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Epidemiologic Profile Urinary Tract Infections: Experience of the Microbiology Laboratory of the University Hospital Mohamed VI in Tangier

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Abstract

Urinary tract infection is one of the most common bacterial infections in humans. The urine cytobacteriological examination is the key test for its diagnosis. This work aims to Evaluate the prevalence of urinary tract infection at the Microbiology Laboratory of the University Hospital Mohamed VI in Tangier and to highlight its epidemiological and bacteriological characteristics. It was a descriptive study with retrospective data collection which took place from January 2021 to June 2022, at the Microbiology Laboratory of the university hospital Mohamed VI in Tangier. It covered all urine cytobacteriological examinations (ECBU) during the study period. We identified 77 cases of urinary tract infections out of 300 requests for (ECBU), that is a positivity rate of 25 %. The mean age was 55 years. The male gender was predominant. The epidemiological profile of the isolated strains was dominated by Enterobacteriaceae 81 %, followed by Gram-positive cocci 11 % and non-fermenting gram-negative bacteria 8 %. The main bacteria responsible for urinary tract infections in order of frequency: Escherichia coli 42 %, Klebsiella pneumoniae 20 %, Enterobacter cloacae 9 %, Staphylococcus aureus 6 %, Pseudomonas aeruginosa 5 % and Acinetobacter baumannii 3%. Most of the analyzed organisms showed resistance, especially to the beta-lactam antibiotic; the enterobacteria strains isolated had revealed resistance to amoxicillin: 74%, to amoxicillin-clavulanic acid in 40% of cases, and to third-generation cephalosporins in 24%. In terms of resistance mechanisms, 11 % of the Enterobacteriaceae were extended-spectrum β-lactamase producers and 9 % of the specimens were identified as carbapenemase producers. Of the Staphylococcus aureus strains isolated, 75% were resistant to meticillin. The Glycopeptides and linezolid were the most active molecules on these isolated strains. 15% of Enterococcus species isolated in our laboratory were resistant to glycopeptides (vancomycin and teicoplanin).

Keywords

Epidemiology, Urinary Tract Infection, Cytobacteriological Urinary Test, Uropathogens, Multiresistant Bacteria, Antibiotic Sensitivity, Morocco

1. Introduction

Urinary tract infections are a heterogeneous group of infections of one of the components of the urinary tract or its appendages. What they have in common is the presence of a pathogen in the urinary tract [1]. Micro-organisms can reach the urinary tract by haematogenous or lymphatic spread; However, substantial clinical and experimental evidence indicates that the most common route to a UTI is the ascent of micro-organisms from the urethra, particularly those of enteric origin such as Escherichia coli [2]. The most uropathogen-causing UTIs colonize the colon, the perianal region, and in females, the periurethral region forming a biofilm that usually resists the body's immune response [3]. These uropathogens generally develop in the lower urinary tract (urethra and bladder) and if not properly treated, they ascend to the upper urinary tract (ureters and kidneys) and cause severe damaged to the kidneys. Other complications caused by UTIs are bladder infection (cystitis), urethra infection(urethritis), kidney infection (pyelonephritis) and ureter (ureteritis) [4].

Urethritis is simply an inflammation of the urethra, which is a tube that carries urine out of the body. It is often caused by sexually transmitted infection or due to an injury from an instrument such as urinary catheter or even exposure to an irritating chemical such as antiseptic or spermicide. Urethritis can either be gonococcal urethritis caused by gonorrhea bacteria or non-gonococcal urethritis caused by bacteria other than gonorrhea, such as *Chlamydia trachomatis*, *Ureaplasma urealyticum*, *Mycoplasma genitalium* and *Trachomonas vaginalis*. Cystitis is a bladder infection caused by abnormal growth of bacteria inside the bladder [4].

Urinary tract infections can have serious consequences, particularly in pregnant women, or in patients with urinary tract anomalies or favouring factors such as diabetes or immunodepression [5]. Reduced immunity in diabetes contributes to the increased risk for acquiring UTI. A few studies have suggested that hyperglycaemic urine promotes rapid bacterial growth and colonization [2].

Urinary tract infection is one of the main reasons for consultations, microbiological investigations and antibiotic prescriptions [6]. It ranks second only to respiratory infection in community pathology, and first in nosocomial infections [7]. The diagnosis is based on the cytobacteriological examination of the urine which imposes rigorous conditions for sampling, storage, production and interpretation.

2. Materials and Methods

It was a descriptive study with retrospective data collection which took place from January 2021 to June 2022, at the microbiology laboratory of Mohamed VI University Hospital in Tangier were included: All patients during the period of our study and presenting a positive cytobacteriological examination of urine. The urinary tract infections caused by specific germs such as Koch's bacillus, viruses, parasites, yeasts and fungi were excluded from our study.

The biological diagnosis of UTI was carried out on a leukocyturia ≥ 104/ml associated with a significant bacteriuria which was interpreted according to the bacterial species involved and the sex of the patient, bearing in mind that Escherichia coli and Staphylococcus saprophyticus are considered specific uropathogens, and their threshold is lowered to 10^3/CFU/Ml.

Identification of isolated bacteria was based on the use of chromogenic media such as Uriselect® from BioRad, Api 20 systems (E, NE, Staph) from BioMérieux™ and immunological identifications by Pastorex® latex agglutination for strains of *Staphylococus aureus*. Antibiotic susceptibility testing was carried out by diffusion on Mueller-Hinton agar according to the standards of the of the CA-SFM (antibiogram committee of the French Microbiology Society). ESBLs were detected by the synergy method between an amoxicillin/clavulanic acid disc and one of the three third-generation cephalosporin discs (cefotaxime, ceftazidime and ceftriaxone), characterized by a "champagne cork" image and indicating the presence of an ESBL. Staphylococcus strains were tested for resistance to meticillin using the diffusion method, using a 30 µg cefoxitin disk with an inhibition diameter around the disk of less than 27 mm.

The results of the Urine Cytobacteriological Examination were collected from the computer system of the Microbiology Laboratory of the same University Hospital, statistical analysis and data entry was carried out by Microsoft Office Excel 2007.

3. Results

A total of 300 individual ECBU's were performed. Among these samples, 77 cases were having the criteria for UTI with a prevalence rate at 25%. The mean age was 55 years. The male gender was predominant with a sex-ratio (M/F) at 0.76. The families of bacteria responsible for urinary tract infection were dominated by Enterobacteriaceae 63 cases (81%) followed by Gram-positive cocci (11%) and Gram-negative bacilli 6 cases (8%) (**Figure 1**).

The main bacteria responsible for urinary tract infections in order of frequency: *Escherichia coli* 42%, *Klebsiella pneumoniae* 20%, *Enterobacter cloacae* 9%, *Staphylococcus aureus* 6%, *Pseudomonas aeruginosa* 5%, *Enterococcus faecalis* 4%, *Acinetobacter baumannii* 3%, and *Enterococcus faecium* 1% (**Table 1**).

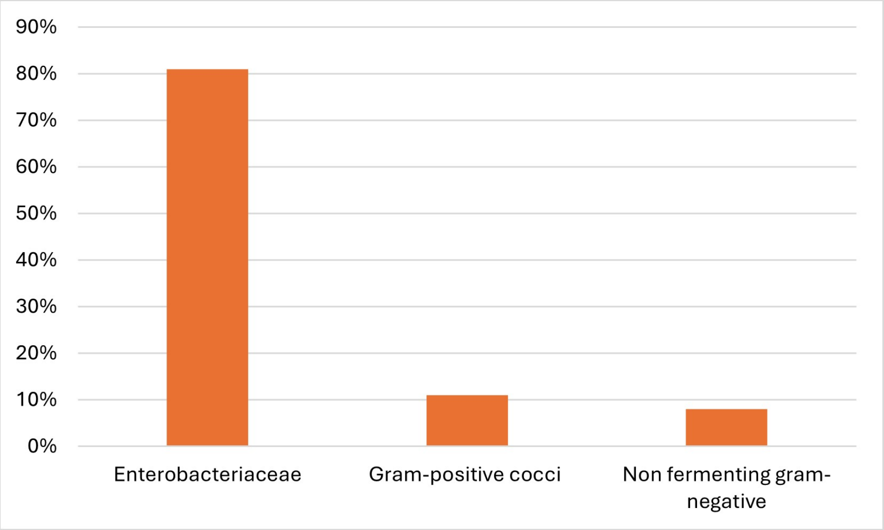

Figure 1. Distribution of bacteria isolated from urine samples processed from the Microbiology Laboratory of the University Hospital of Tangier (n = 77).

Table 1. Identification of the organisms isolated.

Pathogen	Effective	Prevalence
Enterobacteriaceae		
Escherichia coli	32	42%
Klebsiella pneumoniae	15	20%
Enterobacter cloacae	7	9%
Proteus mirabilis	5	6%
Citrobacter freundii	1	1%
Serratia marescens	1	1%
Klebsiella oxytoca	1	1%
Cronobacter	1	1%
Non fermenting gram **Negative bacteria**		
Pseudomonas aeruginosa	4	5%
Acinetobacter baumannii	2	3%
Gram positive cocci		
Staphylococcus aureus	4	6%
Enterococcus faecalis	3	4%
Enterococcus faecium	1	1%
Total (n = 77)	77	100%

The Enterobacteria responsible for urinary tract infections identified in our laboratory, in order of frequency, are as follows: *Escherichia coli* followed by *Klebsiella pneumoniae,* then *Enterobacter cloacae*, *Proteus mirabilis*, *Citrobacter freundii*, *Serratia marescens*, *Klebsiell oxytoca* and *Cronobacter* (**Figure 2**).

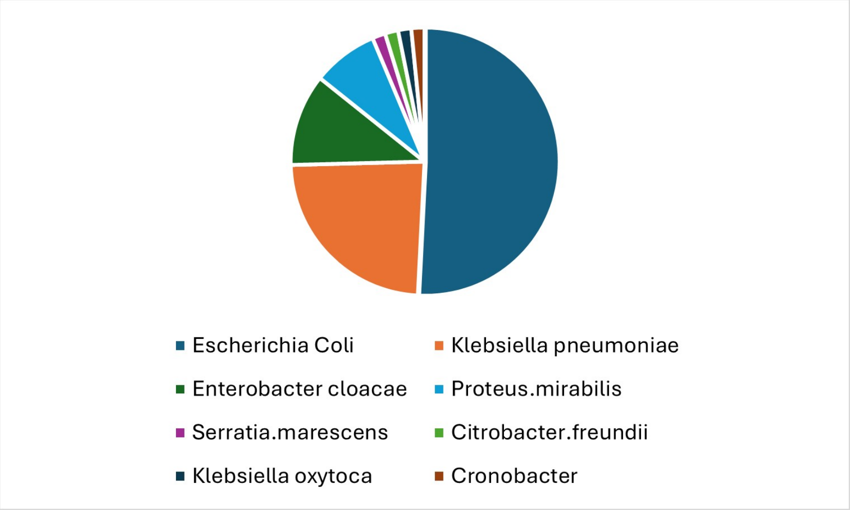

Figure 2. Distribution of *Enterobacteriaceae* responsible for urinary tract.

Most of the analyzed organisms showed resistance, especially to the beta-lactam antibiotic; the enterobacteria strains isolated had revealed resistance to amoxicillin: 74%, to amoxicillin-clavulanic acid in 40% of cases, and to third-generation cephalosporins in 24%. In terms of resistance mechanisms, 11% of the *Enterobacteriaceae* were extended-spectrum β-lactamase producers and 9% of the specimens were identified as carbapenemase producers (**Figure 3**). The Cronobacter strain identified in our study was a wild-type strain. The *Pseudomonas aeuroginosa* and *Acinetobacter baumannii* strains were multiresistant; but they were all sensitive to colistin. Of the Staphylococcus aureus strains isolated, 75% were resistant to meticillin. The Glycopeptides and linezolid were the most active molecules on these isolated strains. 15% of Enterococcus species isolated in our laboratory were resistant to glycopeptides (vancomycin and teicoplanin).

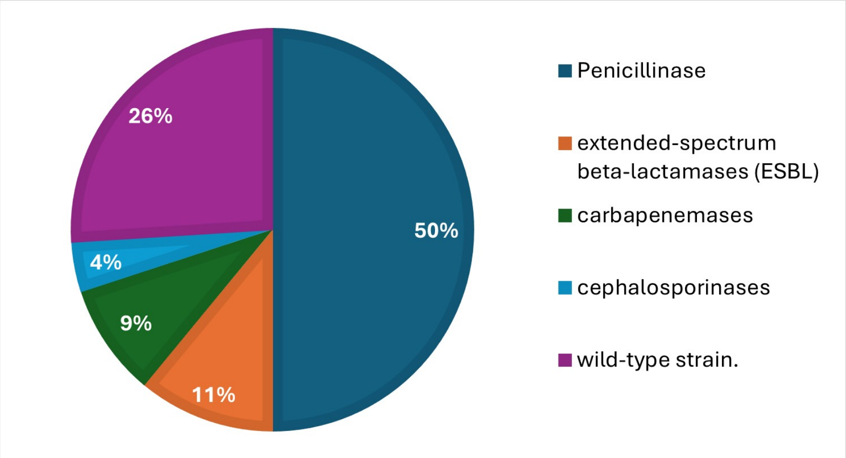

Figure 3. Drug resistance mechanism of *Enterobacteriaceae* strains isolated.

4. Discussion

In our study, the prevalence of UTI was around 25%, which was close to the results of the study carried out by Avicenne Hospital in Rabat, with a culture positivity of 23%; Lower rates were reported in the study carried out by Military Hospital in Marrakech, with culture positivity in 13% of cases. This variability in UTI prevalence could be explained by several risk factors: patient age, gender, diabetes, catheter use, immune compromise, and prior antibiotic history [5].

In the present study, the results showed male predominance (sex-ratio at 2) which could be explained by the fact that ECBU is more systematically requested in men, given the greater risk factors for complications [8]. Most epidemiological studies have shown that females have an increased UTI risk compared with males, predominantly due to the shorter length of their urethra and the shorter distance between their urethra and anus. The mean age was 55 years; similar data was reported by other studies. The incidence of UTIs in men increases after the age of 50, in line with problems of prostatic obstruction and the loss of the bactericidal action of prostate secretions. Urinary tract infections are the most common infections in the elderly. There are many factors that predispose the elderly to UTI, including chronic disease, functional abnormalities and specific medications [2].

The bacterial epidemiology of urinary tract infections in our study was largely dominated by strains belonging to the Enterobacteriaceae family, and Escherichia coli was the most predominant uropathogenic bacterium, which is in line with the literature [9]. The ascending pathophysiology of UTI and the high colonization of the perineum by Enterobacteriaceae of digestive origin, particularly Escherichia coli, combined with specific uropathogenic factors such as bacterial adhesins capable of binding to the urinary epithelium, explain this predominance.

In the present study, the antibiotic susceptibility of Enterobacteriaceae strains isolated and it had revealed resistance to amoxicillin: 74%, to amoxicillin-clavulanic acid in 40% of cases, to third-generation cephalosporins in 24%. Antibiotic resistance is currently on the increase and is a cause for concern [10]. The development of antibiotic resistance is a complex process, often involving host, pathogen and environmental factors. With regard to beta-lactam resistance phenotypes, the essential mechanism of resistance is enzymatic, through the production of beta-lactamase; 11% of the Enterobacteriaceae identified in our laboratory were extended-spectrum β-lactamase producers. Urinary tract infections caused by *Enterobacteriaceae* producing extended-spectrum beta-lactamases (E-BLSE) represent an infectious risk, and a major therapeutic challenge. Today, EBLSEs are the majority of BMRs that are responsible for potentially severe infections and prescriptions for broad-spectrum antibiotics, threatening the future activity of last-line molecules. Their involvement in both nosocomial and community-acquired urinary tract infections (UTIs) is a real public health problem [11]. At present, alternative antimicrobial therapy to treat ESBL-positive UTI on outpatient ba-sis is limited. Carbapenems are highly effective in these cases, but require intravenous or intramuscular administration [2].

In our laboratory, 15% of the enterococcus species isolated were resistant to glycopeptides (vancomycin and teicoplanin). The basic mechanism of vancomycin resistance in enterococci is the formation of peptidoglycan receptors with reduced glycopeptide affinity. This results in decreased binding of vancomycin and decreased inhibition of cell wall synthesis. Peptidoglycan precursors with decreased binding to vancomycin are responsible for this. Instead of the normally occurring peptidoglycan precursor D-alanine-D-alanine, precursors like D-ala-D-lactate or D-ala-D-serine are found on the cell walls of vancomycin-resistant strains of enterococci. D-ala-D-lactate has been found to have an affinity 1000 times less than D-ala-D-ala for vancomycin, whereas D-ala-D-serine has an affinity about 6 times less than the normal cell wall precursors. It has been shown that the substitution of the terminal D-alanine of the cell wall with D-lactate results in repulsive forces in the binding pocket of the vancomycin molecule, leading to a 1000-fold decrease in affinity to the antibiotic [12].

Antimicrobial stewardship involves the careful and responsible use of antimicrobial agents, such as antibiotics, to reduce the risk and spread of antimicrobial resistance (AMR). This approach focuses on optimizing treatment for infections while minimizing the negative impacts of these agents, specifically targeting the prevention of resistance and adverse effects [13].

The WHO, a United Nations agency focused on international public health, has crafted a Global Action Plan to combat antimicrobial resistance (AMR). This plan includes various strategies such as enhancing surveillance, encouraging the development of new antimicrobials, and boosting access to clean water and sanitation [14]. In 2017, the WHO's Expert Committee on Selection and Use of Essential Medicines developed the AWaRe classification system for antibiotics. This system plays a crucial role in promoting effective antibiotic stewardship globally. It sorts antibiotics into three categories: Access, Watch, and Reserve. These categories reflect the potential impact of different antibiotics and their classes on antimicrobial resistance (AMR). The system highlights the vital need for careful and responsible use of antibiotics [15].

5. Conclusion

Urinary tract infections (UTIs) are a real public health problem, both in terms of their frequency and the difficulty of treating them. They are some of the most common bacterial infections and they are usually caused by bacterial invasion of the urinary tract. Among the bacterial species, *Escherichia coli* is the most common organism isolated in our laboratory. The increasing prevalence of antibiotic resistance among uropathogens presents a major challenge to the clinical management of UTIs. This alarming situation of multi-resistance should lead practitioners to prescribe antibiotics rationally, preferably guided by the results of an antibiogram.

Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

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