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Original Research Article

Bacteriological Profile of Paediatric Urinary Tract Infections

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Abstract: The aim of this study was to establish the bacteriological profile of UTIs in children. Method: A retrospective cross-sectional study conducted over one year. Urine samples were taken after local disinfection of the urinary meatus. Children who did not meet the criteria for UTI, i.e., leukocyturia greater than or equal to 104 leukocytes/mL, were excluded from our sample. Susceptibility to antibiotics was studied by agar diffusion. *Results*: Enterobacteriaceae were the most frequently isolated bacterial family in our series (65.65%). Escherichia coli was the most represented bacterial species (49.07%), followed by Klebsiella sp. (14.11%). Gram-positive cocci accounted for 26.38% of germs, including 18.71% Enterococcus sp. and 7.05% coagulase-negative staphylococci. ESBL was observed in 16.74% of enterobacteria. Carbapenem resistance was observed in 6.52% (3/46). Conclusion: E. coli was the germ most frequently isolated in urinary tract infections, with an average rate of resistance to the combination of amoxicillin and clavulanic acid and 3rd generation cephalosporins, but low for ciprofloxacin and cotrimoxazole. ESBL-producing strains.

Keywords: Urinary tract infection; pediatrics; antibiotics.

INTRODUCTION

Urinary tract infection (UTI) is a frequent bacterial infection in pediatrics. Its symptoms are atypical, especially in neonates. It rapidly progresses to chronic renal failure [1]. Appropriate and rapid treatment is therefore essential.

The diagnosis of a urinary tract infection is based on a urine cytobacteriological test (UCBT) [2]. However, the results of this test are only available for 48 hours. This means that a probabilistic antibiotic treatment is required, which is then adapted according to the results of the antibiogram. In addition, the emergence of resistant germs limits the choice of treatment. For this reason, it is important to have a good understanding of the bacterial epidemiology of urinary tract infections in children [3].

The aim of this study is to establish the bacteriological profile of UTIs in children.

MATERIALS AND METHODS

This was a retrospective, cross-sectional study. It took place over a one-year period, from January 1, 2021, to December 31, 2021. Using the registers and computer systems of the central bacteriology laboratory,

we collated all the UCBT performed on children hospitalized in the pediatric wards of CHU Ibn Sina.

Urine was collected under aseptic conditions; local disinfection of the urinary meatus was carried out before urine collection. Urine was collected from the middle of the stream in children and older children and from an adhesive bag in neonates and infants. For catheterized patients, urine was collected by puncture after disinfection at the specific site of the catheter device. The method of urine collection was taken into account when interpreting the culture according to the recommendations of Rémic 2015 [4].

Urine samples that did not meet the criteria for UTI, i.e., leukocyturia greater than or equal to 104 leukocytes/mL, were excluded from our sample. The threshold for significant bacteriuria was interpreted according to the bacterial species involved.

Bacteria were isolated on the basis of morphological, cultural, and biochemical characteristics. Susceptibility to antibiotics was studied both by the Mueller Hinton (MH) agar diffusion technique, using Biomérieux disks, and by the automated method (Phoenix automated system). The results were

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interpreted in accordance with the recommendations of the Antibiogram Committee of the French Microbiology Society (CA-SFM).

Data were collected and entered using Microsoft Excel 2019. Jamovi 2.4.2 was used for data analysis. Fisher's exact test, or Chi2, was used to compare qualitative variables and the t-test for quantitative variables.

RESULTS

Epidemiological aspects

A total of 326 ECBUs were analyzed during the study period. A predominance of females was observed,

with a sex ratio of 0.89. Children aged 0 to 1 year were the most represented, with 57.05% of cases, followed by those aged 1 to 6 years with 27.30%. The median age was 1 year.

Bacteriological aspects

Enterobacteriaceae were the most frequently isolated bacterial family in our series (65.65%). Escherichia coli was the most represented bacterial species (49.07%), followed by Klebsiella sp. (14.11%). Gram-positive cocci accounted for 26.38% of germs, including 18.71% Enterococcus sp. and 7.05% coagulase-negative staphylococci. These data are summarized in Table I.

Table 1: Breakdown of germs isolated from paediatric urinary tract infections

Species	Numbers
Escherichia coli	160 (49,07%)
Enterococcus sp	61 (18,71%)
Klebsielle sp	46 (14,11%)
Coagulase-negative Staphylococcus (CNS)	24 (7,36%)
Pseudomonas aeuginosa	18 (5,52%)
Acinetobacter baumanii	6 (1,84%)
Proteus mirabilis	6 (1,84%)
Enterobacter sp	3 (0,92%)
Staphylococcus aureus (SA)	2 (0,61%)
Total	326 (100%)

Enterobacterial resistance is summarized in Table II. ESBL was observed in 16.74% of enterobacteria. Klebsiella sp. was the most resistant germ in the series. ESBL production was observed in 23.91% (11/46) and carbapenem resistance in 6.52% (3/46). They were the only carbapenem-resistant germs in the series, and one of them is multi-resistant. In addition, cross-resistance to fluoroquinones was observed in 8.69% (4/46). In addition, ESBL production was observed in 15.62 (25/160) E. coli. No KTG phenotype was observed among the Enterobacteriaceae. All our ESBLs are sensitive to amikacin. Tables 2 and 3 summarize these data. Regarding enterococci, the KTG phenotype was observed in 45.90% (28/61) of cases. They were resistant to imipenem in 55.73% (34/61) of cases, to glycopeptides in 18.03% (11/61), and to pristinamycin in 19.67% (12/61). Only one case of resistance to linezolid was observed.

For staphylococci, the KTG phenotype was observed in 26.92% (7/26) of cases. Resistance to methicillin (MRSA) was observed in 57.69% (15/26). However, they were all sensitive to glycopeptides and pristinamycin.

	E. coli (N= 160) %	Klebsiella sp (N=46) %	Proteus mirabilis (N=6) %	Enterobacter sp (N=3) %
Κ	14 (8,75)	3(5,52)	0	0
GM	41(25,62)	12(26,08)	3 (50,00)	0
IMI	1(0,62)	3(5,52)	0	0
AMC	82(51,25)	29(63,04)	1(16,66)	3(100)
TCC	82(51,25)	27(58,69)	0	1(33,33)
PTZ	34(21,25)	13(28,26)	0	1(33,33)
CRO	51(31,87)	20(43,47)	0	1(33,33)
CAZ	51(31,87)	20(243,47)	0	1(33,33)
FEP	35(21,16)	12(26,08)	0	1(33,33)
FOX	16(10,00)	9(19,56)	0	3(100)
CIP	6(3,75)	4(8,70)	2(32,32)	1(33,33)
FOS	80(50,00)	16(34,78)	0	
SXT	13(8,16)	6(13,04)	1(16,66)	0
AN	34(21,25)	13(28,26)	1(16,66)	0

 Table 2: Resistance of isolated Enterobacteriaceae

Table 5. Resistance phenotype of Enterobacter faceae								
	BLSE	КРС	KTG	Résitance croisée	BMR			
				aux Fluoroquinone				
E coli (N=160)	11,63(25/215)	0,46(1/215)	0	0,46(1/215	0			
Klebsiella sp (N=46)	5,12(11/215)	1,53(3/215)	0	1,84(4/215)	0,46(1/215)			
Proteus mirbibis (N=6)	0	0	0	0	0			
Enterobacter sp (N=3)	0	0,46(1/215)	0	0	0			
Total (N=215)	16,7(16,74)	2,32(5/215)	0	5	0,46(1/215)			

KPC= carbapenemase; ESBL extended-spectrum beta-lactamase; MDR= multi-drug resistant bacteria; KTG=amikacin-tobramycin-gentamycin

DISCUSSION

Urinary tract infection is one of the main reasons for consultations and microbiological investigations. Management must be rapid and based on the results of the antibiogram [1]. For this reason, it is important to know the epidemiology of the bacteria involved, as the results of the antibiogram require some time.

Urinary tract infections most often affect infants under 1 year old. Its prevalence is 57.07% in this age group in our series. Moreover, more girls than boys were affected (172 vs. 154). This result is comparable to that of Zahir *et al.*, in Marrekch, Kahindo in the Democratic Republic of the Congo, and Batouche *et al.*, at Oran University Hospital [1, 2, 5].

Of the 326 bacteria isolated, enterobacteriaceae were the most represented, with Escherichia coli in the lead, followed by enterococci, and then Klebsiella sp. Many authors have noted an increase in the predominance of Escherichia coli, followed by Klebsiella. This is the case for Mokni *et al.*, in Tunisia, Duong *et al.*, in Belgium, and Maleb in Oujda [3, 6, 7].

The antibiotic resistance profile of E. coli is 51.25% for the combination of amoxicillin and clavulanic acid, 37.84% for 3rd generation cephalosporins, 8.16% for cotrimoxazole, and 3.75% for ciprofloxacin. These results are similar to those of Cissé et al., for the combination Amoxicillin+clavulanic acid (51.35%) and 3rd generation cephalosporins (37.84%) but are different for Ciprofloxacin (64.86%) and Cotrimoxazole (75.67%). Our results are also comparable to those of Savadogo for the amoxicillin+clavulanic acid combination (76.2%) and 3rd generation cephalosporins (55.8%) [8]. Only one strain of Klebsiella was multi-drug resistant (0.46% of germs), which could reassure prescribers, who thus have a good margin for maneuver. Cissé et al., found 12.16% of multi-resistant germs in their series.

The ESBL rate among E. coli was 11.63% in our series, thus also highlighting the emergence of ESBL-producing E. coli. Frequent and inappropriate use of antibiotics is a risk factor for the carriage of ESBLproducing bacteria. In several developing countries, the inappropriate use of antibiotics by the population is leading to the selection of resistant strains of bacteria, resulting in a real bacteriological disaster. This is due to the free access to antibiotics without a medical prescription in all pharmacies, leading to widespread consumption of broad-spectrum antibiotics without any controls [3].

CONCLUSION

This study showed that E. coli was the most frequently isolated germ in urinary tract infections, with an average rate of resistance to amoxicillin+clavulanic acid and 3rd generation cephalosporins but low resistance to ciprofloxacin and cotrimoxazole. ESBLproducing strains are low but could increase in the future if access to antibiotics is not rigorously regulated.

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Consent for publication: Nil

Availability of data and materials: The datasets used and/or analyzed during the current study are available on reasonable request.

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