrobianos.*

Palabras clave: *Pruebas de sensibilidad microbiana, antibacterianos, bacterias, cocos grampositivos.*

INTRODUCTION

Antibiotics are the most widely used drugs in patients and are key in treating infectious diseases worldwide (1). Their irrational and abusive use of antibiotics, combined with the scarcity of new agents on the market, has led to antibiotic resistance, compromising the efficacy of these drugs (2). Antimicrobial resistance (AMR) in bacteria is considered one of this century's most serious public health threats. During the last decade, increasing levels of resistance to clinically relevant antibiotics, including carbapenems and colistin, considered antibiotics of last resort, have been reported in both human and animal populations (3).

The US Center for Disease Control and Prevention (CDC) estimated that antibiotic-resistant infections affect more than two million people in the USA yearly. At least 23,000 die as a result of the infection (4) in Europe each year and the number of infections and deaths due to multi-resistant bacteria was estimated between 400 000 and 25 000, respectively (5). The National Healthcare Safety Network of the Centers for Disease Control and Prevention (NHSNDC) of the USA, between the years 2015-2017, reported 311 897 healthcare-associated infections (HAIs) in adults, with a total of 356 633 isolated pathogens, of which the most frequent were *E. coli* (18 %), *S. aureus* (12 %) *K. pneumoniae* (9 %) (Ministries of Health and Social Protection).

According to Anaya et al. (6), the threat of antibiotic-resistant microorganisms is not confined to the USA but is a global concern. Carbapenem-resistant Enterobacteriaceae, methicillin-resistant *Staphylococcus aureus,* and extended-spectrum b-lactamase (ESBL)-producing bacteria are increasingly resistant worldwide. A press release from the World Health Organization (WHO) in February 2017 highlighted the global spread of priority bacterial pathogens resistant to most antibiotics, including carbapenem-resistant *Acinetobacter baumannii*, carbapenem-resistant *Pseudomonas aeruginosa*, carbapenem-resistant Enterobacteriaceae, which produce ESBLs; vancomycin-resistant *Enterococcus faecium,* methicillin-resistant *Staphylococcus aureus*, and those with intermediate sensitivity and resistance to vancomycin. These bacteria are not only spreading rapidly in healthcare facilities but also the environment worldwide through mobile genetic elements (6). The most recent data from the European antibiotic surveillance reports found that antibiotic resistance rates vary markedly between countries (7).

Currently, the most serious infections that threaten human life are caused by a group of antibiotic-resistant bacteria, which the Infectious Diseases Society of America has named the ESKAPE group (*Enterococcus faecium, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa, Enterobacter cloacae*) (8), is an acronym formed with the initial letters of the names of six bacteria that cause serious infectious diseases and whose mechanisms of pathogenicity and antimicrobial resistance are evolutionarily significantly developed, the bacteria of the ESKAPE group are a critical health threat because they cause a substantial percentage of HAIs in the modern hospital (7).

Antimicrobial resistance genes (ARGs) can multiply by the proliferation of their bacterial hosts and be transferred 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-resistant 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). The general objective of the present work was to describe the resistance profiles of pathogenic bacteria isolated in pediatrics at the E.S.E Hospital San Jerónimo during the period 2020 – 2022 in Monteria, Colombia.

METHODOLOGY

A retrospective, cross-sectional descriptive study was conducted between 2020 and 2022, considering the clinical histories of patients treated for bacterial infections at E.S.E Hospital in Monteria. The collected data were analyzed using an Excel data matrix, processed in the IBM Statistical Package for the Social Sciences (SPSS 19.0.0) program.

RESULTS

Clinical samples

During the study period, 3 050 samples were obtained. Most patients were given urine samples (1 138), followed by blood samples (546), secretions (327), wounds (179), and bronchi (177), among others, as shown in Figure 1.

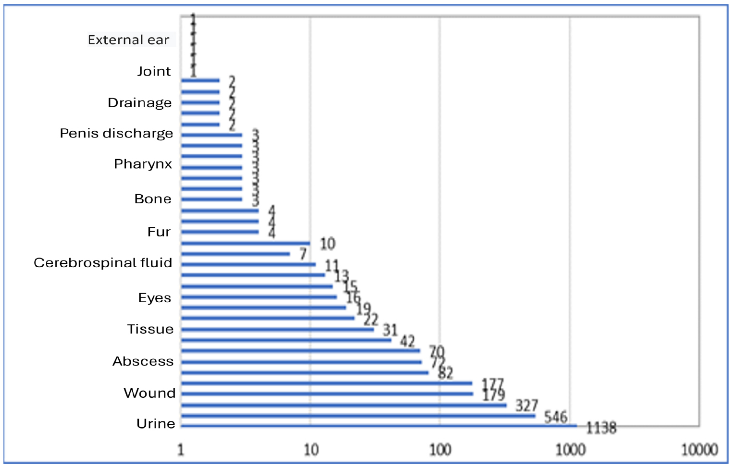

Figure 1. Clinical samples were sent to the laboratory during the study period.

Bacterial pathogens isolated from different clinical samples

Clinically important bacteria that threaten human life are caused by a group of antibiotic-resistant bacteria, which the Infectious Diseases Society of America has named the ESKAPE group (8); in Table 1, several species of the ESKAPE group are reported among which *Staphylococcus aureus* is found with 318 isolated, 95 (30 %) were isolated from blood samples and 44 were isolated from access samples (14 %) and wounds 44; *Klebsiella pneumoniae* were isolated a total of 348, 143 (41 %) were isolated from urine samples and 62 (18 %) from secretions; *Acinetobacter baumannii* was isolated 81 strains, the samples where they were isolated most frequently were secretions 19 (23 %), blood 19 (23 %), and urine 19 (23 %). *Pseudomonas aeruginosa* was isolated in 348 strains, 105 (30 %) were isolated from secretions, followed by bronchial samples 72 (21 %) and urine 52 (15 %); *Enterobacter cloacae* was isolated a total of 92 strains, 33 % were isolated from urine, followed by secretions 20 (22 %) and blood 15 (16 %).

Distribution of positive samples

2 620 samples were taken from January 2018 to December 2022, and the frequency of isolation of Gram-negative bacteria was 2051 (78 %), higher than that of Gram-positive 569 (22 %) bacteria (Figure 2).

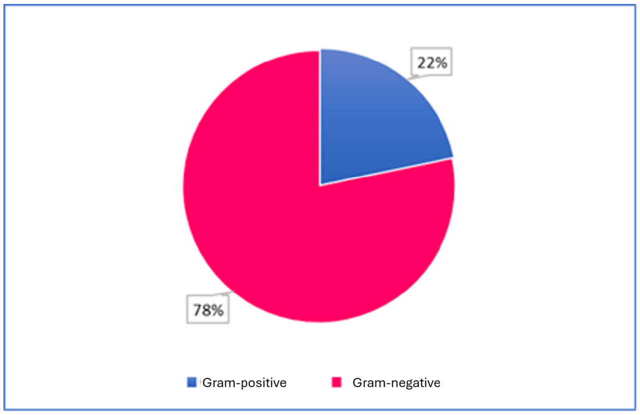

Figure 2. Distribution of positive culture samples from patients with suspected bacterial infections

Frequency of appearance of microorganisms

The most frequently identified Gram-positive bacteria were *Staphylococcus aureus* 318 (43.4 %), *Staphylococcus epidermidis* 97 (13.3 %), *Staphylococcus hominis* 77 (10.5 %), *Staphylococcus haemolyticus* 59 (13.2 %) and *Staphylococcus auricularis* 36 (4.6) (Figure 3).

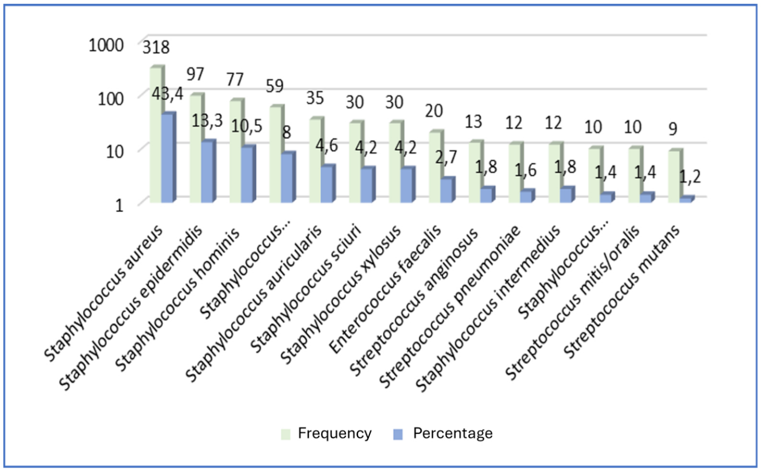

Figure 3. Frequency of Gram-positive bacteria responsible for infections.

The main Gram-negative bacteria identified were *Escherichia coli* 921 (40.8 %), *Pseudomonas aeruginosa* 348 (15.4 %), *Klebsiella pneumoniae* 348 (15.4 %), *Proteus mirabilis* 117 (5.2), *Enterobacter cloacae* 92 (4.1 %), among others (Figure 4).

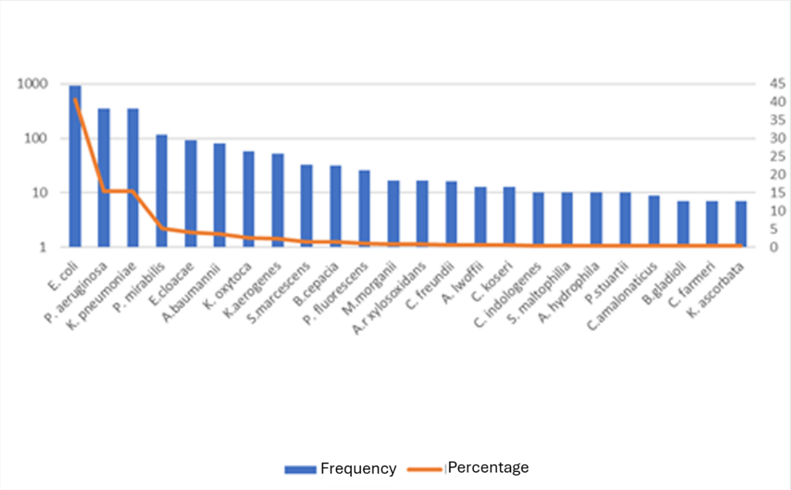

Figure 4. Frequency of Gram-negative bacteria responsible for infections.

Resistance of microorganisms to antimicrobial agents

Tables 2 and 3 show the susceptibility and resistance of Gram-positive and Gram-negative bacteria. Antibiotics used to treat Gram-positive bacterial infections were Amoxicillin/Clavulanic acid, Ampicillin/Sulbactam, Ampicillin, Cefazolin, Ciprofloxacin, Daptomycin, Erythromycin, Gentamicin, Moxifloxacin, Rifampicin, Trimethoprim/Sulfamethoxazole, and Vancomycin.

The sensitivity of Gram-positive bacteria to different drugs was: *Staphylococcus aureus* was 100 % sensitive to Ampicillin/Sulbactam, Daptomycin, and Vancomycin, while *Staphylococcus auricularis, Staphylococcus haemolyticus, Staphylococcus epidermidis, Staphylococcus sciuri*, was 100 % sensitive to Daptomycin, Vancomycin; *Staphylococcus intermedius* Daptomycin, Rifampicin, trimethoprim/sulfamethoxazole, Vancomycin; *Staphylococcus xylosus* was 100 % sensitive to Daptomycin, Rifampicin, trimethoprim/sulfamethoxazole and Vancomycin; *Staphylococcus hominis* was 100 % sensitive to Vancomycin. Antibiotics used to treat Gram-negative bacterial infections were Amikacin, Ampicillin/Sulbactam, Ampicillin, Ciprofloxacin, Colistin, Gentamicin, Levofloxacin, Meropenem, Piperacillin-tazobactam, Tobramycin, Trimethoprim/sulfamethoxazole.

The sensitivity of Gram-negative bacteria to the different drugs were: *Escherichia coli* was 90 % sensitive to Meropenem, Piperacillin-tazobactam; *Enterobacter cloacae* and *Klebsiella oxytoca* were 100 % sensitive to colistin*; Klebsiella pneumoniae* was 99 % sensitive to colistin; *Klebsiella aerogenes* and *Proteus mirabilis* were 100 % sensitive to meropenem; *Pseudomonas aeruginosa* was 96 % sensitive to colistin, *Pseudomonas fluorescens* was 89 % sensitive to levofloxacin; *Serratia marcescens* was 100 % sensitive to meropenem; *Citrobacter freundii* was 100 % sensitive to colistin and meropenem; *Citrobacter amalonaticus* was 100 %

sensitive to all antibiotics used; *Citrobacter koseri* was 100 % sensitive to Colistin, Levofloxacin, Piperacillin-tazobactam, trimethoprim/sulfamethoxazole; *Aeromonas hydrophila* was 100 % sensitive to Amikacin, Colistin, Gentamicin and trimethoprim/sulfamethoxazole; *Achromobacter xylosoxidans* was 36 % sensitive to Levofloxacin and Meropenem; *Providencia stuartii* was 100 % sensitive to Levofloxacin; *Morganella morganii* was 100 % sensitive to Amikacin, Gentamicin, Meropenem and Tobramycin; *Burkholderia cepacia* had the highest sensitivity to Levofloxacin with 67 %; *Chryseobacterium indologenes* had the highest sensitivity to Piperacillin-tazobactam with 67 %; *Stenotrophomonas maltophilia* had the highest sensitivity of 87 % to Levofloxacin and trimethoprim/sulfamethoxazole; *Acinetobacter baumannii* had a sensitivity of 70 % to Amikacin and *Acinetobacter lwoffii* had a sensitivity of 100 % to Amikacin.

DISCUSSION

Given the increasing resistance of bacteria to antimicrobials, surveillance programs have become important to define the species distribution and resistance patterns of pathogens causing infections (11). The increased risk of infections may be due to host- or treatment-related causes; host-related factors include immunodeficiency, comorbid diseases, mucosal ulcerations, previous infections, nutritional deficiency, and stress (12). In the present study, most of the patients were given a urine sample, followed by blood samples. Similar results were reported by Arman et al. (12), who they collected 144 microbial samples, most of them isolated from blood (39.6 %), urine (27.8 %) and sputum (11.8 %). Similar results were reported by Hailemariam et al. (13). The most common bacterial infections in outpatients are urinary tract infections, which are a major public health problem worldwide with an estimated 150 million cases per year, resulting in an extremely negative impact on patient's quality of life and significant financial implications; inappropriate use of antibiotics and consequently the increased incidence of antimicrobial resistance leads to many complications (14).

Urinary tract infections are a major public health problem worldwide, with an estimated 150 million cases yearly (14). In urine samples, the most frequently isolated bacteria were *Escherichia coli* (81 %), followed by *Klebsiella pneumoniae* (41 %) and *Staphylococcus epidermidis* (40 %). Similar studies were conducted by Mahmutovic et al. (14), who performed 122 isolates analyzed in female outpatients; *E. coli* was isolated even in 82 samples, making it the most common cause of urinary tract infections. However, a large body of research reports that *Staphylococcus* is the most common in urinary tract infections. This variation supports the idea that the distribution of organisms causing urinary tract infections and their susceptibility patterns to antibiotics differ from one area to another and over time (15).

Common skin colonizers are the main organisms involved in bloodstream infections (16). In the present study, the most frequently isolated bacteria were *Staphylococcus hominis* (82 %), *Staphylococcus epidermidis* (71 %) and *Staphylococcus haemolyticus* (63 %). *According to* Karlowsky et al. (17), *S. aureus and E. coli* were identified in previous studies as the two most common blood culture isolates from hospitalized patients in the United States and Europe. In the current study, coagulase-negative staphylococci were the most common blood culture isolates from laboratories in the United States (42.0 %). These results agree with those reported by Alam et al. (18) and the present work's results. These results may be due to host risk factors related to immunodeficiency and physical barrier breakdown or contamination during catheter access (16). Differing results were reported by Hailemariam et al. (13), who isolated *E. coli* and *K. pneumoniae* in bloodstream infection, possibly due to poor hygienic care and the higher nosocomial infection in our environment, which significantly contributes to the high proportion.

In the present study, Gram-negative bacteria (78 %) were the most frequent cause of infections. De la Rosa et al. (19) reported similar results in Colombia, where they conducted a prospective, multicenter study in ten hospitals in four cities between September 2007 and February 2008. Likewise, similar results were reported by Mehrad et al. (20) and by Prestinaci (5). 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 as opportunistic pathogens that mainly affect hospitalized patients by remaining on inanimate surfaces and between the hands of health personnel for long periods, which facilitates their dissemination in the hospital setting, continuously increasing the incidence of infections (21).

The main Gram-negative bacteria identified were *Escherichia coli* (40.8 %), *Pseudomonas aeruginosa* (15.4 %), *Klebsiella pneumoniae* (15.4 %), *Proteus mirabilis* (5.2), *Enterobacter cloacae* (4.1 %), among others. According to Hailemariam et al., 2021 (13), the most frequent isolates were *E. coli* and *K. pneumoniae,* consistent with our study. Of course, variation in bacterial isolation of the infection has been observed throughout the region; this could be due to differences between study participants, catheterization, and hospitalization history. The most frequently identified Gram-positive bacteria were *Staphylococcus aureus* (43.4 %), *Staphylococcus epidermidis* (13.3 %), *Staphylococcus hominis* (10.5 %), *Staphylococcus haemolyticus* (13.2 %) and *Staphylococcus auricularis* (4,6). Similar studies agree with our findings; the most common bacterial species are *Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus hominis, and Staphylococcus haemolyticus* (22,23).

As published by the World Health Organization in the United States, antimicrobial-resistant (AMR) microorganisms cause more than 2 million infections. They are associated with approximately 23 000 deaths each year, and the European Union Center for Disease Prevention and Control (ECDC) reported that AMR is associated with approximately 25 000 deaths per year (21). In the present study, the antimicrobial resistance profile of Gram-negative bacteria showed a higher resistance rate than Gram-positive bacteria, as has also been shown in other studies conducted in Ethiopia, Saudi Arabia, and Libya (24,25).

The sensitivity of Gram-positive bacteria to the different drugs was *Staphylococcus aureus* was 100 % sensitive to Ampicillin/Sulbactam, Daptomycin, Vancomycin, while *Staphylococcus auricularis, Staphylococcus haemolyticus, Staphylococcus epidermidis, Staphylococcus sciuri*, was 100 % sensitive to Daptomycin, Vancomycin; *Staphylococcus* the sensitivity of Gram-positive bacteria to different drugs were: *Staphylococcus aureus* was 100 % sensitive to Ampicillin/Sulbactam, Daptomycin, Vancomycin; while *Staphylococcus auricularis, Staphylococcus haemolyticus, Staphylococcus epidermidis, Staphylococcus sciuri*, was 100 % sensitive to Daptomycin, Vancomycin; *Staphylococcus intermedius* Daptomycin, Rifampicin, trimethoprim/sulfamethoxazole, Vancomycin; *Staphylococcus xylosus* was 100 % sensitive to Daptomycin, Rifampicin, trimethoprim/sulfamethoxazole and Vancomycin; *Staphylococcus hominis* was 100 % sensitive to Vancomycin. While in Gram-negative bacteria *Escherichia coli* was 90 % sensitive to Meropenem, Piperacillin-tazobactam; *Enterobacter cloacae* and *Klebsiella oxytoca* were 100 % sensitive to Colistin; *Klebsiella pneumoniae* is 99 % sensitive to Colistin; *Klebsiella aerogenes* and *Proteus mirabilis* are 100 % sensitive to Meropenem; *Pseudomonas aeruginosa* was 96 % sensitive to Colistin, Pseudomonas fluorescens was 89 % sensitive to Levofloxacin; *Serratia marcescens* was 100 % sensitive to Meropenem; *Citrobacter freundii* was 100 % sensitive to Colistin and Meropenem; *Citrobacter amalonaticus* was 100 % sensitive to all antibiotics used; *Citrobacter koseri* was 100 % sensitive to Colistin, Levofloxacin, Piperacillin-tazobactam, trimethoprim/sulfamethoxazole; Aeromonas hydrophila was 100 % sensitive to Amikacin, Colistin, Gentamicin and trimethoprim/sulfamethoxazole; *Achromobacter xylosoxidans* was highly sensitive to Levofloxacin and Meropenem with a maximum sensitivity of 36 %; *Providencia stuartii* was 100 % sensitive to Levofloxacin; *Morganella morganii* was 100 % sensitive to Amikacin, Gentamicin, Meropenem and Tobramycin; *Burkholderia cepacia* was the most sensitive to Levofloxacin with 67 %; *Chryseobacterium indologenes* was the most sensitive to Piperacillin-tazobactam with 67 %; *Stenotrophomonas maltophilia* had the highest sensitivity of 87 % to Levofloxacin and trimethoprim/sulfamethoxazole; *Acinetobacter baumannii* had a sensitivity of 70 % to Amikacin and *Acinetobacter iwoffii* had a sensitivity of 100 % to Amikacin.

CONCLUSIONS

The present investigation observed a high prevalence of antimicrobial resistance, particularly in Gram-negative bacteria. This high prevalence of antimicrobial resistance rates in the region may be due to the excessive use of drugs due to their easy availability.

Ethical Considerations

Under the provisions of section A of article 11 of Resolution 8 430 of 1993, the study was classified as a "risk-free investigation" due to its retrospective nature. In addition, this study was developed to ensure the privacy of patients within the research framework, so no individualized data associated with any name is presented.

The authors declare that there is no conflict of interest for this research.

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SUPPLEMENTARY GRAPHICS AND TABLES

Table 1. Distribution of bacterial pathogens identified from different clinical simples

	Types of samples										
Isolated bacteria	**Abscess**	**Bronchial**	**Catheter**	**Conjunctiva**	**Sputum**	**Faeces**	**Wound**	**Bone**	**Joint fluid**	**Cerebrospinal fluid**	**Total**
Staphylococcus aureus	44	3	6	4	0	0	44	0	1	2	**104**
Staphylococcus haemolyticus	2	0	6	0	0	0	4	1	0	1	**14**
Staphylococcus auricularis	1	1	6	1	0	0	1	0	0	1	**11**
Staphylococcus epidermidis	1	0	6	3	0	0	5	0	0	1	**16**
Staphylococcus saprophyticus	0	0	6	0	0	0	0	0	0	0	**6**
Staphylococcus intermedius	1	0	6	0	0	0	1	0	0	0	**8**
Staphylococcus sciuri	1	0	6	0	0	0	3	0	0	0	**10**
Staphylococcus xylosus	1	0	6	1	0	0	2	0	0	0	**10**
Streptococcus hominis	0	0	6	1	0	0	0	0	0	0	**7**
Streptococcus mutans	0	0	6	1	0	0	0	0	0	1	**8**
Streptococcus pneumoniae	0	3	6	0	0	0	0	0	0	0	**9**
Streptococcus anginosus	0	1	6	0	0	0	0	0	0	0	**7**
Streptococcus mitis	0	0	6	0	2	0	0	0	0	0	**8**
Enterococcus faecalis	0	0	6	0	0	0	1	1	0	0	**8**
Acinetobacter baumannii	2	10	6	0	0	0	2	0	0	0	**20**
Acinetobacter lwoffii	0	3	6	0	0	0	0	0	0	0	**9**
Enterobacter cloacae	1	2	6	0	0	0	7	0	0	3	**19**
Escherichia coli	6	9	6	1	0	7	24	1	0	0	**54**
Enterobacter aerogenes	2	4	6	0	0	0	1	0	0	0	**13**
Klebsiella pneumoniae	8	45	6	0	2	2	12	0	0	1	**76**
Klebsiella oxytoca	0	3	6	0	0	4	2	0	0	0	**15**
Proteus mirabilis	2	7	6	0	0	1	18	0	0	0	**34**
Pseudomonas aeruginosa	1	72	6	4	0	0	33	0	0	0	**116**
Pseudomonas fluorescens	0	1	6	0	0	0	3	0	0	0	**10**
Serratia marcescens	1	1	6	0	0	0	2	0	0	0	**10**
Achromobacter xylosoxidans	0	3	6	0	0	0	2	0	0	0	**11**
Burkholderia cepacia	0	5	6	0	0	0	3	0	0	0	**14**
Burkholderia gladioli	0	0	6	0	0	0	1	0	0	0	**7**
Chryseobacterium indologenes	0	1	6	0	0	0	1	0	0	0	**8**
Citrobacter freundii	0	1	6	0	0	0	0	0	0	0	**7**
Citrobacter koseri	0	1	6	0	0	0	1	0	0	1	**9**
Citrobacter amalonaticus	0	0	6	0	0	0	1	0	0	0	**7**
Citrobacter farmeri	0	0	6	0	0	0	1	0	0	0	**7**
Morganella morganii	0	1	6	0	0	0	0	0	0	0	**7**
stenotrophomonas maltophilia	0	2	6	0	0	0	0	0	0	0	**8**
Kluyvera ascorbata	0	0	6	0	0	1	0	0	0	0	**7**
Aeromonas hydrophila	0	0	6	0	0	0	3	0	0	0	**9**
Providencia rettgeri	0	0	6	0	0	0	1	0	0	0	**7**
Providencia stuartii	0	0	6	0	0	0	1	0	0	0	**7**
TOTAL	**74**	**179**	**234**	**16**	**4**	**15**	**180**	**3**	**1**	**11**	

Continuation in pag. 1032…

…continuation Table 1. Distribution of bacterial pathogens identified from different clinical simples

Isolated bacteria	**Peritoneal fluid**	**Pleural fluid**	**Breast**	**Ear**	**Urine**	**Skin**	**Blood**	**Secretions**	**Tissue**	**Ulcers**	**Total**
Staphylococcus aureus	2	3	1	2	13	16	95	72	5	5	**214**
Staphylococcus haemolyticus	1	0	0	0	4	0	37	3	0	0	**45**
Staphylococcus auricularis	0	0	0	0	3	0	19	1	1	0	**24**
Staphylococcus epidermidis	0	0	0	1	0	1	69	10	0	0	**81**
Staphylococcus saprophyticus	0	0	0	0	4	0	0	0	0	0	**4**
Staphylococcus intermedius	0	0	0	0	0	1	3	0	0	0	**4**
Staphylococcus sciuri	0	0	0	0	2	1	12	5	0	0	**20**
Staphylococcus xylosus	0	0	0	0	1	0	19	0	0	0	**20**
Streptococcus hominis	0	1	0	0	0	0	63	6	0	0	**70**
Streptococcus mutans	0	0	0	0	1	0	0	0	0	0	**1**
Streptococcus pneumoniae	0	1	0	0	0	0	2	0	0	0	**3**
Streptococcus anginosus	0	0	0	0	0	1	3	2	0	0	**6**
Streptococcus mitis	0	0	0	0	0	0	0	2	0	0	**2**
Enterococcus faecalis	1	0	0	0	7	1	1	1	1	0	**12**
Acinetobacter baumannii	0	1	1	0	19	2	19	19	0	0	**61**
Acinetobacter lwoffii	0	0	0	0	1	0	0	3	0	0	**4**
Enterobacter cloacae	0	0	0	0	31	3	15	20	2	2	**73**
Escherichia coli	8	0	0	0	748	7	50	45	4	5	**867**
Enterobacter aerogenes	0	0	0	0	23	5	7	4	1	0	**40**
Klebsiella pneumoniae	5	1	0	0	143	9	47	62	1	4	**272**
Klebsiella oxytoca	3	0	0	0	14	3	11	9	2	1	**43**
Proteus mirabilis	0	0	0	0	27	9	5	27	5	10	**83**
Pseudomonas aeruginosa	2	0	0	1	52	13	42	105	6	11	**232**
Pseudomonas fluorescens	0	0	0	0	2	3	4	7	0	0	**16**
Serratia marcescens	0	0	0	0	7	1	6	7	1	1	**23**
Achromobacter xylosoxidans	0	0	0	0	1	1	1	2	0	1	**6**
Burkholderia cepacia	0	0	0	0	0	2	2	12	1	1	**18**
Burkholderia gladioli	0	0	0	0	0	0	0	0	0	0	**0**
Chryseobacterium indologenes	0	0	0	0	2	0	0	0	0	0	**2**
Citrobacter freundii	0	0	0	0	9	0	0	0	0	0	**9**
Citrobacter koseri	0	0	0	0	4	0	0	0	0	0	**4**
Citrobacter amalonaticus	0	0	0	0	2	0	0	0	0	0	**2**
Citrobacter farmeri	0	0	0	0	0	0	0	0	0	0	**0**
Morganella morganii	0	0	0	0	6	0	0	4	0	0	**10**
stenotrophomonas maltophilia	0	0	0	0	0	0	2	0	0	0	**2**
Kluyvera ascorbata	0	0	0	0	0	0	0	0	0	0	**0**
Aeromonas hydrophila	0	0	0	0	0	0	1	0	0	0	**1**
Providencia rettgeri	0	0	0	0	0	0	0	0	0	0	**0**
Providencia stuartii	0	0	0	0	0	1	1	0	1	0	**3**
TOTAL	**22**	**7**	**2**	**4**	**1126**	**80**	**536**	**428**	**31**	**41**	

Table 2. Resistance of Gram-positive microorganisms to antimicrobial agents

Bacteria		**Amox/A Clav CIM**	**Amp/Sulbactam CIM**	**Ampicilina CIM**	**Cefazolina CIM**	**Ciprofloxacina CIM**	**Daptomicina CIM**	**Eritromicina CIM**	**Gentamicina CIM**	**Moxifloxacina CIM**	**Rifampicina CIM**	**Trimet/Sulfa CIM**	**Vancomicina CIM**
Staphylococcus aureus (275)	S	94(34)	100(36)	12(4)	100(36)	236(86)	275(100)	171(62)	233(85)	265(96)	259 (94)	251(91)	275(100)
	I	0	3(1)	0	0	10(4)	0	25(9)	15(5)	4(1)	5(2)	0	0
	R	181(66)	172(63)	263(96)	175(64)	29(10)	0	79(29)	27(10)	6(3)	11(4)	29(9)	0
Staphylococcus auricularis (28)	S	8(28)	8(28)	8(28)	6(21)	18(64)	28(100)	16(57)	26(93)	26(94)	28(100)	24(86)	28(100)
	I	0	0	0	1(4)	3(11)	0	5(18)	0	1(3)	0	0	0
	R	20(72)	20(72)	20(72)	21(25)	7(25)	0	7(25)	2(7)	1(3)	0	1(4)	0
Staphylococcus haemolyticus (53)	S	1(2)	1(2)	0	1(2)	20(38)	53(100)	8(15)	16(30)	34(64)	48(91)	22(42)	53(100)
	I	0	0	0	0	0	0	1(2)	6(11)	14(26)	0	0	0
	R	52(98)	52(98)	53(100)	52(98)	33862)	0	44(83)	31(59)	5(10)	5(9)	31(58)	0
Staphylococcus epidermidis (87)	S	15(17)	16(18)	0	16(18)	53(61)	87(100)	23(26)	40(46)	74(85)	84(97)	54(62)	87(100)
	I	0	0	0	0	3(3)	0	6(7)	11(13)	11(13)	1(1)	0	0
	R	72(83)	71(82)	87(100)	71(82)	31(36)	0	58(67)	36(41)	2(2)	2(2)	33(38)	0
Staphylococcus intermedius (12)	S	4(33)	4(33)	0	4(33)	10(83)	12(100)	8(67)	8(67)	10(83)	12(100)	12(100)	12(100)
	I	0	0	0	0	0	0	0	2(16)	2(17)	0	0	0
	R	8(67)	8(67)	12(100)	8(67)	2(17)	0	4(33)	2(17)	0	0	0	0
Staphylococcus sciuri (30)	S	0	0	0	0	22(73)	30(100)	4(13)	4(13)	28(93)	28(93)	20(67)	30(100)
	I	0	0	0	0	6(20)	0	10(33)	6(20)	0	2(7)	0	0
	R	30(100)	30(100)	30(100)	30(100)	2(7)	0	16(54)	20(67)	2(7)	0	10(33)	0
Staphylococcus xylosus (30)	S	4(13)	4(13)	0	4(13)	22(73)	30(100)	26(87)	20(67)	22(73)	30(100)	30(100)	30(100)
	I	0	0	0	0	0	0	0	0	0	0	0	0
	R	26(87)	26(87)	30(100)	26(87)	8(27)	0	4(13)	10(33)	8(27)	0	0	0
Streptococcus hominis (64)	S	6(9)	6(9)	0	6(9)	47(73)	0	20(31)	46(72)	54(84)	59(92)	35(55)	64(100)
	I	0	0	0	0	0	0	4(7)	6(9)	4(7)	1(1)	0	0
	R	58(91)	58(91)	64(100)	58(91)	17(27)	64(100)	40(62)	12(19)	6(9)	4(7)	29(45)	0

Table 3. Resistance of Gram-negative microorganisms to antimicrobial agents

Bacteria		**Amicacina CIM**	**Amp/Sulbactam CIM**	**Ampicilina CIM**	**Ciprofloxacin a CIM**	**Colistina CIM**	**Gentamicin a CIM**	**Levofloxacin a CIM**	**Meropenem CIM**	**Pip/Tazo CIM**	**Tobramicin a CIM**	**Trimet/Sulf a CIM**
Escherichia coli	S	851(95)	445(49)	202(22)	706(78)	895(99)	644(71)	579(64)	903(99)	834(92)	770(85)	349(39)
	I	25(3)	241(27)	26(3)	18(2)	0	30(3)	25(3)	0	42(5)	63(7)	0
	R	19(2)	218(23)	677(75)	181(20)	10(1)	231(26)	303(33)	2(1)	29(3)	72(8)	556(61)
Enterobacter cloacae	S	71(87)	0	0	55(68)	81(100)	63(78)	59(73)	75(93)	834(92)	55(68)	45(56)
	I	2(2)	0	0	4(5)	0	3(4)	5(6)	2(2)	42(5)	2(2)	0
	R	8(11)	81(100)	81(100)	22(27)	0	15(18)	17(21)	4(5)	29(3)	24(30)	36(44)
Klebsiella pneumoniae	S	251 (86)	147(50)	0	208(71)	291(99)	194(66)	227(78)	277(95)	228(78)	204(70)	166(57)
	I	12(4)	21(7)	0	14(5)	0	19(7)	14(5)	3(1)	16(5)	15(5)	0
	R	29(10)	124(43)	292(100)	70(24)	1(1)	79(27)	51(17)	12(4)	48(17)	73(25)	126(43)
klebsiella aerogenes	S	43(93)	0	0	33(72)	44(96)	35(76)	35(76)	46(100)	35(76)	38(83)	24(52)
	I	2(4)	0	0	1(2)	0	3(7)	1(2)	0	3(7)	2(4)	0
	R	1(3)	45(100)	45(100)	12(25)	2(4)	5(17)	10(22)	0	8(17)	6(13)	22(48)
Klebsiella oxytoca	S	55(90)	13(21)	0	33(54)	61(100)	38(62)	35(57)	60(98)	51(84)	45/74)	38(62)
	I	0	12(20)	0	1(2)	0	1(2)	2(3)	0	1(2)	3(5)	0
	R	6(10)	36(59)	61(100)	27(44)	0	22(36)	24(40)	1(2)	9(14)	13(21)	23(38)
Proteus mirabilis	S	87(83)	53(50)	44(42)	76(72)	0	78(74)	84(80)	105(100)	89(85)	77(73)	57(54)
	I	3(3)	14(14)	3(3)	5(5)	0	4(4)	7(7)	0	3(3)	5(5)	0
	R	15(14)	38(36)	58(55)	24(23)	105(100)	23(22)	14(13)	0	13(12)	23(22)	48(46)
Pseudomonas aeruginosa	S	211(63)	0	0	175(52)	327(96)	158(47)	191(57)	229(68)	262(78)	265(79)	0
	I	24(7)	0	0	25(7)	1(1)	44(13)	40(12)	26(8)	10(3)	2(1)	0
	R	101(30)	0	0	136(41)	8(3)	134(40)	105(31)	81(24)	64(19)	69(20)	0
Pseudomonas fluorescens	S	15(79)	0	0	14(74)	0	12(63)	17(89)	12(63)	11(58)	12(63)	7(37)
	I	0	0	0	0	0	1(5)	0	1(5)	1(5)	0	0
	R	4(21)	0	0	5(26)	0	6(32)	2(11)	2(32)	7(37)	7(37)	12(63)

Continue in pag 1035…

…continuation Table 3. Resistance of Gram-negative microorganisms to antimicrobial agents

Bacteria		**Amicacina CIM**	**Amp/Sulbactam CIM**	**Ampicilina CIM**	**Ciprofloxacin a CIM**	**Colistina CIM**	**Gentamicin a CIM**	**Levofloxacin a CIM**	**Meropenem CIM**	**Pip/Tazo CIM**	**Tobramicin a CIM**	**Trimet/Sulf a CIM**
Serratia marcescens	S	19(90)	0	0	16(74)	0	19(90)	17(82)	21(100)	20(95)	15(72)	20(95)
	I	0	0	0	0	0	0	2(9)	0	1(5)	2(9)	0
	R	2(10)	21(100)	21(100)	5(24)	21(100)	2(10)	2(9)	0	0	4(9)	1(5)
Citrobacter freundii	S	6(60)	0	0	5(50)	10(100)	4(40)	7(70)	10(100)	7(70)	6(60)	440
	I	0	0	0	2(20)	0	1(10)	1(10)	0	1(10)	1(10)	0
	R	4(40)	10(100)	108100)	3(30)	0	5(50)	2(20)	0	2(20)	3(30)	660
Citrobacter amalonaticus	S	2(100)	1(50)	2(100)	2(100)	2(100)	2(100)	2(100)	2(100)	2(100)	2(100)	2(100)
	I	0	1(50)	0	0	0	0	0	0	0	0	0
	R	0	0	0	0	0	0	0	0	0	0	0
Citrobacter koseri	S	6(56)	6(56)	0	0	7(100)	6(56)	7(100)	6(56)	7(100)	6(56)	7(100)
	I	0	0	0	0	0	0	0	0	0	0	0
	R	1(14)	1(14)	7(100)	0	0	1(14)	0	1(14)	0	1(14)	0
Aeromonas hydrophila	S	4(100)	0	0	3(75)	4(100)	4(100)	1(25)	0	3(75)	0	4(100)
	I	0	0	0	0	0	0	0	0	0	0	0
	R	0	4(100)	4(100)	1(25)	0	0	3(75)	0	1(25)	0	0
Achromobacter xylosoxidans	S	1(9)	0	0	2(18)	0	1(9)	4(36)	4(36)	1(9)	0	1(9)
	I	0	0	0	2(18)	0	0	1(9)	0	3(27)	0	0
	R	10(91)	0	0	7(64)	0	10(91)	6(55)	7(64)	7(64)	11(100)	10(91)
Providencia stuartii	S	3(60)	0	0	4(80)	0	3(60)	5(100)	4(80)	48(80)	2(40)	3(69)
	I	0	0	0	0	0	2(40)	0	1(20)	0	1(20)	0
	R	2(40)	5(100)	5(100)	1(20)	5(100)	0	0	0	1(20)	2(40)	2(40)
Morganella morganii	S	13(100)	0	0	11(85)	0	13(100)	11(84)	13(100)	12(92)	13(100)	7(54)
	I	0	0	0	0	0	0	1(8)	0	0	0	0
	R	0	13(100)	13(100)	2(15)	13(100)	0	1(8)	0	1(8)	0	6(46)

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…continuation Table 3. Resistance of Gram-negative microorganisms to antimicrobial agents

Bacteria		**Amicacina CIM**	**Amp/Sulbactam CIM**	**Ampicilina CIM**	**Ciprofloxacin a CIM**	**Colistina CIM**	**Gentamicin a CIM**	**Levofloxacin a CIM**	**Meropenem CIM**	**Pip/Tazo CIM**	**Tobramicin a CIM**	**Trimet/Sulf a CIM**
Burkholderia cepacia	S	0	0	0	0	0	0	18(67)	16(59)	0	0	18(67)
	I	0	0	0	0	0	0	1(4)	0	0	0	0
	R	0	0	0	0	0	0	8(29)	11(41)	0	0	9(33)
Chryseobacterium indologenes	S	1(25)	0	0	2(50)	0	0	2(50)	2(50)	3(75)	0	2(50)
	I	2(50)	0	0	0	0	2(50)	0	0	0	1(25)	0
	R	1(25)	0	0	2(50)	0	2(50)	2(50)	2(50)	1(25)	3(75)	2(50)
Stenotrophomonas maltophilia	S	0	0	0	0	0	0	7(87)	0	0	0	7(87)
	I	0	0	0	0	0	0	0	0	0	0	0
	R	0	0	0	0	0	0	1(13)	0	0	0	1(13)
Acinetobacter baumannii	S	58(70)	16(19)	0	40(48)	0	40(48)	42(51)	39(47)	0	33(40)	23(28)
	I	5(6)	3(4)	0	3(4)	0	3(4)	20(24)	5(6)	0	22(26)	0
	R	20(24)	64(77)	0	40(48)	0	40(48)	21(25)	39(47)	0	28(34)	60(72)
Acinetobacter lwoffii	S	11(100)	5(46)	0	8(73)	0	9(82)	10(91)	8(73)	0	10(91)	7(54)
	I	0	4(36)	0	0	0	0	0	0	0	1(9)	0
	R	0	2(18)	0	3(27)	0	2(18)	1(9)	3(27)	0	0	4(36)