

Etiology and antimicrobial resistance in pediatric urinary tract infections: a 10-year retrospective study in Hohhot, China

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Abstract

Introduction: Urinary tract infections (UTIs) are among the most common bacterial infections in children, yet regional pathogen distribution and antimicrobial resistance patterns remain understudied in resource-limited settings. This study aimed to characterize UTI pathogens and their resistance profiles in Hohhot, China, including molecular analysis of the *YadC* gene in *Escherichia coli* (*E. coli*).

Methodology: This was a retrospective analysis of 550 pediatric UTI cases from December 2014 to December 2024. Urine cultures, antimicrobial susceptibility testing, and *YadC* gene detection (polymerase chain reaction, PCR) for 46 *E. coli* isolates were performed in 2023. Statistical analysis used χ^2 tests or Fisher's exact tests (SPSS 27.0; $p < 0.05$).

Results: Among 312 culture-positive cases (56.7%), Gram-negative bacteria (64.1%, predominantly *E. coli* [41.7%]), Gram-positive bacteria (35.3%, mainly *Enterococcus faecium* (*E. faecium*) [20.2%]), and 2 yeast isolates (*Candida tropicalis* and *Candida albicans*; 1 strain each; 0.6%) were identified. *YadC*-positive *E. coli* isolates exhibited a significantly higher rate of multidrug resistance compared to *YadC*-negative isolates (83.3% vs. 37.5%, $p = 0.002$). Resistance rates exceeded 70% for penicillin and erythromycin in *E. faecium*, while *E. coli* showed high resistance to ampicillin/sulbactam (73.1%) and third-generation cephalosporins. Nitrofurantoin and β -lactam/ β -lactamase inhibitors (e.g., ampicillin/sulbactam) remained effective for *E. faecalis* isolates.

Conclusions: *E. coli* remains the predominant UTI pathogen in Hohhot. The high *YadC* prevalence (65.2%) and its association with cephalosporin resistance indicate its surveillance potential. Empirical therapy should favor agents like ceftazidime, while managing complicated UTIs requires integrating imaging and susceptibility testing to curb resistance and prevent renal injury.

Key words: children; urinary tract infection; pathogens; antimicrobial resistance; *YadC* gene.

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Introduction

Pediatric urinary tract infection (UTI), characterized by pathogenic invasion and proliferation within the urinary tract with subsequent mucosal or tissue damage, represents one of the most prevalent bacterial infections in children [1–3]. Epidemiological data indicate that UTIs account for 5–14% of annual pediatric emergency department visits, with up to 8% of children experiencing at least one UTI episode between 1 month and 11 years of age. Notably, recurrent infections occur in up to 30% of infants and children within the first 6–12 months following initial diagnosis [4,5].

Clinically, UTIs are classified as acute or chronic based on disease duration [6]. Acute presentations in infants and young children predominantly manifest systemic symptoms, with unexplained fever being the primary presenting feature (76–89%), often accompanied by feeding refusal, vomiting, or diarrhea. Older children typically exhibit fever, chills, and abdominal pain (68–82%) alongside characteristic urinary symptoms including dysuria, frequency, and

urgency [7,8]. Chronic UTIs are associated with systemic complications such as anemia, failure to thrive, growth retardation, and renal insufficiency [9].

While most cases demonstrate favorable prognosis with appropriate treatment, 15–20% of patients experience recurrent infections. Potential complications include renal scarring (8–15% of recurrent cases), acute kidney injury, and uremia. Long-term sequelae may encompass hypertension (3–5 fold increased risk) and end-stage renal disease in adulthood [10]. These clinical implications underscore the critical importance of early recognition and accurate diagnosis.

This retrospective study analyzed microbial distribution and antimicrobial resistance patterns among 550 pediatric UTI cases in Hohhot, China, over a 10-year period from December 2014 to December 2024. The findings aim to optimize empirical antibiotic selection, enhance therapeutic efficacy, and mitigate antimicrobial resistance development in clinical practice. This study includes one of the largest contemporary datasets from Northwestern China, and addresses the critical knowledge gap in region-specific

antimicrobial resistance profiles of pediatric UTIs, providing pivotal evidence for refining local antimicrobial stewardship programs. Furthermore, the analysis was extended to assess the prevalence of the *YadC* gene among isolated strains and its potential association with antimicrobial resistance in *E. coli*.

Methodology

Study design and participants

This retrospective analysis included 550 pediatric patients with clinically confirmed UTIs treated at the Affiliated Hospital of Inner Mongolia Medical University between December 2014 and December 2024. The cohort comprised 211 males (38.4%) and 339 females (61.6%), with ages ranging from 1 month to 16 years (median age: 3 years).

Microbiological and imaging analysis

All pediatric patients met the diagnostic criteria for urinary tract infection specified in Zhu Futang's Practical Pediatrics, defined as: (i) centrifuged urine sediment showing > 5 white blood cells per high-power field (HPF) or presence of clinically compatible urinary symptoms; and (ii) midstream urine culture demonstrating > 10⁵ CFU/mL for Gram-negative bacteria, and >10⁴ CFU/mL for Gram-positive bacteria [11]. For patients with multiple hospital admissions or repeated urine specimens, only the initial positive culture was included to ensure data independence. Clinical data were retrospectively collected from the hospital's electronic medical records, including gender, age, major clinical manifestations, urine culture results, and urinary tract imaging examinations. The imaging studies comprised urinary tract ultrasonography (US), voiding cystourethrography (VCUG), magnetic resonance urography (MRU), and technetium-99m dimercaptosuccinic acid (DMSA) scan [12]. All the aforementioned imaging studies were interpreted by pediatric radiologists using standardized criteria.

Table 1B. Demographic and clinical characteristics by age group.

Group	n	Gender		Fever n (%)	Main clinical manifestations			
		Male n (%)	Female n (%)		Urinary tract irritation n (%)	Atypical manifestations n (%)	Unobvious n (%)	Comorbidities n (%)
<1 year	187	106 (56.7)	81 (43.3)	122 (65.2)	10 (5.3)	26 (13.9)	23 (12.3)	6 (3.2)
1–3 years	96	35 (36.5)	61 (63.5)	20 (20.8)	33 (34.4)	9 (9.4)	19 (19.8)	15 (15.6)
4–7 years	151	42 (27.8)	109 (72.2)	29 (19.2)	61 (40.4)	20 (13.2)	26 (17.2)	15 (9.9)
> 8 years	116	28 (24.1)	88 (75.9)	36 (31.0)	34 (29.3)	15 (12.9)	29 (25.0)	2 (1.7)
χ ² value		42.561				136.023		
p value		< 0.001*				< 0.001*		

* indicates significant differences (*p* < 0.05).

Table 1A. Imaging findings and complications by age group.

Group	Imaging findings	
	Normal n (%)	Abnormal n (%)
< 1 year	138 (73.8)	49 (26.2)
1–3 years	66 (68.8)	30 (31.3)
4–7 years	91 (60.3)	60 (39.7)
> 8 years	71 (61.2)	45 (38.8)
χ ² value	8.787	
p value	0.032*	

* indicates significant differences (*p* < 0.05).

Bacterial identification and antibiotic susceptibility testing

Bacterial identification and antibiotic susceptibility testing were performed using the VITEK-2 Compact fully automated microbial analysis system (bioMérieux, Marcy-l'Étoile, France) and the disk diffusion method. Procedures and interpretation of susceptibility results followed the standards established by the Clinical and Laboratory Standards Institute (CLSI) [13].

YadC gene detection

Polymerase chain reaction (PCR) amplification for the *YadC* gene was performed on 46 randomly selected *E. coli* isolates from a total of 104 collected in the year 2023, using primers (F-5'-ATGTGCAGYACCAGTAARGT -3', R-5'-TGGGTRAARTARGTSACCAGA -3') [14].

Statistical analysis

Statistical analyses were performed using SPSS software (version 27.0; IBM Corp., Armonk, NY, USA). Categorical variables were expressed as percentages and analyzed through Chi-square tests or Fisher's exact tests as appropriate. A two-tailed *α* level of 0.05 was applied, with *p* < 0.05 indicating statistical significance [15,16].

Results

Imaging

Among the 550 pediatric patients, 366 exhibited imaging abnormalities, of whom 248 underwent DMSA scan with a positive detection rate of 45.1%. Among the imaging abnormalities, 61 cases were complicated by

hydronephrosis/hydroureter, 6 by vesicoureteral reflux, 4 by renal calculi, 4 by duplex kidney, 1 by solitary kidney, and 1 by postoperative ureteral stenosis. Imaging abnormalities were common across all groups but were significantly more prevalent in younger patients ($p = 0.032$; Table 1A).

Clinical manifestations

Among the major clinical manifestations, fever was the predominant presentation in infants, whereas urinary tract irritation symptoms were more prominent in older children. Atypical manifestations such as abdominal pain and lumbago were more prominent in younger children (Table 1B).

Pathogen distribution

Urine cultures identified pathogenic organisms in 312 cases (56.7%), yielding 312 isolates: Gram-positive bacteria ($n = 110$, 35.3%), Gram-negative bacteria ($n = 200$, 64.1%), and fungi ($n = 2$, 0.6%).

The Gram-positive spectrum was dominated by *E. faecium* (42.7%, $n = 47$), followed by *Enterococcus faecalis* (*E. faecalis*; 23.6%, $n = 26$), *Staphylococcus epidermidis* (*S. epidermidis*; 12.7%, $n = 14$), and

Enterococcus gallinarum (8.2%, $n = 9$). Among Gram-negative isolates, *E. coli* predominated (65.0%, $n = 130$), with subsequent prevalence of *Klebsiella pneumoniae* (*K. pneumoniae*; 18.0%, $n = 36$), *Proteus mirabilis* (*P. mirabilis*; 7.5%, $n = 15$), and *Enterobacter cloacae* (4.0%, $n = 8$). Fungal isolates comprised *Candida tropicalis* ($n = 1$) and *Candida albicans* ($n = 1$).

Notably, children with radiological abnormalities exhibited higher detection rates of four key pathogens: *E. coli* (20.7% of total cases), *E. faecium* (10.9%), *E. faecalis* (4.9%), and *K. pneumoniae* (2.7%).

Antimicrobial resistance profiles

Resistance patterns of the three most prevalent pathogens from each bacterial category revealed significant variations:

Gram-positive isolates

E. faecium demonstrated high resistance rates to penicillin (82.1%), erythromycin (78.3%), and macrolides (75.6%). *E. faecalis* showed elevated tetracycline resistance (64.7%) but maintained susceptibility to β -lactam/ β -lactamase inhibitors

Table 2. Antimicrobial resistance rates (%) of Gram-positive bacteria.

Antimicrobial agents	<i>Enterococcus faecium</i> (n = 63)	<i>Enterococcus faecalis</i> (n = 23)	<i>Staphylococcus epidermidis</i> (n = 5)
Penicillin	82.5	65.2	80.0
Ampicillin/sulbactam	85.7	8.7	0
Vancomycin	1.6	0	0
Nitrofurantoin	23.8	4.3	0
Levofloxacin	71.4	47.8	40.0
Ciprofloxacin	76.2	60.9	20.0
Tetracycline	57.1	69.6	0
Gentamicin	57.1	39.1	0
Clindamycin	17.5	0	60.0
Amoxicillin/clavulanate	3.2	4.3	0
Erythromycin	77.8	60.9	60.0
Moxifloxacin	7.9	0	0
Oxacillin	1.6	0	60.0

Table 3. Antimicrobial resistance rates (%) of Gram-negative bacteria.

Antimicrobial Agents	<i>Escherichia coli</i> (n = 130)	<i>Klebsiella pneumoniae</i> (n = 14)	<i>Proteus mirabilis</i> (n = 13)
Tobramycin	9.2	7.1	0
Gentamicin	34.6	21.4	0
Aztreonam	18.5	28.6	0
Ampicillin/sulbactam	73.1	35.7	15.4
Ceftriaxone	39.2	21.4	7.7
Cefepime	6.9	7.1	84.6
Cefazolin	35.4	21.4	7.7
Ceftazidime	11.5	7.1	0
Cefuroxime	29.2	21.4	15.4
Cefoperazone/sulbactam	20.0	14.3	0
Trimethoprim/sulfamethoxazole	48.5	28.6	23.1
Piperacillin/tazobactam	3.1	7.1	7.7
Levofloxacin	36.2	14.3	7.7
Nitrofurantoin	3.1	14.3	38.5
Ciprofloxacin	42.3	28.6	15.4

Table 4. Association between *YadC* gene carriage and multidrug resistance in *Escherichia coli* isolates.

Variable	<i>YadC</i> (+) (n = 30)	<i>YadC</i> (-) (n = 16)	<i>p</i> value
Multidrug-resistant (MDR)	25 (83.3%)	6 (37.5%)	0.002*
Non-multidrug-resistant (Non-MDR)	5 (16.7%)	10 (62.5%)	

* χ^2 test; $p < 0.01$.

(93.1%) and nitrofurantoin (89.5%). *S. epidermidis* exhibited > 90% susceptibility to β -lactamase-resistant penicillins, nitrofurantoin, tetracycline, and vancomycin.

Gram-negative isolates

E. coli displayed substantial resistance to ampicillin-sulbactam (68.2%), quinolones (57.8–62.4%), and third-generation cephalosporins (49.3–54.1%). *K. pneumoniae* showed resistance patterns exceeding 50% for ampicillin-sulbactam, aminoglycosides, third-generation cephalosporins, and quinolones. Remarkably, *P. mirabilis* maintained > 80% susceptibility to most β -lactams and aminoglycosides, yet demonstrated 84.6% resistance to cefepime (Tables 2 and 3).

YadC gene and resistance in *E. coli*

Among the 46 *E. coli* isolates tested for *YadC* (2023), 30 (65.2%) were *YadC*-positive. To investigate the association between *YadC* gene carriage and the multidrug resistance (MDR) phenotype, all 46 *E. coli* isolates were categorized as MDR or non-MDR based on their resistance profiles to a panel of 5 antimicrobial agents: cefepime, cefoperazone, ceftriaxone, ceftazidime, and cefotaxime. In this study, MDR was defined as resistance to 3 or more of the aforementioned antimicrobial classes. A significant association was observed between *YadC* carriage and multidrug resistance in *Escherichia coli*, with *YadC*-positive isolates demonstrating markedly higher resistance rates than *YadC*-negative isolates (83.3% vs. 37.5%, $p = 0.002$; Table 4).

Discussion

Epidemiological and microbiological characteristics

UTI constitutes a predominant bacterial infection in the pediatric population. The cohort in this study revealed a striking age distribution, with infants under 1 year representing the largest subgroup, where diaper-associated contamination and congenital urinary tract anomalies served as primary risk factors. The female predominance observed in children > 1 year aligns with established anatomical predisposition—the shorter urethral length in females facilitates ascending bacterial colonization [17].

Clinical manifestations

Regarding the major clinical manifestations, fever was the most common presentation in the infant group. This underscores the need for pediatricians to maintain a high index of suspicion for UTI and perform urinalysis in infants and young children presenting with fever of unknown origin, to avoid missed diagnosis or misdiagnosis [18]. As age increased, the proportion of females among children with UTI also rose. Interestingly, fever remained the most frequent clinical manifestation in adolescents, differing from previous studies. This discrepancy may be attributable to the high prevalence of concurrent respiratory tract infections (RTIs) or pneumonia among older children in this cohort [19–21]. Consequently, when older children present with respiratory illnesses accompanied by fever, urinalysis should be considered when clinically indicated to exclude concurrent UTI.

Diagnostic and pathogenic profile

Urine culture is the gold standard for the diagnosis of UTI [22]. In this study, 312 specimens were positive, yielding a positive culture rate of 56.7%, consistent with reported urine culture positivity rates from other regions in China [23]. Gram-negative bacteria predominated among the isolated pathogens (64.1%), with *E. coli* exhibiting the highest detection rate. This confirms *E. coli* as the primary pathogen causing pediatric UTIs in this region, aligning with prior domestic studies, though contrasting with international reports where *E. coli* alone accounts for 80–90% of pediatric UTIs [24,25].

As a major commensal in the gut, *E. coli* can cause ascending infection via the urethra following inadequate perineal hygiene after defecation. Furthermore, the fimbriae and pili on its surface facilitate adhesion to the urothelium and biofilm formation. This biofilm protects the bacteria from urinary flushing and impedes the bactericidal effects of host-derived antimicrobial peptides, antibiotics, and immune cells [24,26].

Among Gram-positive bacteria, *E. faecium* and *E. faecalis* were prominent, consistent with findings reported by Zheng *et al.* [27]. As opportunistic pathogens, these enterococci not only produce various toxins but also exhibit high intrinsic resistance and complex resistance mechanisms, significantly

increasing the risk of enterococcal infections in children [28]. Notably, the detection rate of *E. faecium* was second only to *E. coli*, warranting vigilance against potential specimen contamination due to improper urine collection techniques. Fungal infections were rare (0.4%), possibly because the study did not include high-risk populations such as immunocompromised individuals or those with long-term catheterization.

Molecular insights into *E. coli* resistance

YadC was detected in 65.2% of *E. coli* isolates. The prevalence of multidrug resistance was significantly higher among *YadC*-positive isolates compared to *YadC*-negative isolates. Due to the adhesin of *Yad* fimbriae in *E. coli*, *YadC* is a crucial factor facilitating adhesion to and invasion of host cells. Bacteria utilize adhesins to attach to the urothelium, resisting urinary clearance and forming biofilms. *E. coli* biofilm antibiotic resistance mechanisms include: limited drug penetration—the extracellular polymeric substance (EPS) matrix acts as a barrier, impeding antibiotic diffusion; enhanced horizontal gene transfer—plasmid-mediated resistance spread is increased within biofilms; reduced metabolic activity—nutrient and oxygen limitation slow growth, lowering susceptibility to growth-dependent antibiotics; and efflux pump upregulation—membrane transporters expel multiple antibiotic classes, promoting multidrug resistance [29,30]. This gene serves as a potential clinical surveillance marker. Where indicated, novel therapeutic approaches for urinary tract infections may include D-xylose, which acts as a binding agent for *YadC*, and inhibitors targeting its receptor ANXA2 on bladder epithelial cells [31].

Antimicrobial susceptibility patterns

Antimicrobial susceptibility testing revealed concerning resistance rates: in Gram-positive isolates, resistance to penicillin and erythromycin exceeded 70% in *E. faecium*, while *E. faecalis* showed high resistance to tetracycline (69.6%), indicating these agents should be avoided in empirical therapy. Notably, penicillin/ β -lactamase inhibitor combinations (e.g., amoxicillin-clavulanate) and nitrofurantoin demonstrated good activity against enterococci and represent preferred options. *E. faecium* exhibited higher resistance rates than *E. faecalis* to ampicillin, quinolones, erythromycin, and nitrofurantoin; a pattern similar to findings in adult UTI studies [32,33].

Among Gram-negative bacteria, *E. coli* exhibited high resistance to ampicillin-sulbactam (73.1%), with significantly increased resistance to third-generation

cephalosporins and quinolones. This trend may be associated with the prevalence of extended-spectrum β -lactamase (ESBL)-producing strains and the horizontal transfer of resistance genes. Notably, the rising incidence of macrolide-nonresponsive *Mycoplasma pneumoniae* pneumonia in recent years has substantially increased the utilization of levofloxacin as first-line therapy. *K. pneumoniae* displayed a similar resistance trend, albeit slightly lower than *E. coli*. Notably, *P. mirabilis* exhibited a high resistance rate to cefepime (84.6%), emphasizing the need to tailor therapy based on susceptibility results, prioritizing highly active β -lactams or aminoglycosides.

Imaging evaluation

Common imaging modalities for pediatric UTI include US, VCUG, MRU, and DMSA scan [34]. Imaging abnormalities were detected in 66.5% of children, with hydronephrosis/ureteral dilation being the most frequent finding (61 cases), suggesting that congenital urinary tract malformations or obstruction were significant predisposing factors for UTI. Importantly, approximately 45.1% of children with imaging abnormalities had positive findings on DMSA scans; these children require long-term follow-up to assess renal functional progression. *E. coli* was the predominant pathogen isolated from children with imaging abnormalities, consistent with findings reported from Shantou [20]. Therefore, routine screening for urinary tract malformations is clinically recommended for children with complicated UTIs, and empirical therapy targeting *E. coli* is justified.

Conclusions

E. coli remains the predominant pathogen causing pediatric UTIs in Hohhot. Clinicians should maintain vigilance for possible concurrent UTI in older children presenting with RTIs accompanied by fever, and particularly in infants with unexplained fever. Penicillin/ β -lactamase inhibitor combinations (e.g., amoxicillin-clavulanate) are recommended as preferred empirical therapy for uncomplicated infections.

In the case of children with complicated UTIs, management should integrate imaging assessments and individualized antimicrobial susceptibility testing to mitigate antibiotic resistance risks and reduce long-term renal injury incidence. Notably, this preliminary analysis revealed a high prevalence of the *YadC* gene (65.2%) in local *E. coli* isolates, and the prevalence of multidrug resistance was significantly higher in *YadC*-positive strains than in *YadC*-negative strains. Future large-scale studies should validate whether *YadC* serves

as a potential biomarker for resistance surveillance.

Additionally, clinical protocols should emphasize urinary tract malformation screening and long-term follow-up to optimize patient outcomes. This study's limitations include its single-center retrospective design; expanding to multicenter cohorts would better elucidate resistance mechanisms linking anatomical abnormalities, molecular markers like *YadC*, and pathogen virulence.

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Ethics approval and consent to participate

This study was conducted with approval from the Ethics Committee of Affiliated Hospital of Inner Mongolia Medical University. This study was conducted in accordance with the Declaration of Helsinki.

Availability of data and materials

The datasets used and/or analyzed during the current study are available from the corresponding author on reasonable request. The materials described in the manuscript, including all relevant raw data, will be freely available to any scientist wishing to use them for non-commercial purposes, without breaching participant confidentiality.

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Authors' contributions

Data acquisition: R-XL, XZ; analysis and interpretation of the data: R-XL, Y-YG; statistical analysis: R-XL, XZ; obtaining funding: Y-YG; manuscript writing: R-XL; critical revision of the manuscript for intellectual content: Y-YG, YZ, QZ. All authors read and approved the final draft.

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Conflict of interest

No conflict of interest is declared.

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