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Original Research

To study the incidence, risk factor, causative organisms associated with urinary tract infection and their antibiotic susceptibility pattern in children aged 1to 15 years in Bebe Nanki Mother and Child Care Centre, Department of Pediatrics, GMC Amritsar

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Abstract
Background: Urinary tract infections are among the most commonly encountered infections in the children.Both Gram-negative, Gram-positive bacteria andCandida species, can cause UTI. Emergence of resistance touropathogens to commonly used antibiotics for the treatment of UTI is a major challenge.
Objectives: To study the incidence, risk factors, causative organisms associated with UTI and their antimicrobial susceptibility pattern in children aged 1 to 15 years.
Methods: A one year hospital based cross sectional study was carried out in the department of Pediatrics BNMCC Hospital, in collaboration with the department of Microbiology, GMC, Amritsar. Urine sample was collected in a wide mouth, screw capped sterile container under aseptic precautions. The sample was processed in the microbiology laboratory as per the standard microbiological procedure.
Results: In our study 2736 urine culture were done, out of which 196 (7.16%)samples were found to have significant bacteriuria.Out of the 196 culture-positive cases, 77.55% had gram-negative isolates, 16.84% had gram-positive isolates, and 4.59% had yeast (Candida) isolates. The most common organism causing UTI was Escherichia coli, found in 73.02%cases.
Conclusion: The findings from this study necessitates the importance of integrating stewardship principles into routine clinical practice and ensuring the sustainability of effective antibiotic therapies for future generations.
(**key words :** urinary tract infection(UTI), Escherichia coli, Antibiotic resistance)

Introduction

Urinary tract infections (UTIs) rank high among infections experienced by children in both outpatient and inpatient hospital setting. The presence of bacteria in urine, along with certain clinical characteristics, or a culture showing more than 100,000 cfu/ml, regardless of symptoms, is what defines a urinary tract infection (UTI). Urinary tract infections (UTIs) encompass a wide spectrum of medical issues, from mild, asymptomatic bacterial infection to life threatening sepsis, which develops in kidneys.[1,2]

Although both Gram-negative and Gram-positive bacteria can cause UTIs, the majority of cases are caused by Gram-negative bacteria. This is because these agents are naturally present in the gut microbiota.[3]Uropathogens that lives in the digestive tract infect the periurethral space, then move on to colonise the urethra and eventually the bladder, causing a urinary tract infection(UTI).[4]

Eighty percent of children who get UTIs have Escherichia coli (E.coli), making it the most frequent uropathogen.[5]In order to evade host defence uropathogenic E.coli strains have unique

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characteristics, such as fimbriae that bind to the surface of uroepithelial cells.[6] Klebsiella, Proteus, Enterobacter and Enterococcus species are among the other prevalent uropathogens.[5,7] Patients with impaired immune systems may be susceptible to infections caused by fungus or low virulence pathogens.

Childhood urinary tract infections (UTIs) can be influenced by a number of factors. These include gender, age, fever, constipation,phimosis , insufficient toilet training, unstable bladder, diabetes, infrequent urination, history of antibiotic usage, vesicoureteral reflux, CAKUT and nitrates in urine.[8,9,10] Other risk factors identified in developing country studies include inadequate sanitation, thread worm infestation, and an impaired immune system.[11]

The management of UTI is increasingly complex due to rising antibiotic resistance among causative agents, which originally emerged in hospital settings but now also affect community-onset infections. This trend underscores the importance of understanding regional antibiotic resistance patterns to guide effective empirical therapy, especially in resource-limited settings lacking facilities for culture and susceptibility testing. The emergence of resistant strains among uropathogens continues to escalate, influenced by both mutational changes within bacterial genetic material and the acquisition of resistance genes from other bacteria .[12,13.]

Objectives

To study the incidence, risk factors, causative organisms associated with UTI and their antimicrobial susceptibility pattern in children aged 1 to 15 years.

Materials and Methods

A one year hospital based cross sectional study was carried out in the department of Pediatrics, BNMCC Hospital, in collaboration with the department of Microbiology, GMC, Amritsar. Urine sample was collected in a wide mouth, screw capped sterile container under aseptic precautions. The sample was sent to microbiology laboratory immediately in case of delay, sample was refrigerated at 4°C to 8°C. Then the sample was processed in the microbiology laboratory as per the standard microbiological procedure.

Inclusion Criteria - All pediatric in-patients and out-patients, with signs and symptoms of UTI, in the age group of 1-15 years.

Exclusion Criteria - Pediatric patients who have received antibiotics in the last two weeks. Children who are suffering from neurodevelopmental disorders and intellectual disability.

Patients fulfilling the inclusion criteria were evaluated by detailed history, sociodemographic profile, associated risk factors, clinical signs and symptoms. Appropriate investigations were assessed and recorded on a designed proforma.

Ethical issues: The study was approved by the institutional ethics committee of Government Medical College, Amritsar, India (Ref. No. 10791/D-26/2021 Batch) on 03-04-2023. Written informed consent was obtained from guardians/parents of the participating children.

Statistical analysis: The results of the different properties of bacteria were subjected to statistical analysis. The statistical analysis was carried out using Chi-Square Test (χ^2), Degree of Freedom (df) andP Value (Probability Value).The collected data was documented, compiled, tabulated and statistically analyzed using the Statistical Package for the Social Sciences (SPSS) version 26.0 (Copyright © SPSS Inc.).

Results

Table 1 shows that the age wise incidence of UTI in age group of 1 to 15 years. The graph 1 shows that the incidence of UTI in male paediatric population between 1 to 15 years of age.

Table 1: Age Wise Incidence Of Uti In Culture Positive Study Subjects

Age in Years	Number of Cases	Incidence (%)
1-5	105 (n = 1095)	9.58
≥5-10	66 (n = 930)	7.09
≥10-15	25 (n = 711)	3.51
Total	196 (n = 2736)	7.16

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Graph 1: Gender Wise Incidence Distribution In Culture Positive UTI

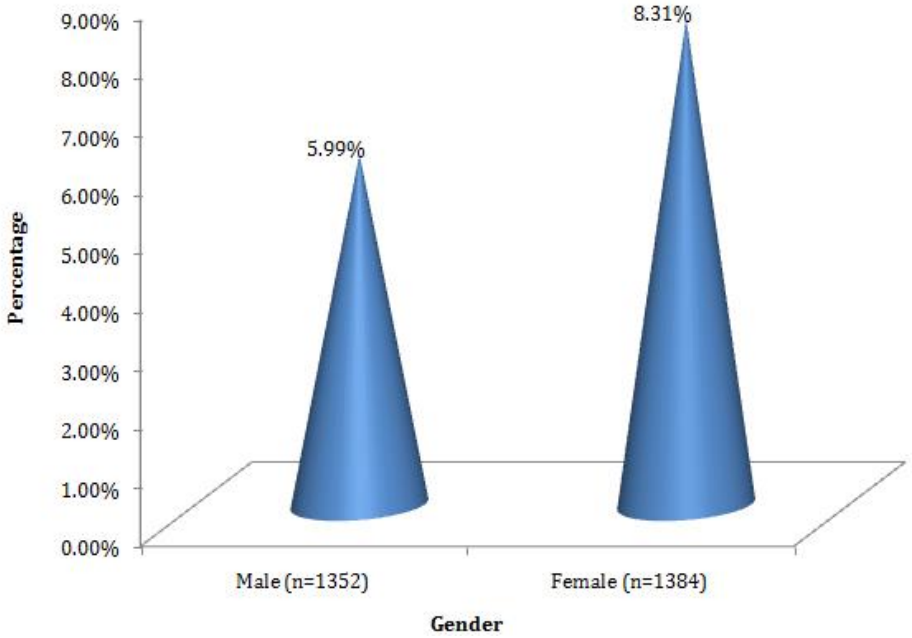

Table 2: Risk Factors Associated With Culture Positive Uti In Study Group

Risk Factors	No. of patients (n=196)	Percentage
Constipation	29	14.80
Phimosis	24	12.24
Nephrotic syndrome	19	9.69
Severe Acute malnutrition	17	8.67
Patient on steroid therapy	16	8.16
Diabetes	14	7.14
Anatomical abnormalities	7	3.57
HIV	0	0.00
No risk factors	70	65.71

X^2=162.57 ; DF=7; P-Value: 0.001

Table: 2 shows that the most common risk factor associated with UTI in our study.

Table 3: Organism Distribution Among Positive Isolates

Type of Organisms	No. of organisms (n=196)	Percentage
Gram positive	33	16.84%
Gram negative	152	77.55%
Yeast (candida)	9	4.59%

X^2=270.67; DF=2; P-Value: 0.02254

Table 3 shows, organism distribution among positive isolates

Table 4: Distribution Of Gram Negative Bacteria

Gram Negative Bacteria	No. of isolates (n=152)	Percentage
E.coli	111	73.02
Klebsiella spp.	33	21.71
Citrobacter spp.	2	1.32
Proteus spp.	4	2.63
Pseudomonas	2	1.32

X^2=343.127; DF=4; P-Value: 0.0009

Table 4 show distribution of gram negative bacteria in our study.

TABLE 5: Distribution Of Gram Positive Bacteria (N=35)

Gram Positive Bacteria	No. of isolates	Percentage
Enterococcus Spp.	16	45.71
MRCONS	13	37.14

DOI: 10.69605/ijlbpr_13.11.2024.135

MSCONS	3	8.57
MSSA	2	5.71
MRSA	1	2.86
Total	35	100.00

X^2=59.64; DF=4; P-Value: 0.003

Table 5 shows, distribution of gram-positive bacteria.

Table 6: Antibiogram Of Gram Negative Isolate Enterobacteriaceae (N=150)

	Sensitivity		Resistance	
Antibiotics	**No. of Cases**	**%age**	**No. of Cases**	**%age**
Ampicillin	11	7.33	139	92.67
Amoxycillin	14	9.33	133	90.67
Amoxy-clavulonate	15	10.00	135	90.00
Ampicillin-Sulbactam	31	20.67	119	79.33
Amikacin	141	94.00	9	6.00
Cefopodoxime	117	78.00	33	22.00
Ceftriaxone	89	59.33	61	40.67
Cefepime	108	72.00	42	28.00
Cotrimoxazole	14	9.33	136	90.67
Gentamycin	116	77.33	33	22.00
Imipenem	150	100.00	0	0.00
Norfloxacin	18	12.00	132	88.00
Nitrofurantoin	135	90.00	15	10.00
Polymixin-B/Colistin	33 (n=33)	100.00	0	0.00
Piperacillin/ Ticarcillin	32	21.33	118	78.66
Pipracillin-Tazobactam	72	48.00	78	52.00
Sulbactam-Ceftriaxone	108	72.00	42	28.00
Sulbactam-Ceftazidime	75	50.00	75	50.00

X^2=1154.00; DF=17; P-Value: 0.00001

Among Enterobacteriaceae family (i.e E. Coli ,klebsiella spp. , Citrobacter spp. and proteus species) imipenem (100%), amikacin (94%) and nitrofurantoin (90%) weresensitive drugs. Isolates showed highest resistance to ampicillin (92.66%), amoxycillin (90.67%) and cotrimoxazole(90.67%).

Table 7: Antibiogram Of E. Coli (N= 111)

	Sensitivity		Resistance	
Causative Organism	**No. of cases**	**Percentage**	**No. of cases**	**Percentage**
Ampicillin	5	4.51	106	95.49
Amoxycillin	6	5.41	105	94.59
Amoxy-clavulonate	11	9.91	100	90.09
Ampicillin-Sulbactam	25	22.52	86	77.48
Amikacin	106	95.49	5	4.50
Cefopodoxime	84	75.67	27	24.32
Ceftriaxone	67	60.36	44	39.64
Cefepime	77	69.37	34	30.63
Cotrimoxazole	8	7.21	103	92.79
Gentamycin	89	80.18	22	19.82
Imipenem	111	100.00	0	0.00
Norfloxacin	7	6.30	104	93.69
Nitrofurantoin	100	90.09	11	9.91
Polymixin-B/Colistin	26 (n=26)	100	0	0.00
Piperacillin/ Ticarcillin	22	19.82	89	80.18
Pipracillin-Tazobactam	47	42.34	64	57.66
Sulbactam-Ceftriaxone	81	72.97	30	27.03
Sulbactam-Ceftazidime	59	53.15	52	46.85

X^2=896.36; DF=17; ‘p’-Value: 0.00045

In our study E. coli showed highest sensitivity to imipenem (100%), amikacin (95.49%) and nitrofurantoin (90.09%). It showed highest resistance to ampicillin (95.49%), amoxycillin (94.59%) and norfloxacin (93.69%).

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TABLE 8: Antibiogram Of Enterococcus Spp. (N=16)

Antibiotics	Sensitivity		Resistance	
	No. of Cases	Percentage	No. of Cases	Percentage
Ampicillin	1	6.25	15	93.75
Ciprofloxacin	3	18.75	13	81.25
Gentamycin	14	87.50	2	12.50
Linezolid	16	100	0	0
Levofloxacin	10	62.50	6	37.50
Norfloxacin	1	6.25	15	93.75
Nitrofurantoin	15	93.75	1	6.25
Streptomycin	16	100	0	0
Tetracycline	13	81.25	3	18.75
Vancomycin	16	100	0	0

X^2=18.37; DF=9; P-Value: 0.0310

Table 8, Enterococcus spp. Showed highest sensitivity to linezolid (100%), streptomycin (100%) and vancomycin (100%). It showed highest resistance to ampicillin (93.75%) and norfloxacin (93.75%).

Discussion

In our study out of 196 patients, the maximum number of patients belonged to the age group of 1-5 years i.e. 54.1% . Findings in this research are similar to thoseDulal Kalita et al;[14] who also reported that majority of UTI cases were in the age group 1 to 5 years (57.3%)

Our study showed that maximum patients were females (58.7%), while males contributed (41.3%) of patients.This is almost in accordance with Kumar GV et al;[15]who have also reported that UTI was more common in girls(52.6%). Pouladfar G et al; in 2017,[16] also reported that frequency of UTI was significantly higher in girls (70.3%) than in boys.

In our study, most common risk factor associated with UTI is constipation which was seen in 29 cases (23%) followed by phimosis seen in 24 cases (19), poor hygiene in 19 (15%) cases, steroid therapy in 16 (13%) cases and diabetes in 14 (11%) cases. In a study done by Andrew J combs et al;[17]association of constipation and/or encopresis with specific lower urinary tract infections.Study done by Uwaezuoke et al;[18]also showed that UTI is more prevalent in malnourished children than in their well-nourished counterparts. Study done by Indurkar et al;[19]reported that about one-sixth of children with Nephrotic Syndrome had UTI.

Out of the 196 culture-positive cases, 152 (77.55%) had gram-negative isolates, 33 (16.84%) had gram-positive isolates, and 9 (4.59%) had yeast (Candida) isolates which is consistent with the study done by Jitendranath A et al;[20] in 2015, 170 out of 932 instances tested positive for the organism with 100 being female and 70 being male .Gram negative bacteria accounted for 85%,gram positive bacteria for 11.56% and fungal for 2.35%.

Out of the 152 gram-negative isolates, the most common organism causing UTI was E. coli, found in 111 (73.02%) cases. This was followed by Klebsiella spp., present in 33 (21.71%) cases. Proteus spp. was identified in 4 (2.63%) cases, while Citrobacter spp. and Pseudomonas were each seen in 2 (1.32%) cases.

This study is in accordance with study done by Pouladfar G et al in 2017,[16] in which out of all the pathogens that were found , Escherichia coli (E.coli) accounts for 51.5%, Klebsiella spp. for 16.8% and Enterococcus spp. for 9.9%. In a study done by Bitew et al;[21] in 79.6% of cases, Escherichia coli and Klebsiella pneumoniae were the micro-organism responsible for infection. In a study by Fenta et al.[22]

In our study E. coli showed highest sensitivity to imipenem (100%), amikacin (95.49%) and nitrofurantoin (90.09%). It showed highest resistance to ampicillin (95.49%), amoxycillin (94.59%) and norfloxacin (93.69%).

In study done by Gessese et al; [23] E. coli isolates showed high resistance to ampicillin (62%) and gentamicin (62%). In a study by Patel et al; [91]E. coli was most susceptible to meropenem (91.89%) and imipenem (91.69%). Susceptibility of E. coli to nitrofurantoin was 72.33%.

In our study, Enterococcus spp. showed highest sensitivity to linezolid (100%), streptomycin (100%) and vancomycin (100%). It showed highest resistance to ampicillin (93.75%) and norfloxacin (93.75%) which is similar to the study done by Kumar et al;[24] in which all enterococcus spps were sensitiveto linezolid (100%) and vancomycin (100%).

Conclusion

This study underscores the importance of tailored approaches considering local epidemiological trends and antibiotic resistance patterns.Escherichia coli, the predominant pathogen identified, exhibited concerning levels of resistance to commonly prescribed antibiotics. By limiting the use of broad-spectrum antibiotics like third-generation cephalosporins, which showed moderate resistance patterns in this study, clinicians can mitigate selective pressure that drives resistance development among UTI pathogens.The findings from this study underscore the importance of integrating stewardship principles into routine clinical practice, emphasizing personalized treatment strategies based on local resistance patterns and ensuring the sustainability of effective antibiotic therapies for future generations.

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