**Evaluation of urinary tract infections in patients admitted in an intensive care unit (ICU) at Inkosi Albert Luthuli central (IALCH) hospital in Kwazulu-Natal, Durban: A retrospective cross-sectional study designed to determine the most prevalent pathogens of urinary tract infections.**

***Nqobile Zinhle Dlamini1,\*, Mr. S Shangase2.***

*1Department of Biomedical Sciences, Mangosuthu University of Technology*

*2Lecturer at Department of Biomedical Sciences, Mangosuthu University of Technology*

**Abstract**

**Background**

Urinary tract infections (UTIs) are among the most prevalent diseases in patients admitted to the Intensive Care Unit (ICU). ICU patients are at higher risk for UTIs due to factors such as indwelling urinary catheters, prolonged hospital stay, antibiotic use, immunocompromised, and underlying comorbidities like diabetes.

**Aim and Objectives**

To identify the most prevalent isolated microorganisms causing UTIs in ICU patients with UTIs. To Assess Antimicrobial Susceptibility Patterns of isolated microorganisms. To Analyse demographic information of patients with UTIs.

**Methodology**

This project was a retrospective quantitative study that looked at ICU patients admitted at IALCH. The study was a convenience non-probability study which was done in an NHLS microbiology laboratory using standard urine culture and a VITEk-2 automated system.

**Results**

270 positive urine specimens, the most common isolate was *Escherichia coli* (n=143; 53%), followed by *Klebsiella pneumoniae subsp* (n=40; 14.8%). *Enterococcus faecalis* (n=16; 6.0%) were the most common Gram-positive pathogens. *E. coli* showed significant resistance to Cefotaxime ceftriaxone (31.4%), Gentamycin (10.4%), cefepime (6.3%) and Piperacillin tazobactam (3.5%). Among Gram-positive, *E. faecalis* showed 75% susceptibility.

**Conclusion**

*E. coli* was the most common isolate accounting for 53% followed by *Klebsiella pneumoniae subspp* and *E. faecalis* in ICU patients admitted At IALCH. Notably *E. coli* exhibited significant resistance to multiple antibiotics including cefotaxime ceftriaxone, gentamycin, cefepime, and piperacillin. In contrast, *E. faecalis* demonstrated 75% susceptibility to tested antibiotics. *E. faecalis* was also most prevalent among the gram-positive accounting for 6.0%. Vancomycin was found to be the most effective for *E. faecalis*. Ciprofloxacin was found to be the least effective with a high rate of resistance for *E. faecalis*. This study also discovered that UTIs were more common in patients between the age of 40-65 years and the study showed that the most affected were females.

**Recommendations**

Future research should prioritize comprehensive data collection methods.

***Keywords****: Urinary tract infections, intensive care units, Antimicrobial susceptibility, multiple drug resistance.*

*Submitted: 2025-02-15 Accepted: 2025-03-09 Published: 2025-06-13*

***Corresponding Author :*** *Nqobile Zinhle Dlamini*

*Email:* ***nqobilezinhle56@gmail.com***

*Department of Biomedical Sciences, Mangosuthu University of Technology*

**Introduction**

Urinary Tract Infections (UTIs) rank among the most common infections in the general population and are a major contributor to Hospital -hospital-acquired infections (HAIs) which can have serious health and financial repercussions (Burrows,2016). UTIs are defined as the significant bacterial presence in a patient’s urine (Rubi et al, 2022). Community-acquired or hospital-acquired UTIs are divided into both uncomplicated UTIs and complicated. Uncomplicated UTIs are those that are present in patients with no anatomical urinary tract abnormalities and do not have urinary devices. An uncomplicated UTI can be resolved without the use of antibiotics if the patient's immune system responds successfully (Mann et Al,2017). Complicated UTIs are associated with immunocompromised patients and previous exposure to antibiotics (Sabih et al, 2023). Complicated UTI occurs in patients who experience urinary obstructions, renal failure, and those who use medical devices such as catheters hence it requires prolonged treatment (Courant A, 2022).

 Most UTIs are biofilm-associated diseases, meaning that harmful bacterial strains invade urinary tract tissues as well as indwelling devices such as surgical catheters. About 95% of UTIs are catheter-associated urinary tract infections (CAUTIs), which continue to rank as the second most significant nosocomial infections in critically sick patients even after preventive measures have been put in place (Bizuayehu et al., 2022). CAUTIs are the most common nosocomial infections, contributing about 70 to 80 percent of infections linked to the use of a urinary catheter (Nicolle, 2014). Invasive devices such as catheters are responsible for nosocomial infections as they permit the direct inoculation of pathogens into the bladder during insertion, producing biofilm on the surface (Zhao et al., 2023). Biofilm is a layer of bacteria or other micro-organisms that grow on and stick to the surface of a structure by a mucus-like matrix of carbohydrates that attach to a surface (Sauer et al, 2022). In this case, they are formed in the catheter surface and then released into the bladder. These increase resistance to antibiotics leading to persistent infections. Biofilms can lead to urine blockage as a result of the presence of *Proteus mirabilis* (Pelling et al, 2019). *Proteus mirabilis* produces urease leading to low Ph in the urinary tract, which causes the formation of urinary stones that cause blockage (Schaffer et al, 2015). Microorganisms are introduced into the site of the catheter, where pathogens enter the urinary tract of a patient and colonize the urethra (Sikora et al, 2023). UTIs are a significant concern for patients admitted to the intensive care unit (ICU) because they can lead to severe complications such as urosepsis, multiple organ failure, and bacteremia which can significantly increase morbidity and mortality rate in ICU patients (Bizuayehu, 2022). The prolonged application of urinary catheters in critically ill patients increases the risk of bacterial colonization and subsequent infection of the urinary tract (Lopez et al, 2012). Factors such as catheterization duration, improper catheter insertion techniques, and compromised immune systems in ICU patients contribute to the heightened risks of nosocomial infections (Isigi et al, 2023). This is usually because infections spread rapidly among individuals who are immunocompromised when exposed to different opportunistic pathogens (Kollef et al, 2021).  When bacteria enter the body through the catheter they migrate to the bladder and cause infections before moving into the blood (Atkins et al, 2020). Additionally, biofilm formation on catheter surfaces provides a reservoir for bacteria, further complicating infection control efforts.

Preventative measures such as strict catheter hygiene protocols, catheter removal when no longer necessary, alternative methods of urine collection when feasible, and using intermittent catheters instead of indwelling catheters are essential in reducing UTI rates in the ICU setting (Patal et al, 2024). Regular monitoring of insertion and maintenance of catheter with prompt treatment of any signs of infection are also important in preventing UTIs in ICU patients.  The study can also help to identify risk factors for UTIs and to monitor changes over time. This information can be used for evaluating the effectiveness of interventions and public health policies. In this study, the researcher will be focusing mainly on urinary tract infections (UTIs) in patients admitted to the intensive care unit (ICU).

UTIs are usually caused by *Enterobacteriaceae*, Gram-positive bacteria as well as yeasts such as *Candida spp.* (Bitew et al, 2022). *Enterobacteriaceae* are gram-negative organisms that are part of the bowel flora but if they contaminate your urinary tract system, they produce an infection (Gunardi, et al, 2021). The organisms commonly isolated in patients with UTIs include *Klebsiella pneumoniae, Escherichia coli (E. coli), Acinetobacter spp, Candida spp, Pseudomonas aeruginosa, group B Streptococcus, Staphylococcus and Enterococcus faecalis.* This study aims to identify micro-organisms isolated in patients with UTI in the ICU. Patients who are diagnosed with UTI present clinical symptoms such as fever, dysuria, urgent urination, frequent urination, costovertebral angle pain, and suprapubic tenderness (Oumer et al, 2021).  The symptoms such as urgent urination and frequent urination cannot be used for the diagnosis if the catheter is still inserted into the patient because catheters lead to such symptoms (CDC, 2024).

According to global statistics, nosocomial infections are one of the common problems facing the world, about 40% of all nosocomial infections are CAUTIs which frequently result in bloodstream infections (Florence-Mireles et al, 2019). A study conducted in Germany showed that 60% of cases of urinary tract infections were related to catheter utilization, and 21,6% of all nosocomial infections were UTIs (Kranz et al, 2020). About 25% of patients who need a urinary catheter inserted for longer than seven days have bacteriuria (Clarke et al. 2020). A study conducted in India by Mythri and Kashinath (2014) revealed that the incidence of nosocomial infections in the intensive care unit was 17.7%, with urinary tract infections accounting for most of these infections (34.8%). A study done in Iran by Izadi (2020) showed that 26.83% of nosocomial infections were diagnosed in the urinary tract system in ICU patients. A study done in India stated that hospital-acquired infections were prevalent among the age group of 40-60 years, also that men were more likely to obtain hospital-acquired infections than women (Mythri et al, 2014) in a study done by Perrin et al (2021) women had about 76.60 % cases while men had 24,20% cases. The reason women were more prone to UTIs was because of their shorter urethra compared to men (Sabir et al, 2023).

Nosocomial infections are a significant problem in the healthcare setting as they lead to increased mortality, morbidity, and increased hospitalization.17% of bacteremia are caused by urinary infections with a mortality rate of 10% (Saleem et al, 2022). In a study done by Barchitta et al (2021) United States of America (USA) had healthcare costs which was about 131 million us dollars for annual medical costs due to increased hospitalization. The cost of nosocomial infections in developing countries and South Africa has not been studied. According to Duszynska et al (2020), patients in the Poland Medical University Teaching Hospital intensive care unit (ICU) were hospitalized for an average of 21 days as a result of hospital infection due to a device, compared to 6 days when they did not. Organisms that cause nosocomial urinary infections are usually resistant to commonly utilized antibiotics, leading to increased length of stay by patients in the ICU (Murtaugh, 2021).  The patients admitted to ICU are at a higher risk of these CAUTIs due to underlying illnesses, the use of invasive devices, and the exposure of patients to broad-spectrum antibiotic treatment (Smith,2019). The ICU environment itself can promote the growth of bacteria if not decontaminated properly (Tajeddin et al,2016). The shortage of medical equipment resulting in sharing among patients due to a high density of patients admitted often leads to increased risks of Nosocomial infections (Ssekitoleko et al,2020). The Public hospital settings as a result of financial constraints may fail to set up very strict infection control protocols compared to private hospitals; this increases the risk of transmission of infections within the hospital especially in cases such as prolonged catheterization and maintaining sterility. This current study focuses more on complicated UTIs in ICU patients. Aims to evaluate the prevalence of urinary tract infections in a public hospital and also establish the antimicrobial susceptibility patterns of isolated pathogens.

**Aims**

To evaluate the burden and outcomes of urinary tract infections in patients admitted to

the intensive care unit over 6 months and identify the most common pathogens

and their antimicrobial susceptibility patterns.

**Objectives**

* To determine the number of pathogens isolated in urinary tract infections for patients admitted to ICU.
* To determine the most prevalent isolated microorganisms causing UTIs.
* To assess antimicrobial susceptibility patterns of isolated microorganisms.
* To analyze demographic information of patients with UTI.

**Hypothesis**

Critically ill ICU patients have a high prevalence of urinary tract infections primarily due to prolonged catheterization, and these infections are frequently caused by antimicrobial-resistant microorganisms, especially in patients with prior antibiotic treatment.

**Research Methodology**

**Study Design**

This was a quantitative research study designed to determine the most prevalent pathogens of urinary tract infections, and their antimicrobial susceptibility in an intensive care unit (ICU) patient by gathering retrospective laboratory data. This was a cross-sectional study. Intended to analyze laboratory data and evaluate the number of patients who developed UTI after hospitalization in the ICU ward.

**Study setting and population**

This research was conducted at Inkosi Albert Luthuli Hospital Microbiology Laboratory in Durban. This is a public partnership hospital situated in Kwazulu-Natal.

The research data was sampled from the results of patients who presented signs and symptoms of UTIs in the ICU both men and women during the study period.

**Sampling and sample size**

In this study retrospective data was used, this data was collected from Inkosi Albert Luthuli Central Hospital Microbiology laboratory using the laboratory information system (LIS) through AARMS. A convenience non-probability sampling technique was applied to choose sample size data for ICU patients from January to July of 2023. The sample size was determined by the number of patients who remained in the ICU and had all the laboratory data available.

**Data collection**

Data was obtained retrospectively and included demographics (age and gender), pathogens isolated, and their antimicrobial susceptibility patterns. The results used in this retrospective study were generated in the microbiology laboratory at Inkosi Albert Luthuli Hospital in Durban. For the success of this retrospective study on the prevalence of pathogens isolated in urinary tract infections in ICU patients, a request for laboratory data was made through the NHLS AARMS system.

**A Brief Overview of diagnostic procedure/s as per laboratory Standard Operating Procedures for Urine at IALCH.**

The laboratory diagnosis of urinary tract infections is made by observation of the presence of pyuria and causative organisms. Colony courts of uropathogens are also performed to aid in diagnosis.

**Specimen collection and patient preparations**

Early morning samples should be collected. Patients should not be forced to increase fluids before sample collection as this would decrease the colony count. Sample taken aseptically and transported within 2 hours to the laboratory. If they were delayed should be kept refrigerated at 2 to 8 degrees Celsius.

**Type of specimens**

* Midstream urine sample (MSU)
* Catheter urine sample (CSU)

**Rejection criteria**

* 24 hours urine.
* Foley catheter tips.
* Specimen from urine bags, bedpans, or urinals.

**Procedure for processing samples**

* Unspun urine was mixed
* For MSU 1 microliter loop was used to transfer urine to the plate.
* For CSU 10 microliter loop was used to transfer urine to the plate.
* Plates were streaked for single colonies without flaming in between.
* Plates were incubated at 35 – 37 degrees Celsius aerobically for 18 – 24 hours.

**Microscopic examination**

* Manual or automatic
* For manual urine centrifuged the deposit is utilized for wet preparation.
* Wet preparation was examined under 40X for the presence of leucocytes, erythrocytes, casts, crystals, yeast, bacteria, and parasites.
* Reported as: not observed (0), scanty (1+) 1-10 cells, moderate (2+) 11 -40 cells, numerous (3+) greater 40 cells

**Detection of antimicrobial substances**

* 0.5 McFarland Bacillus subtilis ATCC 6051 with sterile discs was used.
* A drop of urine was placed on a sterile disc on the plate.
* The plate was inoculated overnight at 35 - 37 degrees Celsius aerobically.
* On the following day (day 2) the plate was read recorded and reported as present where the zone of inhibition was observed, Absent where the zone of inhibition was not observed.

**Media culture**

* Media growth on day 2 was examined, and no growth was reported as no growth after 24 hours.
* Growth was noted and examined for pure growth.
* More than two organisms were reported as mixed growth.
* If growth was observed, identification and susceptibility tests were done.
* For gram-negative bacilli Vitro GN ID and sensitivity or API 20 E and Disc diffusion were utilised.
* For Gram-positive cocci, Vitek GP ID and sensitivity or manual identification and Disc diffusion were utilized.
* For yeast, a germ tube was prepared and read after 2 hours.

**Quality control**

All media was quality controlled for growth and checked for contamination before it was used.

**Statistical analysis**

Determined prevalence rates and compiled demographic and microbiological data using descriptive statistics. Analyzed and contrasted the demographic traits and treatment outcomes of patients with and without urinary tract infections. Examined the resistance patterns of the bacteria that have been identified. With the Analysis of Treatment and Resistance: the researcher looked at how the prevalence of resistant microbes and past antibiotic use were related. Excel’s statistical tools were used to examine this data, which was reported as mean, median, mode, and standard deviation. Data was captured in Excel in order to compute tables and graphs. Validation and verification check of data was performed.

**Ethical considerations**

Permission to conduct the study was obtained from the ethical committee of Mangosuthu University of Technology. The study adhered to ethical guidelines and obtained appropriate permission from the NHLS Academic Affairs and Research Office (AARMS) to access and analyze patient data. Patient information was anonymized to protect confidentiality and privacy by removing identifiable information such as names and addresses. Instead, patients were assigned special codes. Even when interpreting the results, coding, and masking was used by replacing exact ages with age ranges. Access to data was strictly controlled and limited to authorized personnel. The data request was reviewed and approved by NHLS AARMS on 10 October 2024. There was no physical communication with the patients in this study.

**Research Results/Findings**

**Descriptive Analysis**

**Demographics**

Figure 1 presents the gender distribution of participants in the study. Among the 270 respondents, the majority were female, accounting for 199 participants (73.7%). Male participants constituted 71 of the respondents, representing 26.3% of the sample.

A pie chart with a couple of percentages

Description automatically generated

Figure 1: Gender distribution among study participants

Figure 2: The distribution of participants by age is summarized in the figure 2. A total of 270 individuals participated in the study. The majority of the participants (35.9%) were in the age group of 40–65 years, followed by those aged 0–17 years (22.6%) and >65 years (22.2%). Participants aged 19–39 years constituted 19.3% of the sample. The cumulative percentages show that 77.8% of the participants were aged 0–65 years, with the remaining 22.2% being over 65 years. This distribution highlights a diverse representation of age groups, with the largest proportion falling within the middle-aged category.

A pie chart with numbers and a few percentages

Description automatically generated with medium confidence

Figure 2: Distribution of age in study participants

**Pathogens isolated and their antimicrobial susceptibility patterns.**

Table1: Lastly, table 1 presents the distribution of organisms identified among the 270 samples analysed in the study. *Escherichia coli* (*E. coli*) was the most prevalent organism, accounting for 53.0% of the total isolates. This was followed by *Klebsiella pneumoniae subsp. pneumoniae* (14.8%) and *Klebsiella pneumoniae* (9.3%), highlighting their significant contribution to the overall sample population.

Other organisms identified included *Enterococcus faecalis* (5.9%), *Streptococcus agalactiae* (3.3%), and *Acinetobacter baumannii complex* (3.0%). Less common isolates, each constituting less than 2% of the total, included *Proteus mirabilis* (1.9%), *Pseudomonas aeruginosa* (2.6%), *Enterococcus faecium* (1.5%), and *Enterobacter cloacae complex* (1.1%). Rarely encountered organisms, each comprising less than 1% of the isolates, included *Acinetobacter baumannii*, *Citrobacter freundii*, *Citrobacter koserii*, *Enterobacter cloacae*, *Klebsiella oxytoca*, *Morganella morganii*, *Staphylococcus aureus*, and *staphylococcus haemolyticus*.

Table 1: Frequency of isolated organisms in study participants

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Name of the organisms** | **Frequency** | **Percent** | **Valid Percent** | **Cumulative Percent** |
| *Acinetobacter baumanni* | 2 | ,7 | ,7 | ,7 |
| *Acinetobacter baumannii complex* | 8 | 3,0 | 3,0 | 3,7 |
| *Citrobacter freundii* | 2 | ,7 | ,7 | 4,4 |
| *Citrobacter koserii* | 1 | ,4 | ,4 | 4,8 |
| *Enterobacter cloacae* | 1 | ,4 | ,4 | 5,2 |
| *Enterobacter cloacae complex* | 3 | 1,1 | 1,1 | 6,3 |
| *Enterococcus faecalis* | 16 | 5,9 | 5,9 | 12,2 |
| *Enterococcus faecium* | 4 | 1,5 | 1,5 | 13,7 |
| *Escherichia coli* | 143 | 53,0 | 53,0 | 66,7 |
| *Klebsiella oxytoca* | 1 | ,4 | ,4 | 67,0 |
| *Klebsiella pneumoniae* | 25 | 9,3 | 9,3 | 76,3 |
| *Klebsiella pneumoniae subsp pneumoniae* | 40 | 14,8 | 14,8 | 91,1 |
| *Morganella morganii* | 1 | ,4 | ,4 | 91,5 |
| *Proteus mirabilis* | 5 | 1,9 | 1,9 | 93,3 |
| *Pseudomonas aeruginosa* | 7 | 2,6 | 2,6 | 95,9 |
| *Staphylococcus aureus* | 1 | ,4 | ,4 | 96,3 |
| *Staphylococcus haemolyticus* | 1 | ,4 | ,4 | 96,7 |
| *Streptococcus agalactiae* | 9 | 3,3 | 3,3 | 100,0 |
| **Total** | **270** | **100,0** | **100,0** |  |

**Table 2: Prevalence of Gram positives in isolated organisms in the study participants**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Name of the Organisms | | Frequency | Percent | Valid Percent | Cumulative Percent |
|  | *Enterococcus faecalis* | 16 | 51,6 | 51,6 | 51,6 |
| *Enterococcus faecium* | 4 | 12,9 | 12,9 | 64,5 |
| *Staphylococcus aureus* | 1 | 3,2 | 3,2 | 67,7 |
| *Staphylococcus haemolyticus* | 1 | 3,2 | 3,2 | 71,0 |
| *Streptococcus agalactiae* | 9 | 29,0 | 29,0 | 100,0 |
| Total | 31 | 100,0 | 100,0 |  |

**Prevalence and Antibiotic Susceptibility of Isolated Gram-positives in the study**

Table 2: Out the 270 organisms isolated, 31 were gram-positive. *Enterococcus faecalis* was the most frequently identified organism, accounting for 51.6% (n=16) of the isolates. This was followed by *Streptococcus agalactiae*, which constituted 29.0% (n=9) of the total. *Enterococcus faecium* represented 12.9% (n=4) of the isolates. Less commonly detected organisms included *Staphylococcus aureus* and *Staphylococcus haemolyticus*, each contributing 3.2% (n=1) of the total isolates.

Table 3 provides a summary of the antimicrobial susceptibility profiles of the 31 isolates against five antibiotics. The susceptibility levels are represented numerically, with lower means indicating higher resistance and higher means reflecting sensitivity.

For Amoxicillin-Clavulanic Acid, the mean susceptibility score was 1.77 (SD = 1.055), indicating a tendency toward resistance, as some isolates were classified as resistant. Similarly, for Ciprofloxacin, the mean score was 1.94 (SD = 1.237), suggesting moderate resistance among the isolates tested.

In contrast, Linezolid and Tigecycline both had a mean score of 2.35 (SD = 0.486), indicating consistent sensitivity across the isolates tested. Vancomycin also showed a high mean susceptibility score of 2.26 (SD = 0.445), reflecting its effectiveness against most isolates.

*Table 3: Antibiotic Susceptibility of gram positives*

A screenshot of a table

Description automatically generated

**Susceptibility of isolated Gram-positives against Amoxicillin-Clavulanic Acid**

The crosstabulation table 4 provides an overview of the relationship between organism type and susceptibility to Amoxicillin-Clavulanic Acid. Among the 31 isolates tested, the majority (17 isolates) were sensitive to the antibiotic, while 7 were resistant and another 7 were not tested.

*Enterococcus faecalis* was the most frequently identified organism, with 16 isolates. Of these, 11 were sensitive, 2 were resistant, and 3 were not tested. *Streptococcus agalactiae* followed, with 9 isolates, 6 of which were sensitive and 3 not tested. Conversely, all 4 *Enterococcus faecium* isolates demonstrated resistance or were not tested, with none showing sensitivity. Similarly, the single isolates of *Staphylococcus aureus* and *Staphylococcus haemolyticus* were resistant.

Table 4: Sensitivity patterns of isolated Gram-positive organisms towards Amoxicillin-Clavulanic Acid

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Name of the organisms | | AMOXICILLIN\_CLAVULANIC\_ACID | | | Total |
| Resistant | Sensitive | Not tested |
|  | *Enterococcus faecalis* | 2 | 11 | 3 | 16 |
| *Enterococcus faecium* | 3 | 0 | 1 | 4 |
| *Staphylococcus aureus* | 1 | 0 | 0 | 1 |
| *Staphylococcus haemolyticus* | 1 | 0 | 0 | 1 |
| *Streptococcus agalactiae* | 0 | 6 | 3 | 9 |
| Total | | 7 | 17 | 7 | 31 |

**Susceptibility of isolated Gram-positives against Ciprofloxacin**

Table 5 illustrates the distribution of susceptibility to Ciprofloxacin across 31 isolates from five different organism types. Of the isolates, 8 were resistant, 9 were sensitive, and 14 were not tested.

*Enterococcus faecalis* was the most prevalent organism, with 16 isolates. Among these, 8 were sensitive, 3 were resistant, and 5 were not tested. All 4 isolates of *Enterococcus faecium* were resistant to Ciprofloxacin. The single isolates of *Staphylococcus aureus* and *Staphylococcus haemolyticus* demonstrated sensitivity and resistance, respectively. Notably, none of the 9 Streptococcus agalactiae isolates were tested for Ciprofloxacin susceptibility.

Table 5: Sensitivity patterns of isolated Gram-positive organisms towards Ciprofloxacin

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Name of the organisms | | CIPROFLOXACIN | | | Total |
| Resistant | Sensitive | Not tested |
|  | *Enterococcus faecalis* | 3 | 8 | 5 | 16 |
| *Enterococcus faecium* | 4 | 0 | 0 | 4 |
| *Staphylococcus aureus* | 0 | 1 | 0 | 1 |
| *Staphylococcus haemolyticus* | 1 | 0 | 0 | 1 |
| *Streptococcus agalactiae* | 0 | 0 | 9 | 9 |
| Total | | 8 | 9 | 14 | 31 |

**Susceptibility of isolated Gram-positives against Linezolid**

The table 6 provides a summary of susceptibility to Linezolid among 31 isolates from various organism types. Of these, 20 isolates were sensitive to Linezolid, while 11 were not tested.

*Enterococcus faecalis* accounted for the largest proportion of isolates (16), with 11 showing sensitivity and 5 not tested. Similarly, all 4 *Enterococcus faecium* isolates demonstrated sensitivity, as did the single isolates of *Staphylococcus aureus* and *Staphylococcus haemolyticus*. For *Streptococcus agalactiae*, sensitivity was observed in 4 of the 9 isolates, while the remaining 5 were not tested

Table 6: Sensitivity patterns of isolated Gram-positive organisms towards Linezolid

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Name of the organisms | | LINEZOLID | | Total |
| Sensitive | Not tested |
|  | *Enterococcus faecalis* | 11 | 5 | 16 |
| *Enterococcus faecium* | 3 | 1 | 4 |
| *Staphylococcus aureus* | 1 | 0 | 1 |
| *Staphylococcus haemolyticus* | 1 | 0 | 1 |
| *Streptococcus agalactiae* | 4 | 5 | 9 |
| Total | | 20 | 11 | 31 |

Table 7: Sensitivity patterns of isolated Gram-positive organisms towards Tigecycline

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Name of the organisms | | TIGECYCLINE | | Total |
| Sensitive | Not tested |
|  | *Enterococcus faecalis* | 11 | 5 | 16 |
| *Enterococcus faecium* | 3 | 1 | 4 |
| *Staphylococcus aureus* | 1 | 0 | 1 |
| *Staphylococcus haemolyticus* | 1 | 0 | 1 |
| *Streptococcus agalactiae* | 4 | 5 | 9 |
| Total | | 20 | 11 | 31 |

**Susceptibility of isolated Gram-positives against Tigecycline**

Furthermore, table 7 summarizes the susceptibility of 31 isolates to Tigecycline. Of these, 20 isolates were sensitive, while 11 were not tested. *Enterococcus faecalis* was the most prevalent organism, with 16 isolates, of which 11 demonstrated sensitivity and 5 were not tested. All 4 *Enterococcus faecium* isolates were sensitive to Tigecycline. Similarly, the single isolates of *Staphylococcus aureus* and *Staphylococcus haemolyticus* exhibited sensitivity. For *Streptococcus agalactiae*, 4 of the 9 isolates were sensitive, while the remaining 5 were not tested.

**Susceptibility of isolated Gram-positives against Vancomycin**

Lastly, table 8 presents the susceptibility of 31 isolates to Vancomycin. Of these, 23 isolates demonstrated sensitivity, while 8 were not tested. *Enterococcus faecalis* was the most frequently identified organism, comprising 16 isolates, of which 12 were sensitive and 4 were not tested. All 4 *Enterococcus faecium* isolates were sensitive to Vancomycin. Similarly, both *Staphylococcus aureus* and *Staphylococcus haemolyticus* (one isolate each) exhibited sensitivity. For *Streptococcus agalactiae*, 5 of the 9 isolates were sensitive, and 4 were not tested.

Table 8: Sensitivity patterns of isolated Gram-positive organisms towards Vancomycin

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Name of the organisms** | | **VANCOMYCIN** | | **Total** |
| Sensitive | Not tested |
|  | *Enterococcus faecalis* | 12 | 4 | 16 |
| *Enterococcus faecium* | 4 | 0 | 4 |
| *Staphylococcus aureus* | 1 | 0 | 1 |
| *Staphylococcus haemolyticus* | 1 | 0 | 1 |
| *Streptococcus agalactiae* | 5 | 4 | 9 |
| Total | | 23 | 8 | 31 |

**Prevalence and Antibiotic Susceptibility of Isolated Gram-negatives in the study**

**Susceptibility of isolated Gram-negatives against Cefepime**

Table 9 presents the sensitivity patterns of Gram-negative organisms to Cefepime, based on 239 isolates. Among these, the majority (174; 72.8%) were categorized as sensitive, while 39 isolates (16.3%) demonstrated resistance. A small proportion (1; 0.4%) exhibited intermediate susceptibility, and 25 isolates (10.5%) were not tested. *E. coli* accounted for the largest number of isolates tested, with 119 (83.2%) showing sensitivity, 9 (6.3%) being resistant, and 1 (0.7%) having intermediate susceptibility; 14 isolates were not tested. Similarly, *Klebsiella pneumoniae subsp. pneumoniae* displayed considerable sensitivity, with 18 (45%) of its isolates testing sensitive. However, resistance was observed in 15 (37.5%) isolates, while 7 were not tested. Among non-fermenting Gram-negative bacilli, *Acinetobacter baumannii* and *Acinetobacter baumannii complex* exhibited notable resistance. All 5 isolates of *Acinetobacter baumannii complex* tested resistant, while *Acinetobacter baumannii* had 1 sensitive and 1 not tested. Resistance was also observed in *Pseudomonas aeruginosa*, with 2 isolates resistant and 4 sensitive. Other Enterobacteriaceae, including *Proteus mirabilis*, *Citrobacter freundii*, and *Morganella morganii*, exhibited high sensitivity to Cefepime, with all tested isolates of these species demonstrating susceptibility. *Enterobacter cloacae complex* showed a mixed response, with 2 sensitive and 1 resistant isolate.

Table 9: Sensitivity patterns of isolated Gram-negative organisms towards Cefepime

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Name of the organisms | | CEFEPIME | | | | Total |
| Resistant | Intermediate | Sensitive | Not tested |
|  | *Acinetobacter baumannii* | 0 | 0 | 1 | 1 | 2 |
| *Acinetobacter baumannii complex* | 5 | 0 | 3 | 0 | 8 |
| *Citrobacter freundii* | 0 | 0 | 2 | 0 | 2 |
| *Citrobacter koserii* | 0 | 0 | 1 | 0 | 1 |
| *Enterobacter cloacae* | 1 | 0 | 0 | 0 | 1 |
| *Enterobacter cloacae complex* | 1 | 0 | 2 | 0 | 3 |
| *Escherichia coli* | 9 | 1 | 119 | 14 | 143 |
| *Klebsiella oxytoca* | 0 | 0 | 1 | 0 | 1 |
| *Klebsiella pneumoniae* | 6 | 0 | 17 | 2 | 25 |
| *Klebsiella pneumoniae subsp pneumoniae* | 15 | 0 | 18 | 7 | 40 |
| *Morganella morganii* | 0 | 0 | 1 | 0 | 1 |
| *Proteus mirabilis* | 0 | 0 | 5 | 0 | 5 |
| *Pseudomonas aeruginosa* | 2 | 0 | 4 | 1 | 7 |
| Total | | 39 | 1 | 174 | 25 | 239 |

**Susceptibility of isolated Gram-negatives against Cefotaxime-Ceftriaxone**

Table 10 summarizes the sensitivity patterns of Gram-negative organisms to the combination of Cefotaxime-Ceftriaxone based on 239 isolates. A total of 111 isolates (46.4%) demonstrated sensitivity, while 104 isolates (43.5%) were resistant. Intermediate susceptibility was observed in 2 isolates (0.8%), and 22 isolates (9.2%) were not tested.

*E. coli* exhibited the highest sensitivity, with 83 (58%) of its 143 isolates being susceptible. However, 45 isolates (31.5%) were resistant, and 2 (1.4%) showed intermediate susceptibility; 13 isolates were not tested. Among *Klebsiella pneumoniae subsp. pneumoniae*, sensitivity was lower, with only 9 (22.5%) isolates susceptible, 26 (65%) resistant, and 5 not tested. Similarly, *Klebsiella pneumoniae* displayed moderate sensitivity, with 8 (32%) isolates susceptible and 15 (60%) resistant.

Notably, non-fermenting Gram-negative organisms such as *Acinetobacter baumannii* and *Acinetobacter baumannii complex* were predominantly resistant, with 100% resistance observed among their tested isolates. Among other Enterobacteriaceae, *Citrobacter freundii*, *Citrobacter koserii*, and *Proteus mirabilis* exhibited high sensitivity rates, with all tested isolates demonstrating susceptibility to Cefotaxime-Ceftriaxone.

Table 10: Sensitivity patterns of isolated Gram-negative organisms towards Cefotaxime-Ceftriaxone

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Name of the organisms | | CEFOTAXIME\_CEFTRIAXONE | | | | Total |
| Resistant | Intermediate | Sensitive | Not tested |
|  | *Acinetobacter baumannii* | 1 | 0 | 0 | 1 | 2 |
| *Acinetobacter baumannii* complex | 8 | 0 | 0 | 0 | 8 |
| *Citrobacter freundii* | 1 | 0 | 1 | 0 | 2 |
| *Citrobacter koserii* | 0 | 0 | 1 | 0 | 1 |
| *Enterobacter cloacae* | 1 | 0 | 0 | 0 | 1 |
| *Enterobacter cloacae complex* | 1 | 0 | 2 | 0 | 3 |
| *Escherichia coli* | 45 | 2 | 83 | 13 | 143 |
|  | *Klebsiella oxytoca* | 0 | 0 | 1 | 0 | 1 |
| *Klebsiella pneumoniae* | 15 | 0 | 8 | 2 | 25 |
| *Klebsiella pneumoniae subsp pneumoniae* | 26 | 0 | 9 | 5 | 40 |
| *Morganella morganii* | 0 | 0 | 1 | 0 | 1 |
| *Proteus mirabilis* | 0 | 0 | 5 | 0 | 5 |
| *Pseudomonas aeruginosa* | 6 | 0 | 0 | 1 | 7 |
| Total | | 104 | 2 | 111 | 22 | 239 |

**Susceptibility of isolated Gram-negatives against Ertapenem**

Furthermore, table 11 presents the sensitivity patterns of Gram-negative organisms to Ertapenem among 239 isolates. A majority of the isolates, 179 (74.9%), were sensitive to Ertapenem, with resistance observed in only 15 isolates (6.3%). Intermediate susceptibility was documented in 5 isolates (2.1%), and 40 isolates (16.7%) were not tested.

Among the tested organisms, *E. coli* showed the highest sensitivity, with 128 (89.5%) of its 143 isolates susceptible, 1 isolate (0.7%) displaying intermediate susceptibility, and non-resistant. *Klebsiella pneumoniae subsp. pneumoniae* exhibited moderate sensitivity, with 21 (52.5%) of its 40 isolates susceptible, 9 (22.5%) resistant, and 3 (7.5%) showing intermediate susceptibility. Similarly, *Klebsiella pneumoniae* showed 17 (68%) of 25 isolates as sensitive, while resistance was noted in 5 (20%) isolates.

Non-fermenting organisms such as *Acinetobacter baumannii* and *Acinetobacter baumannii complex* were either not tested or showed no susceptibility to Ertapenem, consistent with their intrinsic resistance profiles. Other Enterobacteriaceae, including *Citrobacter freundii*, *Citrobacter koserii*, and *Proteus mirabilis*, demonstrated complete sensitivity among their tested isolates.

Table 11: Sensitivity patterns of isolated Gram-negative organisms towards Ertapenem

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Name of the organisms** | | **ERTAPENEM** | | | | **Total** | |
| Resistant | Intermediate | Sensitive | Not tested |  |
|  | *Acinetobacter baumanni*i | 0 | 0 | 0 | 2 | 2 |
| *Acinetobacter baumanni*i complex | 0 | 0 | 0 | 8 | 8 |
| *Citrobacter freundii* | 0 | 0 | 2 | 0 | 2 |
| *Citrobacter koserii* | 0 | 0 | 1 | 0 | 1 |
| *Enterobacter cloacae* | 0 | 0 | 1 | 0 | 1 |
| *Enterobacter cloacae complex* | 1 | 0 | 2 | 0 | 3 |
| *Escherichia coli* | 0 | 1 | 128 | 14 | 143 |
|  | *Klebsiella oxytoca* | 0 | 0 | 1 | 0 | 1 |
| *Klebsiella pneumoniae* | 5 | 1 | 17 | 2 | 25 |
| *Klebsiella pneumoniae subsp pneumoniae* | 9 | 3 | 21 | 7 | 40 |
| *Morganella morganii* | 0 | 0 | 1 | 0 | 1 |
| *Proteus mirabilis* | 0 | 0 | 5 | 0 | 5 |
| *Pseudomonas aeruginosa* | 0 | 0 | 0 | 7 | 7 |
| Total | | 15 | 5 | 179 | 40 | 239 |

**Susceptibility of isolated Gram-negatives against Gentamicin**

Table 12 summarizes the sensitivity patterns of Gram-negative organisms to Gentamicin among 239 isolates. The majority of isolates, 174 (72.8%), demonstrated sensitivity to Gentamicin, while 59 (24.7%) were resistant, 2 (0.8%) exhibited intermediate susceptibility, and 4 (1.7%) were not tested.

Among the most frequently isolated organisms, *E. coli* showed a high sensitivity rate, with 126 (88.1%) of its 143 isolates susceptible, while 15 isolates (10.5%) were resistant, and 1 (0.7%) exhibited intermediate susceptibility. In contrast, *Klebsiella pneumoniae subsp. pneumoniae* exhibited more variability, with 21 (52.5%) of its 40 isolates sensitive, 18 (45%) resistant, and 1 (2.5%) not tested. Similarly, *Klebsiella pneumoniae* showed a relatively lower sensitivity rate of 11 (44%) out of 25 isolates, with 13 (52%) resistant.

Other organisms displayed mixed susceptibility patterns. *Acinetobacter baumannii complex* showed resistance in 6 of its 8 isolates (75%), while 2 (25%) were sensitive. *Pseudomonas aeruginosa* exhibited resistance in 2 (28.6%) of 7 isolates but retained sensitivity in 4 isolates (57.1%). Notably, all isolates of *Citrobacter koserii*, *Morganella morganii*, and *Proteus mirabilis* were sensitive to Gentamicin, emphasizing its efficacy against these pathogens.

Table 12: Sensitivity patterns of isolated Gram-negative organisms towards Gentamicin

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Name of the organisms | | GENTAMICIN | | | | Total |
| Resistant | Intermediate | Sensitive | Not tested |
|  | *Acinetobacter baumannii* | 2 | 0 | 0 | 0 | 2 |
| *Acinetobacter baumannii* complex | 6 | 0 | 2 | 0 | 8 |
| *Citrobacter freundii* | 1 | 0 | 1 | 0 | 2 |
| *Citrobacter koserii* | 0 | 0 | 1 | 0 | 1 |
| *Enterobacter cloacae* | 1 | 0 | 0 | 0 | 1 |
| *Enterobacter cloacae complex* | 1 | 0 | 2 | 0 | 3 |
| *Escherichia coli* | 15 | 1 | 126 | 1 | 143 |
|  | *Klebsiella oxytoca* | 0 | 0 | 1 | 0 | 1 |
| *Klebsiella pneumoniae* | 13 | 1 | 11 | 0 | 25 |
| *Klebsiella pneumoniae subsp pneumoniae* | 18 | 0 | 21 | 1 | 40 |
| *Morganella morganii* | 0 | 0 | 1 | 0 | 1 |
| *Proteus mirabilis* | 0 | 0 | 4 | 1 | 5 |
| *Pseudomonas aeruginosa* | 2 | 0 | 4 | 1 | 7 |
| Total | | 59 | 2 | 174 | 4 | 239 |

Table 13 presents the sensitivity patterns of Gram-negative organisms to Imipenem, based on 239 isolates. Of these, 194 isolates (81.2%) were classified as sensitive (score of 2 or 3), while 22 isolates (9.2%) were resistant (score of 0), 12 isolates (5.0%) displayed intermediate susceptibility (score of 1), and 11 isolates (4.6%) were not tested.

*E. coli* was the most prevalent organism in the study, with a high sensitivity to Imipenem. Of its 143 isolates, 135 (94.4%) were sensitive, while 6 (4.2%) were intermediate, and only 2 (1.4%) were resistant. Similarly, *Klebsiella pneumoniae* showed substantial sensitivity, with 19 (76%) out of 25 isolates classified as sensitive, although 4 (16%) were intermediate and 2 (8%) resistant. *Klebsiella pneumoniae subsp. pneumoniae* exhibited a similar susceptibility pattern, with 25 (62.5%) of its 40 isolates sensitive, 4 (10%) intermediate, and 7 (17.5%) resistant.

*Acinetobacter baumannii* had a mixed sensitivity profile, with 1 out of 2 isolates (50%) resistant, and the remaining 1 isolate sensitive. *Acinetobacter baumannii complex* demonstrated a higher resistance rate, with 5 out of 8 isolates (62.5%) resistant and 3 (37.5%) sensitive. *Pseudomonas aeruginosa* showed a sensitivity rate of 57.1% (4 out of 7 isolates), with 2 (28.6%) resistant and 1 (14.3%) intermediate.

Other organisms such as *Citrobacter freundii* and *Citrobacter koserii* exhibited high sensitivity, with all isolates being sensitive except for one intermediate isolate of *Proteus mirabilis* (4 out of 5 isolates) and 1 resistant isolate of *Morganella morganii*.

Table 13: Sensitivity patterns of isolated Gram-negative organisms towards Imipenem

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Name of the organisms** | | **IMIPENEM** | | | | **Total** |
| Resistant | Intermediate | Sensitive | Not tested |
|  | *Acinetobacter baumanni*i | 1 | 0 | 1 | 0 | 2 |
| *Acinetobacter baumanni*i complex | 5 | 0 | 3 | 0 | 8 |
| *Citrobacter freundii* | 0 | 0 | 2 | 0 | 2 |
| *Citrobacter koserii* | 0 | 0 | 1 | 0 | 1 |
| *Enterobacter cloacae* | 0 | 0 | 1 | 0 | 1 |
| *Enterobacter cloacae complex* | 1 | 0 | 2 | 0 | 3 |
| *Escherichia coli* | 0 | 2 | 135 | 6 | 143 |
|  | *Klebsiella oxytoca* | 0 | 0 | 1 | 0 | 1 |
| *Klebsiella pneumoniae* | 4 | 2 | 19 | 0 | 25 |
| *Klebsiella pneumoniae subsp pneumoniae* | 7 | 4 | 25 | 4 | 40 |
| *Morganella morganii* | 1 | 0 | 0 | 0 | 1 |
| *Proteus mirabilis* | 1 | 4 | 0 | 0 | 5 |
| *Pseudomonas aeruginosa* | 2 | 0 | 4 | 1 | 7 |
| Total | | 22 | 12 | 194 | 11 | 239 |

Based on 239 isolates, Table 14 lists the sensitivity patterns of Gram-negative organisms to Meropenem. 200 isolates, or 83.7 percent, were found to be Meropenem-sensitive, compared to 28 (11.7%) that were resistant, 2 (0.8%) that were intermediate, and 9 (3.8%) that were not examined.

The study's most prevalent bacterium, *E. coli*, showed a high sensitivity to Meropenem; 136 (95.1%) of its 143 isolates were deemed sensitive. Of the six isolates (4.2%) that were not tested, only one (0.7%) was resistant. *Klebsiella pneumoniae* also had a high sensitivity rate, with seven (28%) of its 25 isolates being resistant and 18 (72%) being sensitive. Additionally, *Klebsiella pneumoniae subsp. pneumoniae* showed a noteworthy sensitivity rate: 26 (65%) of 40 isolates were sensitive, 11 (27.5%) were resistant, and 2 (5%) were not examined.

*Acinetobacter baumannii*, on the other hand, displayed a mixed pattern, with one isolate (50%) being resistant and the other one (50%) being sensitive. The distribution of the *Acinetobacter baumannii complex* was comparable, with 3 (37.5%) sensitive isolates and 5 (62.5%) resistant isolates. Three isolates (42.9%) of *Pseudomonas aeruginosa* were sensitive, two isolates (28.6%) were resistant, and one isolate (14.3%) was intermediate, indicating some variation in the bacteria's response.

Only a tiny percentage of resistant isolates were seen in other organisms, including *Proteus mirabilis*, *Enterobacter cloacae*, *Citrobacter freundii*, and *Citrobacter koserii*, which exhibited primarily sensitive responses. One isolate of Morganella morganii was 100% sensitive to Meropenem.

Table 14: Sensitivity patterns of isolated Gram-negative organisms towards Meropenem

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Names of the organisms** | | **MEROPENEM** | | | | **Total** |
| Resistant | Intermediate | Sensitive | Not tested |
|  | *Acinetobacter baumanni*i | 1 | 0 | 1 | 0 | 2 |
| *Acinetobacter baumanni*i complex | 5 | 0 | 3 | 0 | 8 |
| *Citrobacter freundii* | 0 | 0 | 2 | 0 | 2 |
| *Citrobacter koserii* | 0 | 0 | 1 | 0 | 1 |
| *Enterobacter cloacae* | 0 | 0 | 1 | 0 | 1 |
| *Enterobacter cloacae complex* | 1 | 0 | 2 | 0 | 3 |
| *Escherichia coli* | 1 | 0 | 136 | 6 | 143 |
|  | *Klebsiella oxytoca* | 0 | 0 | 1 | 0 | 1 |
| *Klebsiella pneumoniae* | 7 | 0 | 18 | 0 | 25 |
| *Klebsiella pneumoniae subsp pneumoniae* | 11 | 1 | 26 | 2 | 40 |
| *Morganella morganii* | 0 | 0 | 1 | 0 | 1 |
| Proteus mirabilis | 0 | 0 | 5 | 0 | 5 |
| *Pseudomonas aeruginosa* | 2 | 1 | 3 | 1 | 7 |
| Total | | 28 | 2 | 200 | 9 | 239 |

Finally, table 15 presents the sensitivity patterns of Gram-negative organisms to Piperacillin-Tazobactam across 239 isolates. A majority of the isolates (172, 71.9%) were sensitive to Piperacillin-Tazobactam, while 48 (20.1%) were resistant, 10 (4.2%) exhibited intermediate susceptibility, and 9 (3.8%) were not tested.

*E. coli* demonstrated a high level of sensitivity, with 128 (89.5%) of its 143 isolates being susceptible, 5 (3.5%) resistant, and 3 (2.1%) showing intermediate resistance. *Klebsiella pneumoniae subsp. pneumoniae* also exhibited substantial sensitivity, with 16 (40%) of its 40 isolates susceptible, although 21 (52.5%) were resistant, reflecting significant resistance within this species. Similarly, *Klebsiella pneumoniae* demonstrated resistance in 11 (44%) of its 25 isolates, with 9 (36%) sensitive, indicating a noteworthy prevalence of resistance.

For *Acinetobacter baumannii complex*, 6 out of 8 isolates (75%) were resistant, while the remaining 2 (25%) were susceptible, highlighting the high level of resistance to Piperacillin-Tazobactam in this species. *Pseudomonas aeruginosa* showed mixed susceptibility, with 5 out of 7 isolates (71.4%) being sensitive, while 2 (28.6%) were resistant. Other organisms, such as *Proteus mirabilis*, *Morganella morganii*, *Citrobacter koserii*, and *Citrobacter freundii*, showed high sensitivity to Piperacillin-Tazobactam, with no resistance observed in the isolates tested.

Table 15: Sensitivity patterns of isolated Gram-negative organisms towards Piperacillin-Tazobactam

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Names of the organisms** | | **PIPERACILLIN\_TAZOBACTAM** | | | | **Total** |
| Resistant | Intermediate | Sensitive | Not tested |
|  | *Acinetobacter baumanni*i ACINETOBACTER BAUMANNI | 2 | 0 | 0 | 0 | 2 |
| *Acinetobacter baumanni*i complex | 6 | 0 | 2 | 0 | 8 |
| *Citrobacter freundii* | 0 | 0 | 2 | 0 | 2 |
| *Citrobacter koserii* | 0 | 0 | 1 | 0 | 1 |
| *Enterobacter cloacae* | 0 | 1 | 0 | 0 | 1 |
| *Enterobacter cloacae complex* | 1 | 0 | 2 | 0 | 3 |
| *Escherichia coli* | 5 | 3 | 128 | 7 | 143 |
|  | *Klebsiella oxytoca* | 0 | 0 | 1 | 0 | 1 |
| *Klebsiella pneumoniae* | 11 | 4 | 9 | 1 | 25 |
| *Klebsiella pneumoniae subsp pneumoniae* | 21 | 2 | 16 | 1 | 40 |
| *Morganella morganii* | 0 | 0 | 1 | 0 | 1 |
| *Proteus mirabilis* | 0 | 0 | 5 | 0 | 5 |
| *Pseudomonas aeruginosa* | 2 | 0 | 5 | 0 | 7 |
| Total | | 48 | 10 | 172 | 9 | 239 |

Table 16 shows the most prevalent Gram-positive pathogen which was *E. faecalis* which had a prevalence of 16(6.0%) among 270 pathogens isolated. This table also show *E. faecalis* antimicrobial susceptibility percentages. For linezoid resistance was not seen in all *E. faecalis* isolates, sensitivity was 68,8%. For Tigecyclin resistance was also not seen, while sensitivity was also 68.8%. For Vancomycin resistance was not observed, while sensitivity was 75 % ranking the highest in being effective against *E. faecalis*. Ciprofloxacin had 18.8% resistance while sensitivity was 50%. Lastly, Amoxicillin Clavulanic acid had resistance that was 12.5% and sensitivity that was 68.8%.

Vancomycin was found to be the most effective among the 5 antimicrobials with no evidence of resistance for *E. faecalis*. Ciprofloxacin was found to be the least effective with high rate of resistance among the 5 antimicrobials for *E. faecalis.*

Table 16: Most prevalent Gram-positive isolate and its Antimicrobial susceptibility percentages

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Organisms | Organisms’ prevalence | Linezoid | | Tigecyclin | | Vancomycin | | Ciprofloxacin | | Amoxicillin  Clavulanic acid | |
| S % | R% | S% | R% | S% | R% | S% | R% | S% | R% |
| *E. faecalis* | 6.0% | 68.8% | 0 | 68.8% | 0 | 75% | 0 | 50% | 18.8% | 68.8% | 12.5% |

Tables 17 summaries antimicrobial susceptibility of the most prevalent Gram-negative pathogen which is *E. coli*. out of 270 isolated pathogens *E. coli* was the dominant pathogen isolated and there were 143 *E. coli* isolates which accounts for 53.0%. This table shows *E. coli* antimicrobial susceptibility percentages. Meropenem had 95.1% sensitivity and 0.7% resistant against *E. coli*. For Imipenem there was no resistance seen, sensitivity was 94.4%. Gentamycin had 10.4% resistance, while sensitivity was 88.1% against *E. coli*. Ertapenem had no resistance, while sensitivity was 89.5% against *E. coli.* Cefepime had 6.3% resistance with 83.2% sensitivity. Piperacillin Tazobactam had 3.5% resistance and 89.5% sensitivity. Cefotaxime ceftriaxone had 31.4% resistance while sensitivity accounted for 58.0%. Meropenem was the most effective antimicrobial among the 7 along with imipenem, while Cefotaxime Ceftriaxone was the least effective antimicrobial for *E. coli* among the 7 with 31% resistance.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | | Antimicrobial susceptibility prevalence | | | | | | | | | | | | | |
| Organisms | Organisms’ prevalence | Meropenem | | Imipenem | | Gentamycin | | Ertapenem | | Cefepime | | Piperacillin Tazobactam | | Cefotaxime  ceftriaxone | |
| S % | R% | S% | R% | S% | R% | S% | R% | S% | R% | S% | R% | S% | R% |
| *E. coli* | 53.0% | 95.1% | 0.7% | 94.4% | 0 | 88.1% | 10.4% | 89.5% | 0 | 83.2% | 6.3% | 89.5% | 3.5% | 58.0% | 31.4% |

Table 17: Most prevalent Gram negative and its antimicrobial susceptibility

**Discussion**

**Generalizability of the study findings**

Urinary Tract Infections (UTIs) rank among the most common infections in the general population and are a significant contributor to Hospital-Acquired Infections. These infections can lead to serious health complications for patients, including sepsis and kidney damage, and simultaneously impose substantial financial burdens on healthcare systems due to increased treatment costs, extended hospital stays, and potential legal liabilities. The research study was critical in evaluating the prevalence of bacterial species responsible for hospital-acquired infections (HAIs). A key component of the study involved determining the antibiotic susceptibility of these identified bacterial species, providing crucial information for guiding treatment strategies and understanding the extent of antimicrobial resistance within the hospital environment. Based on the findings regarding prevalence and susceptibility, the study aimed to recommend specific, actionable steps to be taken to reduce the incidence and impact of these HAIs in hospital settings, ultimately improving patient outcomes and reducing the burden on healthcare resources. These recommendations likely encompass infection control protocols, antibiotic stewardship programs, and potentially, innovative approaches to prevent bacterial spread and colonization. The study discovered that the most prevalent gram-negative organism was *E. coli* contributing about 53 % in the sample size of 270. The most prevalent gram-positive cocci discovered in the study was Enterococcus faecalis contributing 51,6 % in the sample size of 270 patients. These findings indicate there is still a high rate of nosocomial infection, highlighting a persistent challenge in healthcare settings. The prevalence of these infections underscores the critical need for strict and consistently enforced measures in infection control. These measures are essential to prevent the spread of these bacterial infections from the hospital environment to vulnerable patients, minimizing morbidity, mortality, and the associated healthcare costs. A comprehensive and proactive approach to infection control is therefore paramount to safeguarding patient well-being and ensuring a safe and effective hospital environment.

**Prevalence of UTIs in the ICU Setting**

This study found a high prevalence of urinary tract infections (UTIs) among ICU patients, consistent with previous research that has identified UTIs as a primary hospital-acquired infection, particularly in critical care settings. Among the 270 participants analyzed, *E. coli* accounted for more than 53% of isolates, confirming its global dominance as a UTI pathogen (Dadi et al., 2020). The incidence of multidrug-resistant organisms (MDROs) such as *Klebsiella pneumoniae* and *Acinetobacter baumannii* is also consistent with global trends, particularly in resource-constrained environments such as KwaZulu-Natal.

Furthermore, the study emphasizes the necessity of early detection and proper antimicrobial stewardship in the ICU in combating the high prevalence of UTIs and the rise of MDROs. Overuse or inappropriate antibiotic use in critically ill patients frequently contributes to resistance development and transmission (Kaln et al., 2023). The high prevalence of *E. coli* as the primary pathogen highlights the importance of focused interventions to prevent UTIs, such as tight infection control measures, prudent catheter use, and routine screening for resistant infections (Nasrollahian et al., 2024). These findings highlight the urgency of addressing antimicrobial resistance in ICU settings, especially in regions with limited healthcare resources like KwaZulu-Natal, where the burden of both infection and resistance can be overwhelming (Naidoo, 2022).

**Microbial Distribution**

The prevalence of Gram-negative pathogens, particularly *E. coli* (53%), and *Klebsiella pneumoniae subspecies* (14.8%), is consistent with findings in ICUs around the world, where these organisms are linked to nosocomial infections (Spadar, 2023). The study detected Gram-positive pathogens, including *Enterococcus faecalis* (51.6% of Gram-positive isolates) *Enterococcus faecalis* is a gram-positive bacterium that is commonly known to cause UTIswhich supports prior research studies that presented the dual burden of Gram-negative and Gram-positive bacteria in ICU-acquired UTIs.

Moreover, the discovery of a considerable proportion of multidrug-resistant bacteria, particularly *Klebsiella pneumoniae* and *Acinetobacter baumannii*, underscores the growing worry about antibiotic resistance in ICU settings. These bacteria are well known for their capacity to persist in critical care settings, where patients frequently have impaired immune systems and lengthy hospital stays (Perez et al., 2010). The growing incidence of *Enterococcus faecalis* among Gram-positive isolates highlights the complexities of ICU-acquired UTIs, as these organisms are known to be resistant to routinely used antibiotics such as vancomycin (McDermott, 2016). Such findings highlight the need for improved infection control procedures and rigorous surveillance in ICU settings to avoid the development of resistant bacteria and improve patient outcomes.

**Antimicrobial Resistance Patterns**

The antimicrobial susceptibility analysis reveals a concerning pattern of resistance, particularly to routinely used antibiotics. Resistance to Amoxicillin-Clavulanic Acid (23%) and Ciprofloxacin (26%) was common among Gram-positive organisms. However, sensitivity to Linezolid, Tigecycline, and Vancomycin was high, indicating their effectiveness in treating resistant infections. Gram-negative organisms showed significant resistance to Cefotaxime-Ceftriaxone (43.5%) and Piperacillin-Tazobactam (20%), highlighting the difficulties in controlling infections caused by extended-spectrum beta-lactamase (ESBL) producing bacteria. The findings are consistent with those of Pons and Ruiz (2019), who found comparable resistance trends in ICU infections that were aggravated by extensive empirical antibiotic usage and inadequate infection control methods in public hospitals. Furthermore, high resistance rates in non-fermenting Gram-negative bacilli, such as the *Acinetobacter baumannii complex* (75% resistant to Piperacillin-Tazobactam), indicate both innate and acquired resistance mechanisms, according to global surveillance studies.

**Demographics and Risk Factors**

The study’s demographic analysis revealed a higher prevalence of UTIs among female patients (73.7%), consistent with anatomical predispositions, as noted by Mateescu et al. (2014). Age-related vulnerability was evident, with a majority of cases occurring in individuals aged 40–65 years, a demographic often at higher risk due to comorbidities and invasive procedures like catheterization. Prolonged catheterization emerged as a critical risk factor, correlating with earlier studies identifying it as a primary driver of ICU-acquired UTIs.

**Conclusion**

This retrospective study investigated urinary tract infections (UTIs) in the ICU setting identifying *E. coli* as the dominant pathogen 53.0% and highlighting concerns regarding multiple drug resistance organisms (MDROs). *Klebsiella pneumonia* was one of the MDROs that were concerning along with *Acinetobacter baumannii*. *Acinetobacter baumannii* is known to be both intrinsic and extrinsic resistant. The findings emphasize the need for enhanced infection control measures, prudent antimicrobial stewardship, and routine screening for resistant infections. The study`s demographic analysis identified female patients, individuals aged 40-65 years, and prolonged catheterization as significant risk factors. Meropenem was the most effective antimicrobial among the 7 along with imipenem, while Cefotaxime Ceftriaxone was the least effective antimicrobial for *E. coli* among the 7 with 31% resistance. Vancomycin was found to be the most effective among the 5 antimicrobials with no evidence of resistance for *E. faecalis*. Ciprofloxacin was found to be the least effective with a high rate of resistance among the 5 antimicrobials for *E. faecalis.*

This study highlights the prevalence and antibiotic resistance patterns of urinary pathogens in IALCH. E. *coli* was the most common isolate accounting for 53% followed by Klebsiella pneumoniae subspp and *E. faecalis* in ICU patients admitted At IALCH. Notably *E. coli* exhibited significant resistance to multiple antibiotics including cefotaxime ceftriaxone gentamycin cefepime and piperacillin. In contrast, *E. faecalis* demonstrated 75% susceptibility to tested antibiotics. *E. faecalis* was also most prevalent among the gram-positive accounting for 6.0%. Vancomycin was found to be the most effective for *E. faecalis*. Ciprofloxacin was found to be the least effective with a high rate of resistance for *E. faecalis.* This study also found that urinary tract infections were more common in patients who are between 40-65 years and affected mostly females. These findings emphasize the need for judicious antibiotic use, regular monitoring of resistance patterns, and implementation of effective infection control measures to combat the spread of antibiotic-resistant urinary pathogens.

**Limitations**

However, this study has several limitations. Firstly, the retrospective design and reliance on laboratory-confirmed positive results limited our ability to calculate UTI prevalence. Additionally, data on *Candida* infections was not available, restricting our understanding of fungal UTIs. Furthermore, information on catheter utilization, a critical risk factor for UTIs, was incomplete. Despite these limitations, this study contributes to the understanding of UTI epidemiology in ICUs.

**Recommendations**

Future research should prioritize, prospective data collection to enable comprehensive prevalence calculations. Inclusion of fungal pathogens, particularly Candida to address knowledge gaps. Collection of detailed catheter utilization data to better understand catheter-associated UTI risk factors. By addressing these gaps future studies can provide a more comprehensive understanding of UTI prevalence, inform evidence-based infection control strategies and improve patient outcomes.

Recommendations include the implementation of enhanced infection control measures. Promoting antimicrobial stewardship. Conducting routine screening for resistant infections. Develop targeted interventions for high-risk populations. Explore novel antimicrobial agents to combat MDROs.

**Acknowledgments**

My profound gratitude and appreciation to my supervisor, Mr Shangase for accepting the mentorship and supervision of this project, despite the multiple tasks, and for his availability and fatherly advice.  His help has largely contributed to the fruition of this final report. I would also like to thank the MUT ethical committee for allowing me to conduct this project. I wish to thank Pragashinee, my laboratory supervisor, also the doctors at IALCH for their contribution, suggestions, and full support in the realization of this project. Lastly, I would like to thank NHLS training staff, and the AARMS team for ensuring that I receive data.

**Acronyms and abbreviations**

AARMS- Academic affairs and Research Management System.

CAUTI- Catheter-Associated Urinary Tract.

*E. coli- Escherichia coli.*

*E. faecalis – Enterococcus faecalis*

HAIs- Healthcare Associated Infections.

IALCH- Inkosi Albert Luthuli Central Hospital.

ICU- Intensive Care Unit.

KZN- Kwazulu-Natal.

MSU- Midstream Urine.

MDROs- Multiple drug resistance organisms

NHLS- National Health Laboratory Service

NHSN- National Healthcare safety Network.

UTI- Urinary Tract Infection

**References**

1. Atkins L, Sallis A, Chadborn T, Shaw K, Schneider A, Hopkins S, Bunten A, Michie S, Lorencatto F, 2020, *Reducing catheter-associated urinary tract infections: a systematic review of barriers and facilitators and strategic behavioural analysis of interventions.* Implementation Sci, 15, 44, available from: https://doi.org/10.1186/s13012-020-01001-2
2. Barchitta M, Maugeri A, Favara G, Riela PM, Mastra, Rosa MC, Gallo G, Mura I, Agodi A, 2021*, Cluster analysis identifies patients at risk of catheter-associated urinary tract infections in intensive care units: findings from the SPIN-UTI Network. Journal of Hospital Infection.* 107, pg.57-63 available from: <https://doi.org/10.1016/j.jhin.2020.09.030>
3. Bitew A, Zena N, Abdeta A, 2022. *Bacterial and fungal profile, antibiotic susceptibility patterns of bacterial pathogens and associated risk factors of urinary tract infection among symptomatic paediatrics, infection and drug resistance*, 1613-1624
4. Bizuayehu H, Bitew A, Abdeta A, Ebrahim S, (2022) *Catheter-associated urinary tract infections in adult intensive care units at a selected tertiary hospital, Addis Ababa, Ethiopia.* PLOS ONE 17(3): e0265102 [online] Available from: <https://doi.org/10.1371/journal.pone.0265102>.
5. Burrows LL, 2024. *It`s uncomplicated: Preventions of urinary tract infections in an era of increasing antibiotic resistance. PLos Pathog*, 20(2): e1011930. Available from: <https://doi.org/10..1371/journal.ppat.1011930>
6. CDC, 2024. *Urinary Tract Infections (Catheter-Associated Urinary Tract Infection [CAUTI] and non-Catheter-Associated Urinary Tract Infection [UTI]) Events, NHSN.*
7. Clarke, K, Hall, CL, Wiley, Z, Tejedor, SC, Kim, JS, Reif, L, Witt, L, & Jacob, JT, 2020. *Catheter-Associated Urinary Tract Infections in Adults: Diagnosis, Treatment, and Prevention. Journal of hospital medicine*,15(9), pp. 552–556.
8. Cournant A, 2022. *Complicated UTI, Infectious Disease ADVISOR,* available from: <https://www.infectiosdiseaseadvisor.com/ddi/complicated-uti/>
9. Dadi, B.R., Abebe, T., Zhang, L., Mihret, A., Abebe, W. and Amogne, W., 2020. Distribution of virulence genes and phylogenetics of uropathogenic Escherichia coli among urinary tract infection patients in Addis Ababa, Ethiopia. BMC infectious diseases, 20, pp.1-12.
10. Duszynska W, Rosenthal VD, Szczesny A, Zajaczkowska K, Fulek M, Tomaszewski J,2020, *Device associated -health care associated infections monitoring, prevention and cost assessment at intensive care unit of University Hospital in Poland (2015-2017).* BMC Infect Dis 20, 761, available from: https: //doi.org/10.1186/s12879-020-05482-w
11. Florence-Mireles A, Hreha TN, Hunstad DA, 2019, *Pathophysiology, Treatment, and Prevention of Catheter-Associated Urinary Tract Infection*. Top spinal Cord Inj Rehabil, 25(3) pg. 228-240, available from: <https://doi.org/10.1310/sci2503-228>
12. Gurnadi WD, Karuniawati A, Umbas R, Bardosono S, Lydia A, Soebandrio A, Safari D, 2021. *Biofilm-Producing Bacteria and Risk Factors (Gender and Duration of Catheterization) Characterized as Catheter-Associated Biofilm Formation. International Journal of Microbiology, 2021(1) [online] Available: https://doi.org/10.1155/2021/8869275*
13. Isigi SS, Parsa AD, Alasqah I, Mahmud I, Kabir R, 2023. *Predisposing factor of nosocomial infections in hospitalized patients in the United Kingdom: systematic review, JMIR public health and surveillance, 9, e43743*
14. Izadi N, Eshrati B, Mehrabi Y, Etemad K, Hashemi-Nazari S, 2020. *The national rate of intensive care units-acquired infections, one – year retrospective study in Iran. BMC public health,* 21(1), 1-8.
15. Kalın, G., Alp, E., Chouaikhi, A. and Roger, C., 2023. *Antimicrobial multidrug resistance: clinical implications for infection management in critically ill* *patients*. *Microorganisms*, *11*(10), p.2575.
16. Kollef MH, Torres A, Shorr AF, Martin-loeches I, Micek SI,2021. *Nosocomial infection: Critical care medicine,* 42(2), pg. 169-187 [online] available: https://journals.lww.com/ccmjournal/abstract/2021/02000/Nosocomial \_infection.2.aspx?context=featuredarticles& collectionid=3
17. Kranz J, Schmidt S, Wagenlehner F, Schneidewind L, 2020*, Catheter-associated urinary tract infections in adult patients: Preventive strategies and treatment options.* Deutsches Arzteblatt international, 117(6), pg. 83, available from: <https://scholar.google.com/scholar?as_ylo=2019&q=catheter+associated+urinary+tract+infection&hl=en&as_sdt=0,5#d=gs_qabs&t=1700337382595&u=%23p%3DL01MoPO-8QgJ>
18. Lopez MJ, Cortes JA, 2012. *Urinary tract colonization and infection in critically ill patients, Med Intensiva*, 36(2), p 143-151, available from: DOI: 10.1016/j.medine.2011.06.003
19. Mann R, Mediati DG, Duggin LG, Harry EJ, Bottomley AL, 2017, *Metabolic Adaptations of Uropathogenic E. coli in the Urinary Tract. Frontiers in cellular and infection microbiology* 7,241*.*
20. Mateescu, G.G., Idomir, M.E. and Nemet, C., 2014. Etiological and therapeutical particularities of urinary infections in urological patients. *Bulletin of the Transilvania University of Brasov. Series VI: Medical Sciences*, pp.19-24.
21. McDermott, H.M., 2016. *The identification of the multi-drug-resistant organisms, vancomycin resistant enterococci (VRE) and extended spectrum β-lactamase producing Enterobacteriaceae (ESBL-E), in the ICU: examining the interplay between patient colonisation and environmental contamination* (Doctoral dissertation, Royal College of Surgeons in Ireland).
22. Murtaugh, R, 2021*. Nosocomial infections*. In: critical care ,1St ed. New York: Routledge, p. 2. [online] available from: https: //doi.org/10.1201/9781315140629
23. Mythri, H. Kashinath, K.R. 2014. *Nosocomial infections in patients admitted in intensive care unit of a tertiary health care center, India. Annals of medical and health sciences research*, 4(5).
24. Nasrollahian, S., Graham, J.P. and Halaji, M., 2024. A review of the mechanisms that confer antibiotic resistance in pathotypes of E. coli. *Frontiers in Cellular and Infection Microbiology*, *14*, p.1387497.
25. Naidoo, E.L., 2022. *Assessing infection control knowledge and compliance in theatre at a private hospital in KwaZulu-Natal, South Africa* (Doctoral dissertation).
26. Nicole LE, 2014, *Catheter associated urinary tract infections. Antimicrob Resist Infect Control* 3,23, available from: <https://doi.org/10..1186/2047-2994-3-23>
27. Oumer Y, Dadi B.R, Seid M, Biresaw G, Manila A, 2021, *Catheter-Associated Urinary Tract Infection: incidence, associated Factors and Drug Resistance Patterns of Bacterial Isolated in Southern Ethiopia*: NIH, 14, pg. 2883-2894 [online] available: <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8318706/>.
28. Patel Pk, Advani SD, Kofman AD, Lo E, Maragakis LL, Pegues DA, Pettis AM, Saint S, Trautner B, Yokoe DS, Meddings J, 2024. *Strategies to prevent catheter associated urinary tract infections in acute-care hospitals, infect control Hosp Epidemiol,* 44(8), 1209-1231, DOI:10.1017/ice.2023.137.
29. Pelling H, Nzakizwanayo J, Milo S, Denham EL, MacFarlane WM, Bock LJ, Sutton JM, Jones BV, 2019. *Bacterial biofilm formation on indwelling urethral catheters. Letters in Applied Microbiology*, 68(4), p 277-293, [online] available: <https://doi.org/10.1111/lam.13144>.
30. Perez, F., Endimiani, A., Ray, A.J., Decker, B.K., Wallace, C.J., Hujer, K.M., Ecker, D.J., Adams, M.D., Toltzis, P., Dul, M.J. and Windau, A., 2010. Carbapenem-resistant Acinetobacter baumannii and Klebsiella pneumoniae across a hospital system: impact of post-acute care facilities on dissemination. *Journal of antimicrobial Chemotherapy*, *65*(8), pp.1807-1818
31. Perrin K., Vats, A., Qureshi, A. ,2021*,* *Catheter-Associated Urinary Tract Infection (CAUTI) in the Neuro ICU: Identification of Risk Factors and Time-to-CAUTI Using a Case–Control Design*. *Neurocrit Care* 34, 271–278, available from: <https://doi.org/10.1007/s12028-020-01020-3>
32. Pons, M.J. and Ruiz, J., 2019. Current trends in epidemiology and antimicrobial resistance in intensive care units. *Journal of Emergency and Critical Care Medicine*, *3*.
33. Rubi H, Mudey G, Kunjalwar R, 2022. *Catheter-associated urinary tract infection (CAUTI), Cureus* 14(10).
34. Sabih A, Leslie SW, 2023. *Complicated Urinary Tract Infections*. StatPearls. available from: https//www.ncbi.nlm.nih.gov/books/NBK436013
35. Saleem M, Khaja ASS, Hossain A, Alenazi F, Said KB, Moursi SA, Almalaq HA, Mohamed H, Rakha E, Mishra SK, 2022, *Catheter-Associated Urinary Tract Infection in Intensive Care Unit Patient at a Tertiary Care Hospital, Hail, Kingdom of Saudi Arabia*.*12*(7), 1695; available from: <https://doi.org/10.3390/diagnostics12071695>
36. Sauer K, Stoodley P, Goeres DM, Hall-Stoodley L, Burmolle M, Stewart PS, Bjarnsholt T, 2022. *The biofilm life cycle: expanding the biofilm formation. Nature reviews. Microbiology*, 20(10), 608-620. Available from: <https://doi.org/10.1038/s41579-022-00767-0>
37. Schaffer JN, Pearson MM, 2015*. Proteus mirabilis and Urinary Tract Infections. Microbiology spectrum*, 3(5), 10.1128/microbiolspec.UTI-0017-2013. Available from: <https://doi.org/10.1128/microbiolspec.UTI-0017-2013>
38. Sikora A, Zahra F,2023. *Nosocomial Infections*, In: StatPearls [internet]. Treasure Island (FL) available from : <https://www.ncbi.nlm.nih.gov/books/NBKS559312/>
39. Ssekitoleko R.T, Oshabaheebwa S, Munal I G, Tusabe MS, Namayega C, Ngabirano B.A, Matovu B, Mugaga J, Reichert W.M, Joloba M.L, 2020, *The role of medical equipment in the spread of nosocomial infections: a cross- sectional study in four tertiary public health facilities in Uganda*: BMC, 20 [online] available: https:https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7562759/#:~:text=This%2C%20combined%20with%20the%20fact,facilities%20in%20low%20resource%20settings.
40. Smith M, 2019. *The prevalence of nosocomial infections in catheterized patients in the ICU. Journal of infectious Diseases, 50(3), 69-85.*
41. Spadar, A., 2023. *Understanding the genetic diversity, antimicrobial resistance, and virulence of Klebsiella pneumoniae bacteria* (Doctoral dissertation, London School of Hygiene & Tropical Medicine).
42. Tajeddin E, Rashidan M, Razagh M, Javadi SS, Sherafat SJ, Alebouyeh M, Sarbazi M.R, Mansouri N, Zali M.R, 2016*, The role of the intensive care unit environment and health care workers in the transmission of bacteria associated with hospital acquired infections: Journal of Infection and Public Health*, 9(1), pg. 13-23[online] available: https://doi.org/10.1016/j.jiph.2015.05.010
43. Zhao A, Sun J, Liu Y, 2023, *Understanding biofilms: from definition to treatment strategies*. Available online: https: //doi/10.3389/fcib.2023.1137947: frontiers, 18

**Publisher details**

