STUDY OF PREVALENCE AND BACTERIAL CAUSES OF UTI AMONG CHILDREN WITH FEVER AT ALEXANDRIA UNIVERSITY CHILDREN'S HOSPITAL

Hassan Heshmat Hassan[1] , Marwa Ahmed Meheissen[2], Eman Hamza Hassan[1] , Ahmed Farid Ahmed[1]

Department of Pediatrics[1], Department of Medical Microbiology&Immunology[2], Faculty of Medicine, Alexandria University

Introduction

UTI is among the most common infections in the pediatric age group affecting nearly 150 million cases worldwide. It is the third most common cause of fever and in developed countries, febrile UTI is the most common cause of morbidity after respiratory tract infection in children younger than two years old.

The bacteria causing UTI commonly gain access to the urinary system through ascending route, less commonly through hematogenous spread. The most common causative bacteria are Escherichia coli, followed by others like Klebsiella, Proteus, Enterobacter, and Enterococcus species.

Aim of the work

The aim of our study was to estimate the prevalence of urinary tract infection among febrile children admitted at Alexandria University Children's Hospital and to identify the common bacterial causes of urinary tract infection among febrile children and their antibiotic susceptibility pattern.

Patients and Methods

This study was conducted in all febrile children with proven urinary tract infection who were admitted to Alexandria University Children's Hospital over a period of six months from June 2021 to November 2021. The patients were subjected to detailed history taking and all the data was collected including the demographic data, symptoms, and signs, lab investigations, treatment received and samples were collected for microbiological diagnosis including blood and urine samples.

Finally, the data were fed to the computer and analyzed using IBM SPSS software package version 20.0. (Armonk, NY: IBM Corp) Qualitative data were described using number and percent. The Kolmogorov-Smirnov test was used to verify the normality of distribution Quantitative data were described using range (minimum and maximum), mean, standard deviation, median and interquartile range (IQR). Significance of the obtained results was judged at the 5% level.

Results

1536 febrile patients were admitted during the study period, among which 103 were eligible in the current study. The prevalence of UTI among febrile children was 6.7% (103/1536 * 100) There was increase in the resistant pattern among the isolated organisms [82.5% (n=85)] and low prevalence of susceptible organisms [17.5% (n=18)]. The MDR organisms were the most common isolated in 66.0% (n=68), followed by XDR in 15.6% (n=16) and PDR organisms were the least common isolated in only 1% (n=1) of cases. The most common organism isolated was E. Coli which was MDR in 74.5% (n=38), XDR in 9.8% (n=5), PDR in 1% (n=1) and susceptible in 13.7% (n=7). The second and third common organism were Klebsiella pneumoniae and Enterococcus which was MDR in 60.0%(n=18), XDR in 26.7% (n=8), and susceptible in 18%(n=4) and MDR in 80% (n=8), and 10% (n=1) in XDR and susceptible group respectively. 63% (n=65) of the isolated organisms in urine culture had a concomitant positive blood culture result (bacteremic UTI) compared to non-bacteremic UTI 37% (n=38).

Table (1): Distribution of the studied cases according to their demographic and clinical characteristics.

Demographic characteristics	No.	
Sex		
Male	47	45.6
Female	56	54.4
Age (months)		
<12	47	45.6
12 – 36	47	45.6
>36	9	8.8
Min. – Max.	1.0 – 72.0	
Clinical characteristics		
Fever	103	100.0
Vomiting	45	43.7
Diarrhea	9	8.7
Malodorous urine	15	14.6
Change urine color	14	13.6
Urine retention	7	6.8
Burning micturition	12	11.7
Degree of fever (Celsius)		
Min. – Max.	38.0 – 39.20	
Median (IQR)	38.30 (38.10–38.50)	
Meam±SD.	3.8.32±0.27	

Table (2): Distribution of organisms isolated from bacteremic and non-bacteremic UTI. (n=103).

Bacterial isolates	Bacteremic UTI (n=65) (63.0%)		Non–bacteremic UTI (n=38) (37.0%)	
	No.	%	No.	%
Klebsiella pneumoniae	21	32.3	8	21.1
ESBL-Klebsiella pneumoniae	0	0.0	2	5.3
E. coli	32	49.2	15	39.5
ESBL E. coli	0	0.0	4	10.5
Pseudomonas aeruginosa	3	4.6	3	7.9
Enterococcus	6	9.2	4	10.5
Citrobacter	2	3.1	0	0.0
Acinetobacter	1	1.5	0	0.0
Proteus	0	0.0	1	2.6
Enterobacter	0	0.0	1	2.6

Conclusion

The prevalence of UTI among febrile children was 6.7%. Gram-negative organisms were the most common cause of febrile UTI (90.3%), and gram-positive organisms were represented in 9.7% of cases. Among gram negative E. coli was the most common isolated organism, followed by Klebsiella pneumoniae, pseudomonas and Citrobacter. The prevalence of resistant organisms (82.5%) was so high compared to the prevalence of susceptible organisms (17.5%). The MDR organisms were the most common (66.0%) followed by XDR (15.6%) and PDR organisms were the least common (1%).

The Extended spectrum B-Lactam (ESBL) was detected in 5.8%. The most frequent ESBL pathogens were E-coli [7.8% (n=4)] and klebsiella pneumoniae [6.7% (n=2).