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ANTIMICROBIAL RESISTANCE. AN OBSERVATIONAL RETROSPECTIVE STUDY FROM A SINGLE CENTER IN SOUTH-EAST ROMANIA

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Abstract: Antimicrobial resistance (AMR) is a major global health concern, contributing to prolonged hospitalizations, treatment failures, and increased mortality. The aim of this study was to analyze antimicrobial resistance patterns among clinical isolates in the Microbiology Laboratory of the Emergency Clinical Hospital "Sfantul Andrei," Constanta, Romania. This observational, retrospective study was conducted between April 15 and September 30, 2025. A total of 11179 clinical samples were analyzed, including 4771 urine cultures and 6408 other clinical samples (blood cultures, exudates, and bacterial cultures). Antimicrobial resistance testing was performed using both disk diffusion assays and the VITEK automated system, following CLSI and INSP guidelines. Among urine cultures, multidrug-resistant organisms (MDROs) were identified in 2.24% of samples and extensively drug-resistant organisms (XDROs) in 0.90%. The most prevalent resistances included glycopeptide-resistant isolates (1.32%), vancomycin-resistant Enterococcus (1.19%), and extended-spectrum β-lactamase (ESBL) production (1.04%). Among other clinical samples, notable resistance patterns included β-lactam resistance (3.97%), cefoxitin screen resistance (4.38%), and penicillin-binding protein modifications (2.09%). Overall, MDR prevalence exceeded XDR, suggesting a moderate level of resistance within the hospital setting. The study revealed a generally low prevalence of high-level antimicrobial resistance, though β-lactam and cefoxitin screen resistances were relatively elevated, suggesting the possible presence of MRSA and antibiotic misuse. Continuous surveillance and strict infection control measures are essential to prevent the spread of resistant strains. These findings provide a foundation for strengthening local AMR monitoring systems and guiding antimicrobial stewardship programs within the hospital.

Keywords: Antimicrobial resistance, Multidrug-resistant organisms, Antimicrobial stewardship, Resistance

Introduction

Antimicrobial resistance (AMR) is a major public health challenge in both developed and developing countries. Infections caused by AMR bacteria can lead to health complications such as extended hospitalization, treatment failure, and mortality. The misuse of antibiotics in healthcare facilities, inadequate compliance with infection control programs, and the lack of surveillance systems to track both unique and common resistant phenotypes have contributed to development and emergence of AMR bacteria. The World Health Organization (WHO) has initiated the Global Action Plan on Antimicrobial Resistance which includes, among other pillars, the increased knowledge about AMR through surveillance and data collection. Therefore, one of the first steps in building an AMR surveillance system in a country is to explore and analyze available resistance data in clinical isolates from hospital settings. (1)

Infections due to multidrug-resistant organisms (MDR) account for 31.6% of hospital infections and are a major threat in intensive care unit (ICU) settings, where their prevalence may reach up to 50%. Indeed, factors associated with an increased MDR infection risk include characteristics largely seen in ICUs such as critical illness, broad-spectrum antibiotic use, use of invasive procedures (mechanical ventilation, endotracheal tubes, central venous access, urinary catheters, feeding tubes, etc.), and hospital/healthcare exposures related to prolonged hospital stay. Therefore, patients with chronic illnesses who require frequent hospitalizations and/or antibiotic treatments as well as invasive procedures are at risk of developing MDR infection along with various complications. (2)

The emergence of multidrug-resistant (MDR) bacteria, followed by extensive drug-resistant (XDR) bacteria, has posed a threat to the lives of patients with infectious diseases. About 25,000 patients in Europe die each year from infectious diseases caused by MDR bacteria, and more than 50% of cases are associated with high mortality rates. (3)

The spread of extended spectrum β-lactamase (ESBL)-producing bacteria has increased over the last two decades in the hospital setting as well as in the community, emerging as a serious public health threat. Infections caused by antimicrobial-resistant Escherichia coli proportionally contributed the most to the burden of antimicrobial resistance in Europe, both as number of cases and number of attributable deaths. (4)

Since their emergence in the 1980s, VRE has remained a significant threat to some patients in hospital settings. The ability of enterococci species to colonize the human gastrointestinal tract and their persistence on environmental surfaces increase their ability to be transmitted between individuals in healthcare settings, leading to healthcare-associated infections (HAIs). Despite the advent of effective antibiotic therapies for VRE, VRE-associated and overall mortality rates are higher in patients infected with VRE than for those with vancomycin susceptible enterococci (VSE), and VRE infection is usually associated with higher costs and length

of hospital stay. In addition, there remains a risk that the genes responsible for glycopeptide resistance in VRE will spread to other organisms. A priority is to prevent the spread of VRE in the healthcare setting (5)

Glycopeptides (GPs) are a class of compounds containing the carbohydrate moieties (glycans or sugars) attached to the peptide core. Glycopeptide antibiotics are a kind of antibacterial agents that possess a similar macromolecular structure and basic mechanism of action. GPs exhibit strong antibacterial properties against numerous bacteria. GPs are a primordial class of antimicrobials exhibiting activity against Streptococcus, Enterococcus species and Staphylococcus aureus strains that are methicillin-resistant (MRSA) as well. (6)

Linezolid, the first clinically available oxazolidinone, is active against most Gram-positive bacteria, including MRSA, VRE and penicillin-resistant pneumococci. Pharmacokinetic properties of this drug allow its use for treatment of meningitis, endocarditis, sepsis, osteomyelitis and surgical infections. The oxazolidinone molecule has potential for development of new compounds with lower toxicity and broader spectrum, including Gram-negative respiratory tract infection pathogens, and new concepts such as quinolone-oxazolidinone hybrid drugs, which may cover Gram-positive and Gram-negative bacteria. There is only one resistance mechanism described for linezolid and that is target modification. No transferable resistance is described yet for oxazolidinones. (7)

The proportion of isolates resistant to β-lactams is increasing in several countries worldwide, and this has emerged by the acquisition of β-lactamases, the modification of penicillin-binding protein 3 (PBP3) encoded by the ftsI gene, or both. The importance of increasing resistance amongst H. influenzae isolates has been recognized by the WHO, and it is considered one of the bacterial priority pathogens for antimicrobial resistance. β -lactamases are frequently of TEM-1 or ROB-1 types, which usually confer resistance to ampicillin and amoxicillin but not against third-generation cephalosporins (3GC) and are inactivated by clavulanic acid. These isolates are usually referred to as β-lactamase-positive ampicillin-resistant (BLPAR) isolates. The mutations in PBP3 involve several key residues that result in the decreased affinity of β-lactams for PBP3 and subsequently confer resistance to ampicillin and amoxicillin. Recently, mutations in additional residues of PBP3 were reported to also confer resistance to 3GC. PBP3 and its corresponding isolates are classified accordingly into several groups (8)

The most prevalent mechanism of high-level aminoglycoside resistance in clinical bacteria is their enzymatic modification. Three families of aminoglycoside modifying enzymes have been recognized: phosphotransferases (APH), acetyltransferases (AAC), and nucleotidyltransferases (ANT). Genes for aminoglycoside modifying enzymes are often plasmidic, with bacteria-to-bacteria dissemination. (9)

Over the last 20 years, many new β-lactam antibiotics have been developed that were specifically designed to be resistant to the hydrolytic

action of β-lactamases. However, with each new class that has been used to treat patients, new β-lactamases emerged that caused resistance to that class of drug. Presumably, the selective pressure of the use and overuse of new antibiotics in the treatment of patients has been selected for new variants of β-lactamase. One of these new classes was the oxyimino-cephalosporins, which became widely used for the treatment of serious infections due to Gram-negative bacteria in the 1980s. Currently, more than 150 different ESBLs have been described. These β-lactamases have been found worldwide in many different genera of Enterobacteriaceae and P. aeruginosa. ESBLs represent an important mechanism of resistance with significant epidemiological implications. (10)

Methicillin-resistant staphylococci (MRS), including methicillin-resistant Staphylococcus aureus (MRSA) and methicillin-resistant coagulase-negative staphylococci (MRCoNS) strains have become an additional threat for human and animal health, contributing significantly to morbidity, mortality, and socio-economic costs. Resistance in MRSA and MRCoNS is caused by the acquisition of the mecA gene that encodes a modified penicillin-binding protein 2a (PBP2a) which has a low binding affinity for all β-lactam antibiotics (11)

Some strains have demonstrated resistance to multiple antibiotics, which may occur through various mechanisms such as the production of hydrolyzing enzymes, loss of outer membrane proteins, efflux systems, and mutations in target sites. These resistant isolates are classified as MDR, XDR, and PDR (pandrug-resistant), based on the severity of their resistance. Infections caused by these resistant strains can lead to higher rates of morbidity and mortality due to the limited availability of effective antimicrobial treatments. MDR is usually characterized by acquired resistance to at least one agent in three or more antimicrobial categories, while XDR is defined as resistance to at least one agent in all but two or fewer categories (meaning the bacteria remain susceptible to only one or two categories), and PDR is defined as resistance to all agents across all antimicrobial categories. To accurately apply these definitions, bacterial isolates must be tested against nearly all antimicrobial agents within the relevant categories, and selective reporting or suppression of results should be avoided. (12)

β-lactamases were first described in Escherichia coli shortly after the clinical use of penicillin that began in the 1940s. These enzymes may be encoded chromosomally or on transposons or plasmids. The hundreds of β-lactamases can be organized by their structure. This classification divides β-lactamases into 4 groups (A–D). The classes A, C, and D have serine at their active site, while class B, the metallo–β-lactamases, have zinc at the active site. β-lactamases are also found primarily in Gram-negative bacteria, but they have also been described in Staphylococcus aureus. Although Staphylococcus aureus possessed β-lactamase even before the discovery of penicillin, the prevalence of β-lactamase–producing Staphylococcus aureus increased rapidly after its introduction into clinical

use. (13)

Resistance to antibiotics is typically the result of antibiotic destruction or modification, target alterations (target replacement, target site mutations, target site enzymatic alterations, target site protection, target bypass or target overproduction), and reduced antibiotic accumulation due to either increased efflux or decreased permeability. Alternatively, antibiotic resistance can be the result of a global adaptation of the bacterial cell. β-Lactamases are the best example of antibiotic resistance mediated by the destruction of the antibiotic molecule. These enzymes destroy the amide bond of the β-lactam ring essentially rendering the antimicrobial ineffective. (14)

High-throughput DNA sequencing and bioinformatics have dramatically changed the way AMR is investigated by identifying the genes or mutations that convey resistance. Culture-based approaches may be used to investigate AMR in the clinical setting using antibiotic sensitivity assays. These methods depend on the ability of an organism to be grown in culture, while this is an effective way to determine if an organism can resist a particular antimicrobial agent. The ability to sequence DNA from environmental and clinical samples (metagenomics and whole genome sequencing) to determine gene content presents the opportunity to identify ARGs as well as understand the mechanism of how organisms acquire ARGs. It also presents tools to determine the extent of spread of ARGs among diverse populations without the need to first grow the organism in pure culture. (15)

Materials and Methods

This was an observational retrospective study conducted at the Emergency Clinical Hospital “Sfantul Andrei” from Constanta, Romania. This study analyzed the antimicrobial resistance patterns between April 15 and September 30, 2025. The main aim was to evaluate the specific antimicrobial resistance profile of microorganisms isolated from urine cultures and other clinical samples (blood cultures, exudates and bacterial cultures). The main resistance patterns analyzed included: XDRO (Extensively Drug-Resistant Organism), MDRO (Multidrug-Resistant Organism), ESBL (Extended Spectrum β -Lactamses), VRE (Vancomycin-Resistant Enterococcus), Polypeptide-Resistant, Glycopeptide-Resistant, Oxazolidinone-Resistant, β-Lactamases, Gentamicin High-Level Resistant, Kanamicin High-Level Resistant, Streptomycin High-Level Resistant, Extended Spectrum β-Lactamase, Carbapenem resistance mechanisms, Carbapenemase, Cefoxitin screen resistance, PBP modifications, Glycopeptides Hetero-Visa, Mupirocin High Level Resistance. Samples were collected from hospitalized patients in the Emergency Hospital “Sfantul Andrei” from Constanta, Romania and microbiological analyses were processed in the microbiology laboratory of the same hospital.

Data were collected from the records of the microbiology laboratory of the hospital, which included related information: patient code, date of

collection, type of sample, XDRO test results, MDRO test results, ESBL results, and specific resistances like VRE), Polypeptide-Resistant, Glycopeptide-Resistant, Oxazolidinone-Resistant, β -Lactamases, Gentamicin High-Level Resistant, Kanamicin High-Level Resistant, Streptomycin High-Level Resistant, Extended Spectrum β-Lactamase, Carbapenem resistance mechanisms, Carbapenemase, Cefoxitin Screen Resistance, PBP modifications, Glycopeptides Hetero-Visa, Mupirocin High Level Resistance.

The inclusion criteria were the following: hospital admission and the presence of clinical signs of infection. No age or sex restrictions were applied. The patients were selected from all wards of the hospital.

Bacteriologic testing was performed in the microbiology laboratory of the hospital, according to standard protocols and using automated and manual culture and identification methods. Antimicrobial susceptibility testing was performed by disk diffusion assay and VITEK automated system (bioMérieux). The determinations were performed according to CLSI (Clinical and Laboratory Standards Institute) guidelines and INSP (National Institute of Public Health from Romania) guidelines.

Data was manually compiled in an Excel file, following consultation of antibiograms and laboratory records and results for all cases recorded between April 15 and September 30, 2025. Each patient was included in a database with variables organized into columns: Number of isolates, XDR, MDR, ESBL, VRE, Polypeptide-Resistant, Glycopeptide-Resistant, Oxazolidinone-Resistant, β-Lactamases, Gentamicin High-Level Resistant, Streptomycin High-Level Resistant, Extended Spectrum β-Lactamase, Carbapenem resistance mechanisms, Carbapenemase, Cefoxitin Screen Resistance, PBP modifications, Glycopeptides Hetero-Visa, Mupirocin High Level Resistance. The study did not involve direct patient intervention, and all data were anonymized in accordance with ethical standards.

Results

In total, 11,179 patient samples were analyzed in the 6 months of the study, of which 4,771 were urine cultures and 6,408 were other clinical samples. Of these, 3,011 were positive and 8,168 were negative. There were 1,249 positive urine culture samples, 3,522 negative samples, 1,762 positive samples from other clinical samples and 4,646 negative samples. The other clinical samples also include 1,556 blood cultures and 756 exudates. The highest number of urine culture samples was recorded in July 2025 (317) and the fewest in April 2025 (97). The monthly average was 208 samples of urine cultures. Regarding other clinical samples, most samples were in August 2025 (526) and the fewest in May 2025 (99). No samples were recorded in April, as processing non-urine specimens began in May. The monthly average was 352 samples. Overall, there were a total of 3,011 samples, with most samples in July 2025 (774) and the fewest in April 2025 (97). The average is 502 samples monthly. The distribution of positive samples by month is illustrated in Table 1.

Table 1. The distribution of positive samples

	APRIL	MAY	JUNE	JULY	AUGUST	SEPTEMBER	TOTAL
URINE CULTURES	97	253	208	317	198	176	1,249
OTHER CULTURES	0	99	238	457	526	442	1,762
TOTAL	97	352	446	774	724	618	3,011

Regarding the urine culture samples and the resistances, there are notable differences. Of the total of 4,771 samples, 1,249 were positive, 3,522 were negative, 107 samples were MDRO (2.24%) and only 43 samples were XDRO (0.90%). There were 57 samples of VRE (1.19%) and 50 samples of ESBL (1.04%). Other significant resistances are Glycopeptides Resistances which were 63 samples (1.32%) and β Lactams which were 48 samples (1%). The fewest were Extended Spectrum β Lactamase, which were only 2 samples in May 2025 (0.04%). The numerical distribution of resistances from urine culture samples is illustrated in Table 2.

Table 2. Numerical distribution of resistances from urine culture samples (XDRO - Extensively Drug-Resistant Organism, MDRO - Multidrug-Resistant Organism, ESBL - Extended Spectrum B-Lactamses, VRE - Vancomycin-Resistant Enterococcus, RES – Resistance)

Culture	**Nr.**	**%**
XDRO	43	0.90%
MDRO	107	2.24%
ESBL	50	1.04%
VRE	57	1.19%
POLYPEPTIDE RES	15	0.31%
GLYCOPEPTIDES RES	63	1.32%
OXAZOLIDINONE RES	28	0.58%
β LACTAMS	48	1.00%
GENTA HIGH LEVEL RES	8	0.16%
KANA HIGH LEVEL RES	14	0.29%
STREPTO HIGH LEVEL RES	7	0.14%
EXTENDED SPECTRUM β -LACTAMASE	2	0.04%
CARBAPENEM RESISTANCE MECHANISMS	4	0.08%
CARBAPENEMASE	4	0.08%
CEFOXITIN SCREEN	13	0.27%

Regarding other clinical samples and resistances, there are also some differences. Of the total of 6,408 samples, 1,762 were positive, 4,646 were negative, 30 samples were MDRO (0.46%) and only 10 samples were XDRO (0.15%). There were 26 samples of VRE (0.40%) and 18 samples of ESBL (0.28%). Other significant resistances are β-lactam resistance which were 255 samples (3.97%) and Cefoxitin screen which were 281 samples (4.38%). The lowest frequency was observed for Kanamicin High-Level Resistant and Streptomycin High-Level Resistant, which were only 1 sample in May 2025 (0.01%). Other significant resistances are PBP modifications which were 134 samples (2.09%) and Glycopeptides resistance which were 118 samples (1.84%). The numerical distribution of resistances from other secretion samples is illustrated in Table 3.

Table 3. Numerical distribution of resistances from other secretion samples (XDRO - Extensively Drug-Resistant Organism, MDRO - Multidrug-Resistant Organism, ESBL - Extended Spectrum β-Lactamses, VRE - Vancomycin-Resistant Enterococcus, RES – Resistance)

Culture	**Nr.**	**%**
XDRO	10	0.15%
MDRO	30	0.46%
ESBL	18	0.28%
VRE	26	0.40%
POLYPEPTIDE RES	10	0.15%
GLYCOPEPTIDES RES	118	1.84%
OXAZOLIDINONE RES	35	0.54%
β LACTAMS	255	3.97%
KANA HIGH LEVEL RES	1	0.01%
STREPTO HIGH LEVEL RES	1	0.01%
CEFOXITIN SCREEN	281	4.38%
PBP MODIFICATIONS	134	2.09%
GLYCOPETIDES HETERO-VISA	9	0.14%
MUPIROCIN HIGH LEVEL RES	8	0.12%

The distribution of MDR and XDR organisms by month and sample type was also analyzed. The laboratory used VITEK only in April, May and June so from July were used only disk diffusion assay which did not provide a result for XDRO and MDRO so only these three months were included in the comparison. According to the collected data, from urine cultures the most XDRO were in May 2025 (15 samples), in the other months were only 14. The most MDRO were also in May 2025 (44 samples), in the other months were 24 and 39 samples. From other clinical samples, the most samples were in June (8 samples of XDRO and 25 of MDRO), and no cases were recorded in April because the laboratory started working other clinical samples only in May.

β lactams and cefoxitin screen resistances are very important to study. Regarding the β lactams from other clinical samples, the most were in July (72 samples), and only zero in May. From urine cultures, the most were in June (31 samples) and only zero in August. Regarding the Cefoxitin screen resistance from other clinical samples, the most were in July (90 samples) and the fewest in May (only 8). From urine cultures, the most were in September (5 samples) and only zero in August. These results indicate that there are a lot more β lactams and Cefoxitin screen resistances from other clinical samples towards urine cultures (48 β lactams and 13 cefoxitin screen res from urine cultures compared with 255 β lactams and 281 cefoxitin screen from other clinical samples). The monthly evolution of β Lactams and Cefoxitin screen resistance from all samples (including negative) is illustrated in Figure 1.

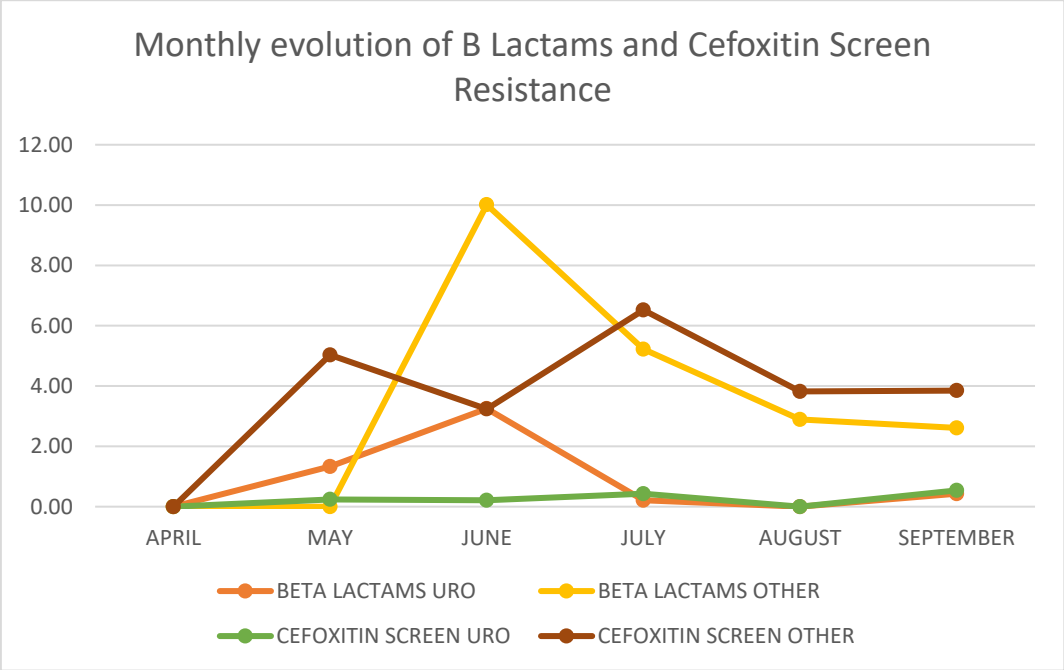

Figure 1. Monthly evolution of β Lactams and Cefoxitin Screen Resistance

Discussions

A higher number of other clinical samples was observed compared to urine cultures, although processing of these samples began one month later. This can be explained by the fact that other clinical samples include blood cultures, exudates and bacterial cultures so there are three types of samples instead of one. Bacterial cultures include axillary skin, inguinal skin and ocular infections. The most frequent bacterial cultures that were processed in the microbiology laboratory were skin infections. A higher incidence of skin infections was observed, particularly among pediatric and neonatal patients. Regarding the distribution of urine cultures, a decrease was observed in the last months, in the last months there were fewer patients with urine cultures. In contrast, an increase was observed regarding the other clinical samples in the last months. This is likely because in last months the laboratory has expanded and a substantial number of samples which were sent to other hospitals in the first months are now being collected and processed in our laboratory. Another contributing factor may be that in the summer season there were more patients than in the spring.

As an analysis of the distribution of resistances from urine culture samples, there was a higher prevalence of MDR organisms, followed by Glycopeptides Resistance, VRE, ESBL and β Lactams. In other clinical samples, a high prevalence of cefoxitin resistance, β-lactam resistance, PBP modifications, and glycopeptide resistance were observed. Comparatively, both have a high prevalence of Glycopeptides Resistance and β Lactams which show the increased incidence of these resistances in hospital.

The XDRO and MDRO distribution is very important for reporting. In the case of urine cultures, uniform distribution was observed. Instead, in

the case of other clinical samples there was an increased distribution. There are more MDRO than XDRO (147 samples of MDRO compared with 53 samples of XDRO) indicating that there are fewer Extensively Drug-Resistant Organism than Multidrug-Resistant Organism, this suggests that multidrug resistance is more prevalent than extensive drug resistance in this setting.

A total of 303 β-lactam-resistant isolates and 294 cefoxitin-resistant isolates were identified. There are a lot more other clinical samples instead of urine cultures. The most numbers are also in the summer season compared with the spring and autumn season.

Conclusions

This observational retrospective study revealed a relatively low prevalence of most resistance patterns, with higher rates observed for β-lactam and cefoxitin resistance.

The results suggest a relatively low prevalence of multidrug-resistant organisms and a controlled rate of nosocomial infections. The high number of cefoxitin screen resistance suggests that many bacterial isolates tested in the lab showed resistance to cefoxitin and also suggest a high prevalence of MRSA or other multidrug-resistant bacteria. This could indicate increased antibiotic misuse in the area, a potential hospital or community outbreak, need for stricter infection control measures and fewer effective antibiotic options for treatment. The high number of β lactams suggest that many bacterial strains are no longer killed or inhibited by β-lactam antibiotics (penicillins, cephalosporins, carbapenems, monobactams). The high resistance to β lactams is a problem because it reduces treatment options, this leads to limited therapeutic options, increased treatment complexity, prolonged hospital stays, and higher healthcare costs.

The analysis provides an important starting point for the development of surveillance strategies, and the study highlights the importance of continuous monitoring of bacterial resistance, the evolution of susceptibility and resistance and the need for well-structured data management systems in our hospital.

Data Availability Statement

The data supporting the findings of this study are available from the corresponding author upon reasonable request. The data are not publicly available due to institutional and ethical restrictions.

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