Etiological profile and antimicrobial resistance of urinary tract infections in Western Santa Catarina

Perfil etiológico e resistência antimicrobiana das infecções do trato urinário no oeste catarinense

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Abstract

Introduction: Urinary tract infections (UTIs) are among the most frequent bacterial infections, with high prevalence in women and the elderly. The growing antimicrobial resistance hampers treatment, making it essential to monitor the main etiological agents and their sensitivity profiles. This study aimed to retrospectively analyze the etiology of UTIs and antimicrobial resistance patterns in a municipality in Western Santa Catarina, contributing to more effective therapeutic strategies. **Methodology:** This is a retrospective, cross-sectional, and analytical study based on the analysis of 22,274 urine cultures performed between 2018 and 2024 in a clinical laboratory in Concórdia-SC. Samples with ≥100,000 CFU/mL were considered positive, following CLSI guidelines until 2019 and BrCAST from 2020 onwards. Bacterial identification was performed using selective media and mass spectrometry (Maldi-TOF), and antimicrobial susceptibility testing was done by the disk diffusion method. **Results:** Of the 22,274 samples, 1,613 (7.2%) were positive, with a predominance in women (92.87%). *Escherichia coli* was the main pathogen (78.2%), followed by *Proteus mirabilis* (3.94%) and *Enterococcus* spp. (3.08%). High resistance rates were observed for ampicillin (28.08%), sulfamethoxazole + trimethoprim (16.15%), and quinolones. Fosfomycin and nitrofurantoin maintained good efficacy. **Conclusion:** The findings highlight the need for continuous antimicrobial resistance surveillance and rational antibiotic use. Control strategies, including education on appropriate antimicrobial use and strengthened infection prevention practices, are essential to preserve treatment efficacy.

Keywords: Urinary tract infections; Drug resistance, Microbial; *Escherichia coli*.

Resumo

Introdução: As infecções do trato urinário (ITUs) são uma das infecções bacterianas mais frequentes, com alta prevalência entre mulheres e idosos. A resistência antimicrobiana crescente dificulta o tratamento, tornando essencial o monitoramento dos principais agentes etiológicos e de seus perfis de sensibilidade. Este estudo teve como objetivo analisar retrospectivamente a etiologia das ITUs e os padrões de resistência antimicrobiana em um município do Oeste Catarinense, contribuindo para uma abordagem terapêutica mais eficaz. **Metodologia:** Estudo retrospectivo, transversal e analítico, com análise de 22.274 uroculturas realizadas entre 2018 e 2024 em um laboratório clínico de Concórdia–SC. Consideraram-se positivas as amostras com ≥100.000 UFC/mL, seguindo diretrizes do CLSI até 2019 e do BrCAST a partir de 2020. A identificação bacteriana foi feita por cultivo em meios seletivos e por espectrometria de massas (MALDI-TOF); a sensibilidade antimicrobiana, por disco-difusão. **Resultados:** Dos 22.274 exames, 1.613 (7,2%) foram positivos, com predominância em mulheres (92,87%). *Escherichia coli* foi o principal agente (78,2%), seguido por *Proteus mirabilis* (3,94%) e *Enterococcus* spp. (3,08%). Observou-se elevada resistência à ampicilina (28,08%), ao sulfametoxazol + trimetoprima (16,15%) e às quinolonas. Fosfomicina e nitrofurantoína mantiveram boa eficácia. **Conclusão:** Os resultados reforçam a importância do monitoramento contínuo da resistência antimicrobiana e do uso racional de antibióticos. Estratégias de controle, como educação para uso adequado de antimicrobianos e práticas de prevenção de infecções, são fundamentais para preservar a eficácia terapêutica.

Palavras-chave: Infecções Urinárias; Resistência Microbiana a Medicamentos; *Escherichia coli*.

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INTRODUCTION

Urinary tract infections (UTIs) are recognized as the most common bacterial infections in both outpatient and hospital settings, representing a significant cause of morbidity, especially among women, the elderly, and patients with chronic comorbidities.[1] It is estimated that up to 60% of women will experience at least one episode of UTI during their lifetime, and in most cases, treatment is empirical, without complementary laboratory testing.[2]

The primary route of contamination in UTIs is ascending, where microorganisms from the intestinal microbiota colonize the urethra and subsequently reach the bladder. When treatment is inadequate or the infection persists, it may ascend to the ureters and kidneys, resulting in pyelonephritis, a potentially serious condition.[3] In this scenario, the correct identification of the etiological agent and its sensitivity profile is essential to ensure therapeutic efficacy and prevent recurrence.

The most frequent etiological agent of UTIs is *Escherichia coli*, responsible for 70–90% of uncomplicated urinary tract infections. However, other microorganisms may also be involved, such as *Klebsiella pneumoniae*, *Proteus mirabilis*, *Enterococcus faecalis*, *Pseudomonas aeruginosa*, and *Staphylococcus saprophyticus*, especially in nosocomial infections, in patients with catheters, or with a history of recurrent infections.[4,5]

In recent years, the growing bacterial resistance to antimicrobials has become a global public health concern, directly impacting the therapeutic success of UTIs. This phenomenon is driven by the indiscriminate and inappropriate use of antibiotics, both in clinical practice and through self-medication.[6] Resistance can limit treatment options and lead to longer hospital stays, clinical complications, and increased healthcare costs.[7,8]

Among the resistance mechanisms, β-lactamase production stands out, such as extended-spectrum β-lactamases (ESBL), and the presence of efflux pumps, which reduce the intracellular concentration of antimicrobials. Additionally, mutations in regulatory genes can confer resistance to quinolones, aminoglycosides, and sulfamethoxazole + trimethoprim, which are widely used in the treatment of UTIs.[9,10]

Given this context, local epidemiological studies are essential for monitoring antimicrobial resistance and supporting more effective and safer therapeutic protocols. Sensitivity profiles may vary according to geographic region, population habits, and implemented health policies.[11]

Therefore, this study aims to analyze the etiological profile of UTIs and the antimicrobial resistance patterns of bacteria isolated from urine cultures performed at a clinical laboratory in the Western region of Santa Catarina between 2018 and 2024, contributing to the updating of therapeutic guidelines and the rational use of antimicrobials in the regional context.

METHODOLOGY

Study design and period

This is a cross-sectional, retrospective, and analytical study based on laboratory data from urine cultures processed between January 2018 and March 2024 at a clinical analysis laboratory located in the municipality of Concórdia, Santa Catarina, Brazil.

Sample collection and processing

All urine samples collected either spontaneously or by bladder catheterization were included, provided they were accompanied by the minimum required clinical information and showed significant growth in the urine culture. Cultures were considered positive when presenting counts $\geq 10^5$ colony-forming units per milliliter (CFU/mL) for the general population, according to the criteria established by the Clinical and Laboratory Standards Institute (CLSI) guidelines[11] up to 2019, and from 2020 onwards, by the Brazilian Committee on Antimicrobial Susceptibility Testing (BrCAST).[12]

Samples were plated on selective chromogenic media for uropathogen identification and incubated at 35 ± 2 °C for 18 to 24 hours. Microorganism identification was performed by mass spectrometry using the Matrix-Assisted Laser Desorption/Ionization-Time of Flight (MALDI-TOF) technique.

Antimicrobial Susceptibility Testing

Susceptibility testing was performed using the disk diffusion method on Mueller-Hinton agar, following standardized protocols from CLSI[11] and BrCAST.[12] The antimicrobials tested included the most commonly used agents for urinary infections in clinical practice, such as ampicillin, ampicillin-sulbactam, amoxicillin, amoxicillin + clavulanate, piperacillin-tazobactam, benzylpenicillin, cephalexin, cefaclor, cefazolin, cefuroxime, cefotaxime, ceftriaxone, cefepime, aztreonam, ciprofloxacin, norfloxacin, levofloxacin, nitrofurantoin, fosfomycin, gentamicin, amikacin, and sulfamethoxazole + trimethoprim, among others, depending on availability and clinical indication.

Results were classified as "susceptible," "intermediate," or "resistant" and later analyzed based on the resistance rates of the isolated microorganisms.

Statistical analysis

Data were tabulated in Microsoft Excel spreadsheets and analyzed using descriptive statistics, with calculations of absolute and relative frequencies. Proportion comparison tests were applied when appropriate, with a significance level of 5% ($p<0.05$). The analysis was conducted using GraphPad Prism software.

Ethical considerations

The study was submitted to and approved by the Research Ethics Committee of the University of Contestado (UNC), under opinion no. 7.108.400, in accordance with Resolution no. 466/2012 of the Brazilian National Health Council and the principles of the Declaration of Helsinki.

RESULTS AND DISCUSSION

Between January 2018 and March 2024, a total of 22,274 urine samples were analyzed. Among these, 1,613 showed significant bacterial growth (≥10^5 CFU/mL), resulting in a positivity rate of 7.2%. Most of the positive samples came from female patients (n = 1,498; 92.87%), with the highest concentration of cases in the age groups of 18 to 40 years (32.5%) and over 60 years (28.1%).

Urinary tract infections (UTIs) are among the leading causes of medical consultations and antimicrobial prescriptions in primary care and emergency services. The high prevalence in women observed in this study (92.87%) is consistent with previous data, which attribute this pattern to the shorter length of the female urethra, its proximity to the anus, and hormonal variations that affect the local microbiota.[14,16]

Regarding the identified etiological agents, *Escherichia coli* was responsible for 1,262 (78.2%) of the infections. *Proteus mirabilis* ranked second (n = 63; 3.94%), followed by *Enterococcus* spp. (n = 49; 3.08%), *Klebsiella pneumoniae* (n = 42; 2.60%), and *Staphylococcus saprophyticus* (n = 36; 2.23%). Less prevalent microorganisms included *Pseudomonas aeruginosa*, *Citrobacter freundii*, and *Morganella morganii*, collectively accounting for approximately 9.85% of the isolates. *Escherichia coli* was consistently the main etiological agent isolated (78.2%), confirming its predominant role in both community-acquired and nosocomial UTIs. These findings are in agreement with national and international studies, which report prevalence rates ranging from 70% to 90% for this bacterium.[3,15-19] Table 1 presents the distribution of the main isolated uropathogens.

Table 1

Microorganisms isolated and their relative occurrence in positive urine cultures

Microorganisms	%
Escherichia coli	78.2
Proteus mirabilis	3.94
Enterococcus spp.	3.08
Staphylococcus saprophyticus	3.07
Enterobacter spp.	2.72
Klebsiella spp.	2.32
Staphylococcus aureus	1.17
Streptococcus viridans	0.81
Pseudomonas aeruginosa	0.71
Coagulase-negative *Staphylococcus* spp. (CoNS)	0.58
Klebsiella pneumoniae	0.38
Streptococcus agalactiae	0.34
Klebsiella ozaenae	0.32
Pseudomonas spp.	0.32
Citrobacter spp.	0.26
Morganella morganii	0.22
Proteus spp.	0.21
Enterobacter cloacae	0.18
Providencia stuartii	0.14
Citrobacter koseri	0.12
Serratia spp.	0.12
Streptococcus of groups C, G or F	0.11
Hafnia alvei	0.1
Serratia marcescens	0.08
Streptococcus of group D	0.08
Citrobacter freundii	0.07
Enterobacter sakazakii	0.06
Citrobacter braakii	0.04
Proteus vulgaris	0.04
Klebsiella oxytoca	0.03
Edwardsiella hoshinae	0.02
Enterobacter aerogenes	0.02
Enterobacter amnigenus	0.02
Escherichia fergusonii	0.02
Escherichia hermannii	0.02
Proteus penneri	0.02
Pseudomonas fluorescens	0.02
Pseudomonas oryzihabitans	0.02
Acinetobacter spp.	0.01
Streptococcus anginosus	0.01
TOTAL	100

Source: Research data (2024).

The antimicrobial susceptibility analysis of *E. coli* revealed high resistance rates to ampicillin (28.08%) and sulfamethoxazole + trimethoprim (16.15%). On the other hand, most strains demonstrated susceptibility to fosfomycin (98.7%) and nitrofurantoin (94.5%). Resistance to quinolones was notable: ciprofloxacin (8.57%) and norfloxacin (9.13%). *Proteus mirabilis* showed higher resistance to nitrofurantoin (72.2%) and ampicillin (41.3%), with high sensitivity to ceftriaxone (92.1%) and gentamicin (88.9%). *Enterococcus* spp. exhibited moderate resistance to ampicillin (22.5%) and norfloxacin (30.2%), while maintaining broad susceptibility to nitrofurantoin (91.8%). Table 2 summarizes the resistance patterns of the main isolated bacteria to the tested antibiotics.

Table 2

Microorganism resistance to different antimicrobials

Microorganism	Antibiotic	% Resistance
Escherichia coli	Ampicillin	28.08
	Sulfamethoxazole + Trimethoprim	16.15
	Norfloxacin	9.13
	Ciprofloxacin	8.57
	Levofloxacin	8.25
Proteus mirabilis	Nitrofurantoin	72.20
	Ampicillin	41.30
	Sulfamethoxazole + Trimethoprim	17.74
	Nalidixic Acid	6.72
	Fosfomycin	5.11
Klebsiella spp.	Ampicillin	41.00
	Fosfomycin	15.48
	Nitrofurantoin	6.69
	Cefuroxime	5.44
	Sulfamethoxazole + Trimethoprim	5.02
Enterococcus spp.	Norfloxacin	30.20
	Ampicillin	22.50
	Ciprofloxacin	11.90
	Gentamicin	11.43
	Levofloxacin	11.43

Source: Research data (2024).

The resistance of *E. coli* to ampicillin (28.08%) and to sulfamethoxazole + trimethoprim (16.15%) is concerning, especially since these drugs are widely used as first-line empirical therapy. *E. coli* resistance to ampicillin and sulfamethoxazole-trimethoprim (TMP-SMX) is also a growing global concern. Reported resistance rates for ampicillin range from 28% to over 60%, and for TMP-SMX from 16% to over 40%, with some regions reporting even higher rates. These rates indicate the potential inefficacy of these antibiotics as empirical treatment options in our region, reinforcing the importance of local resistance profiles to guide rational clinical practice.[14,20,30]

The sustained high susceptibility rates to fosfomycin (98.7%) and nitrofurantoin (94.5%) support the use of these drugs as effective alternatives for empirical treatment, particularly in uncomplicated cases.[15,26] These antibiotics, due to their lower selective pressure and localized action in the urinary tract, have demonstrated good performance even in the face of global increases in bacterial resistance.[31-33]

The second most prevalent pathogen, *Proteus mirabilis*, showed high resistance to nitrofurantoin, which is expected due to its intrinsic resistance to this drug. *P. mirabilis* is intrinsically resistant to nitrofurantoin, with resistance rates typically exceeding 85-99%.[34,35] However, the high susceptibility to ceftriaxone (92.1%) and gentamicin (88.9%), that have been consistently reported across multiple studies and regions, supports their effectiveness in complicated infections or cases requiring parenteral therapy.[36-39]

The presence of *Enterococcus* spp. (3.08%) aligns with the profile of UTIs in elderly, immunosuppressed, and hospitalized patients. The moderate resistance to ampicillin and norfloxacin warrants special attention when treating such cases, with nitrofurantoin remaining a viable option.[32,33]

The increasing resistance to quinolones observed in *E. coli* and other microorganisms reflects a concerning global trend. The indiscriminate use of these drugs, along with the selection of multidrug-resistant strains, compromises their effectiveness and promotes the spread of resistance mechanisms such as extended-spectrum β-lactamases (ESBLs) and carbapenemases.[4,5,39-41] Chromosomal mutations in the quinolone resistance-determining regions (QRDRs) of gyrA, gyrB, parC, and parE are primary drivers of high-level resistance.[34,35,42,43]

Plasmid-mediated quinolone resistance (PMQR) genes (qnrA, qnrB, qnrS, aac(6')-Ib-cr, qepA, oqxAB) enable horizontal transfer of resistance and often co-occur with ESBL and carbapenemase genes, compounding the problem.[47] Many quinolone-resistant *E. coli* also produce ESBLs (e.g., CTX-M) and, increasingly, carbapenemases, leading to limited treatment options and higher rates of therapeutic failure.[43]

The 7.2% positivity rate in urine cultures may be attributed to the outpatient profile of most samples and to collections performed without clear symptomatology in some cases. Nonetheless, the findings remain relevant to guide empirical management in the region, especially in settings with limited resources or restricted access to microbiological culture.

One limitation of this study is the lack of individual clinical and comorbidity data, which could allow for more stratified analyses. However, the large number of samples and the extended study period provide statistical robustness and epidemiological relevance for the region.

CONCLUSION

This study demonstrated that *Escherichia coli* remains the main etiological agent of urinary tract infections in the Western region of Santa Catarina, with a predominance of cases in young and elderly women. The high resistance rates to commonly used antibiotics such as ampicillin and sulfamethoxazole + trimethoprim highlight the need for periodic review of empirical treatment protocols, considering local particularities.

Fosfomycin and nitrofurantoin showed high efficacy against *E. coli* and other uropathogens, consolidating their role as safe therapeutic options for uncomplicated infections. The growing resistance to quinolones warrants special attention due to their widespread use and potential for disseminating multidrug-resistant strains.

Therefore, it is essential to implement continuous epidemiological surveillance strategies with regionally focused monitoring of bacterial susceptibility profiles. These actions are fundamental to support evidence-based clinical decisions, contributing to the rational use of antimicrobials and the fight against bacterial resistance.

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