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(RESEARCH ARTICLE)

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Profile of enterobacteria isolated at Ibn Tofail Hospital, Marrakech

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Abstract

Enterobacteriaceae are a family of Gram-negative bacteria. Some species can become pathogenic, causing a variety of infections such as urinary tract, digestive, respiratory, and bloodstream infections, especially in immunocompromised or hospitalized patients. In this study, different clinical samples were analyzed to identify the presence of Enterobacteriaceae. The aim is to assess the epidemiological characteristics of these isolates and to evaluate their antimicrobial susceptibility profiles to help clinicians select appropriate treatment strategies.

Keywords: Enterobacteriaceae; Antibiotic Resistance; Extended-Spectrum Beta-lactamase-Producing Enterobacteriaceae; Multidrug Resistance

1. Introduction

Bacterial resistance to antibiotics represents a major clinical and public health challenge [1]. Among the pathogens responsible for infections, Enterobacteriaceae are particularly concerning due to their ability to produce β-lactamases—enzymes that inactivate β-lactam antibiotics, including penicillins, cephalosporins, carbapenems, and monobactams. In addition to β-lactamase production, they also possess other resistance mechanisms that further limit treatment options [2,3,4,5,6]

They are implicated in a wide range of both intestinal and extraintestinal infections, with the urinary tract being the most common site of isolation. They are also frequently identified in blood, the respiratory tract, the peritoneal cavity, surgical sites, and wound isolates. These infections may be acquired in either hospital or community settings and can affect individuals regardless of underlying health conditions. [7,8,9]

The emergence and spread of resistance among Enterobacteriaceae are complicating the treatment of serious nosocomial infections and threatening to create species resistant to all currently available agents.[10]

The aim of this work is to describe the epidemiological profile of Enterobacteriaceae strains isolated in our hospital structure, as well as the resistance profile of these bacteria to the various ATBs to guide clinicians in the adjustment of therapeutic regimens.

2. Materials and methods

This retrospective, descriptive study was conducted in the medical microbiology laboratory of Ibn Tofail Hospital in Marrakech over a period of 3 years and 2 months, from January 1, 2022, to April 2025.

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Bacterial isolates were obtained from clinical specimens sent to the medical microbiological laboratory for diagnostic purposes. The specimens were urine, blood, catheters, puncture fluid, wound and surgical site specimens, biopsy and cerebrospinal fluid samples

The clinical samples were processed according to the routine laboratory diagnostic protocol, which included identifications by morphological, biochemical and culture characteristics. The identification of purified isolates was carried out withAPI gallery (Biomerieux).

Antibiotic susceptibility testing was performed using the disk diffusion method on agar media, and results were interpreted according to the guidelines of the Antibiogram Committee of the French Society for Microbiology (CA-SFM).

Extended-spectrum Betalactamase-producing Enterobacteriaceae (EBLSE) are identified using the positive synergy test, which consists of a synergy test between the clavulanic acid present on the CoAmoxiclave (AMC) disc and Ceftriaxone (CRO) or Cefotaxime (CTX). When EBLSE is present, this test produces a characteristic image resembling a "champagne cork".

We used Microsoft Excel 2016 for statistical data analysis.

3. Results

During the study period, a total of 324 bacterial isolates were recovered from clinical specimens received at the Bacteriology Laboratory of ibn Tofail Hospital in Marrakech. Enterobacteria accounted for 88.27% of all bacterial isolates, representing a total of 285 strains. Among these strains, 186 were from the surgical departments, and 64 from the intensive care unit. Strains isolated from outpatient samples accounted for 12.28% of all Enterobacteriaceae isolates (35 strains). The mean age of patients was 28 months, and the male-to-female sex ratio was 1.04.

The majority of isolates were obtained from wound and surgical site samples (42%), followed by urine (27%) and respiratory specimens (9%). Other sources included cerebrospinal fluid (5%), medical devices (5%), blood (4%), puncture fluids (4%), and biopsy samples (4%). (Figure 1)

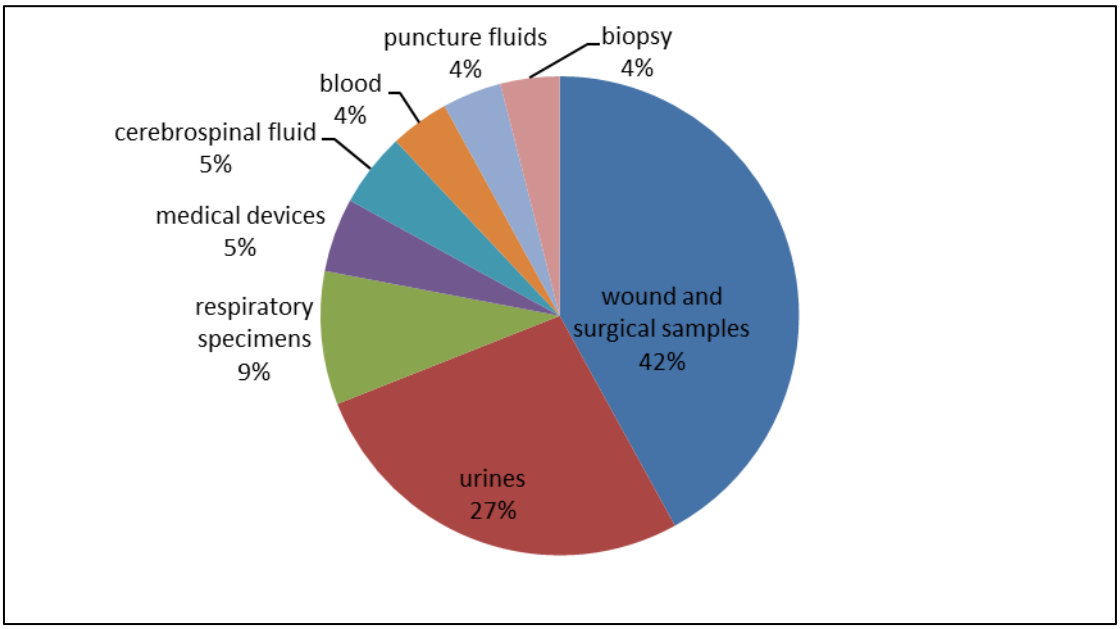

Figure 1 Distrubition of recieved specimens

In wound and surgical site specimens (n=148), *Enterobacter* spp. was the predominant organism (54/148), followed by *Klebsiella pneumoniae* (28/148), *Proteus* spp. (27/148), and *Escherichia coli* (23/148). *Enterobacter* spp. was also the predominant pathogen isolated from cerebrospinal fluid samples.

In urine samples (n = 74), *Escherichia coli* was the most frequently isolated species (46/74), followed by *Enterobacter* spp. (17/74) and *Klebsiella pneumoniae* (9/74).

In blood cultures (n=12), *Klebsiella pneumoniae* was the most commonly identified pathogen (7/12). It was also the most frequently isolated organism in respiratory specimens (9/24), followed by *Proteus* spp. (7/24) *Enterobacter* spp. (6/24), *Escherichia coli* (1/24) and *citrobacter spp.* (1/24). In biopsy samples, medical devices, and puncture fluids, *Klebsiella pneumoniae* was also the most frequently isolated organism. **(table 1)**

Table 1 Distribution of Enterobacteriaceae across various sample types

Microoganisms /Specimens	**wound and surgical sites**	**Urine**	**respiratory specimens**	**blood**	**puncture fluids**	**Medical devices**	**Cerebrospinal fluid**	**biopsy**
Escherichia coli	23	46	1	2	2	4	0	0
Enterobater spp.	54	17	6	2	1	4	2	0
Klebsiella pneumoniae	28	9	9	7	2	6	0	4
Proteus spp.	27	1	7	0	1	0	0	0
Citrobacter spp.	5	1	1	1	0	1	0	0
Morganella Morganii	5	0	0	0	0	0	0	0
Providencia spp.	4	0	0	0	0	0	0	0
Serratia spp.	2	0	0	0	0	0	0	0

Among these, *Enterobacter spp*. was the most frequently isolated (30%), followed by *Escherichia coli* (27%), *Klebsiella pneumoniae* (23%), *Proteus spp.* (13%), and *Citrobacter spp* (3.15%). Other species, including Morganella, Providencia, and Serratia, were also detected in lower proportions, accounting for 1.7%, 1.3%, and 1% of isolates, respectively**. (**Figure 2**)**

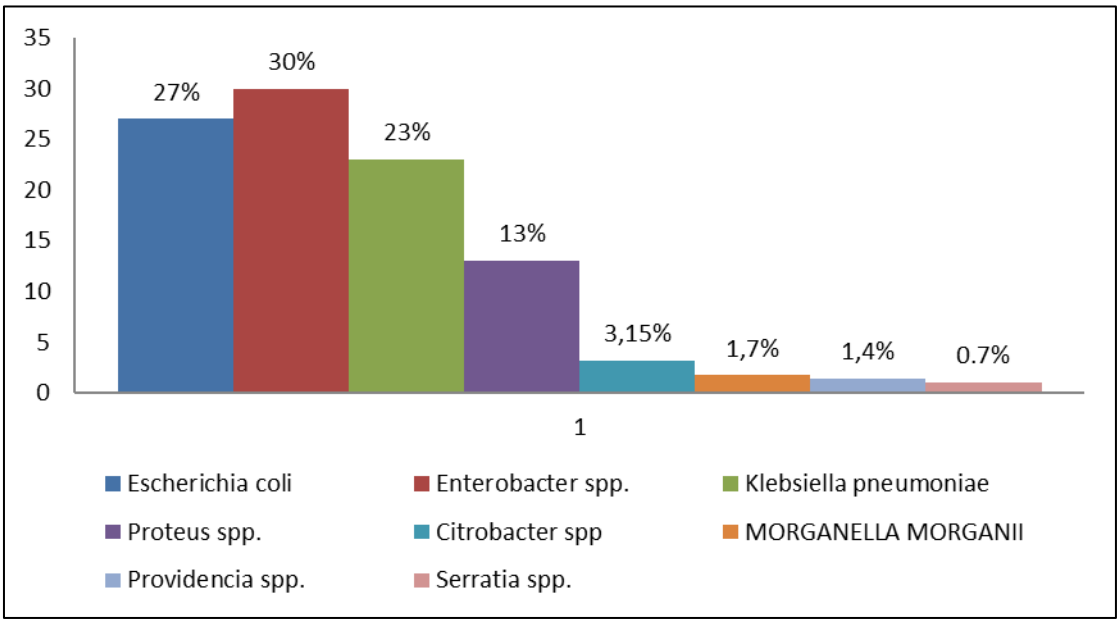

Figure 2 Distribution of the different Enterobacteriaceae strains

The antibiotic resistance profiles varied according to the bacterial species. Among the main Enterobacteriaceae isolates, resistance to aminopenicillins was notably high (85.4%). When combined with clavulanic acid, this resistance dropped to 78%. (Figure 3)

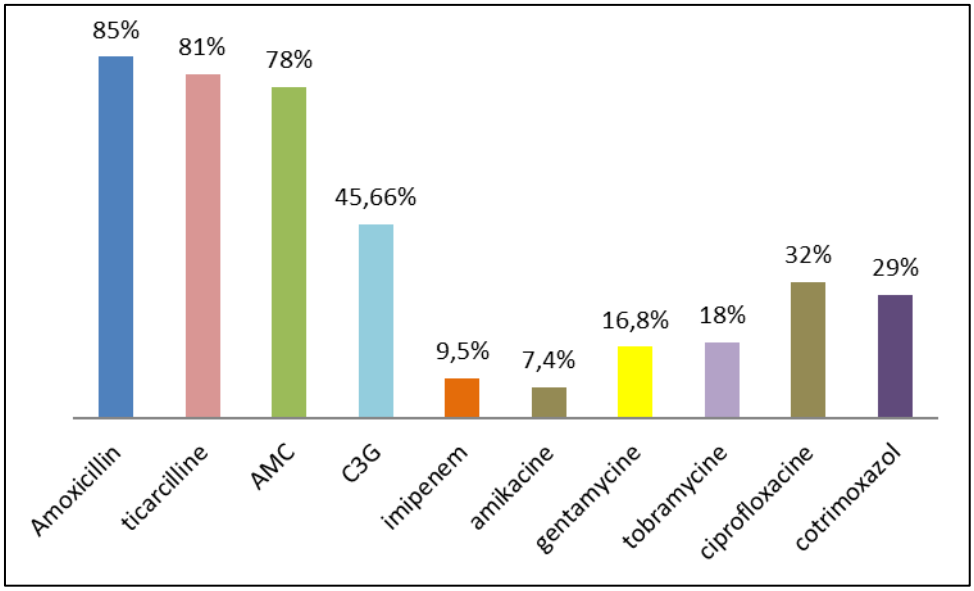

Figure 3 Resistance rates of Enterobacteriaceae isolates

Escherichia coli exhibited the lowest resistance to third-generation cephalosporins (30.6%), followed by Enterobacter spp. (39%) and Klebsiella pneumoniae (56.14%). *Escherichia coli* also showed the lowest resistance to gentamicin, with a rate of 4.7%.

Resistance to imipenem was detected in 14 strains of *Klebsiella pneumoniae*, 7 strains of *Escherichia coli*, and 5 strains of *Enterobacter cloacae*.

Regarding fluoroquinolones, *Klebsiella pneumoniae* had a 51% resistance for ciprofloxacin, higher than *E. coli* and *E. cloacae* showing a resistance ranging from 27% to 36%

Among the isolated strains, 52 were extended-spectrum β-lactamase (ESBL) producers, representing 18.2% of the isolates. The distribution of ESBL-producing *Enterobacteriaceae* by species showed a predominance of *Klebsiella pneumoniae* (38.4%), followed by *Escherichia coli* (36.5%) and *Enterobacter cloacae* (25%). Among the other resistance phenotypes observed in *Enterobacteriaceae* were: 10 high-level penicillinase producers (3.5%), 26 low-level penicillinase producers (9.12%), 18 high-level cephalosporinase producers (6.31%), 41 low-level cephalosporinase producers (14.3%), 8 carbapenemase producers (2.8%), and 6 isolates producing both ESBL and carbapenemase (2.1%). Additionally, 112 isolates (39.1%) were wild-type strains, showing no acquired resistance mechanisms.(Figure 4)

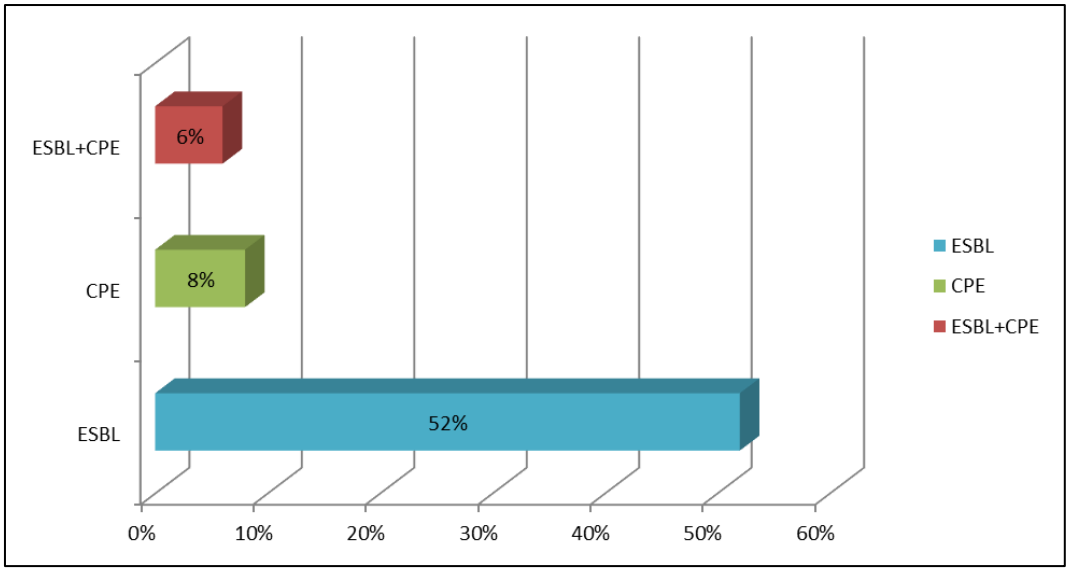

Figure 4 Distribution of Multidrug-Resistant Strains

Among the antibiotics tested, Amikacin and Imipenem were the most effective against Enterobacteriaceae

4. Discussion

In our study, the most frequently isolated species was *Enterobacter spp.* followed by *Escherichia coli*. This profile differs from most data reported in the literature, where *E. coli* generally predominates, especially in urinary and community-acquired infections [11,12]. The predominance of *E. cloacae* may be explained by the specific context of our study population. This species is frequently associated with nosocomial infections, particularly related to the use of invasive devices (catheters, urinary probes) and prolonged antibiotic exposure [13, 14]. Several hospital-based studies have reported high rates of *E. cloacae* in intensive care units and surgical wards [15].

the prevalence of these microbial pathogens is increasing in different regions of the world, which is a wake-up call and prompts us to take initiatives to address this phenomenon.The ability of these bacterial species to acquire various resistance mechanisms, notably to β-lactams, fluoroquinolones, and aminoglycosides, significantly complicates therapeutic management.

The observed resistance rate of 85.4% to aminopenicillins is alarmingly high and reflects the widespread inefficacy of these antibiotics as monotherapy in treating infections caused by this bacterial family. This finding is consistent with several reports in the literature, which have reported similarly elevated resistance rates ranging from 80% to over 90% for ampicillin and amoxicillin, particularly in *Escherichia coli* and *Klebsiella* spp. [16,17].

In our study, *Klebsiella pneumoniae* exhibited the highest resistance to ciprofloxacin among the tested *Enterobacteriaceae* followed by *Escherichia coli* and *Enterobacter cloacae.*This pattern reflects the well-documented tendency of *K. pneumoniae* to acquire and accumulate multiple resistance mechanisms, including plasmid-mediated quinolone resistance (PMQR) genes, mutations in DNA gyrase (gyrA) and topoisomerase IV (parC), and overexpression of efflux pumps.[18]

In our study, 38.4% of the ESBL-producing isolates were *Klebsiella pneumoniae* strains, followed by *Escherichia coli* (36.5%) and *Enterobacter cloacae* (25%). This finding is consistent with several reports indicating that *K. pneumoniae* is often the predominant species responsible for ESBL production [19,20,21]. However, other international studies have reported a different distribution, with *E. coli* being the most frequently identified ESBL producer, followed by *Klebsiella* spp. For instance, the study conducted in Monastir reported 41% of ESBL-producing isolates as *E. coli* and 39% as *Klebsiella* spp. [22], while a study from China showed 71.7% for *E. coli* and 28.3% for *Klebsiella pneumoniae* [23]. These differences may be attributed to geographical variability, differences in sample origin, and local antimicrobial use practices.These enzymes are often plasmid-encoded, enabling horizontal gene transfer and the rapid dissemination of resistance across different bacterial species, especially in hospital settings where antibiotic pressure and close contact among patients facilitate their spread. [24]

Imipenem and amikacin showed good activity against *Enterobacteriaceae* isolates. These findings have also been reported in studies conducted in Spain [25] and in various regions of Africa [26,22].

Antibiotic susceptibility testing of *Enterobacteriaceae* demonstrated a high level of resistance to most antibiotics tested. This observation, consistent with findings from other studies, mainly attributed to inappropriate use and prescription of broad-spectrum antibiotics in both hospital and community settings. [27][28]

5. Conclusion

Antibiotic resistance among bacteria represents a major global public health concern. In response to the growing prevalence of multidrug-resistant organisms, particularly within *Enterobacteriaceae*, national and international guidelines emphasize the importance of regular microbiological surveillance, prudent antibiotic use, and strengthened infection control measures. In this context, close collaboration between clinicians and microbiologists is essential to ensure timely and appropriate patient management based on microbiological evidence.

Compliance with ethical standards

Disclosure of conflict of interest

Disclosure of conflict of interest There is no conflict of interest.

Statement of informed consent

Informed consent was obtained from all individual participants included in the study by signing the Free and Informed Consent Form.

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