

Community Circulation of Multidrug-Resistant *Escherichia coli* Associated with Urinary Tract Infections

ARTICLE INFO

Article Type Original Article

Authors

Patrícia Guedes Garcia, *PhD*^{1,2*}
Bianca Silva Soares, *BPharm*¹
Janita Soraia de Oliveira da Silva,
*BPharm*¹
Luzia Miranda da Silva, *BPharm*²
Luciana Debortoli de Carvalho,
*PhD*³
Marcio Roberto Silva, *PhD*^{2,4}
Marcelo Silva Silvério, *PhD*²
Natalia Maria da Silva Fernandes,
*PhD*³

¹ Department of Pharmaceutical Sciences, Faculty of Pharmacy, Federal University of Juiz de Fora, Brazil.

² Postgraduate Program in Collective Health, Federal University of Juiz de Fora, Juiz de Fora, Minas Gerais, Brazil.

³ Department of Internal Medicine, Faculty of Medicine, Federal University of Juiz de Fora, Juiz de Fora, Minas Gerais, Brazil.

⁴ Embrapa Dairy Cattle, Brazilian Agricultural Research Company, Juiz de Fora, Minas Gerais, Brazil.

* Correspondence

Department of Pharmaceutical Sciences, Faculty of Pharmacy, Federal University of Juiz de Fora, Brazil.
E-mail: patricia.guedes@ufjf.br

How to cite this article

Guedes Garcia P., Silva Soares B., Oliveira da Silva J., Miranda da Silva L., Debortoli de Carvalho L., Roberto Silva M., Silva Silvério M., Fernandes N.M.S. Community Circulation of Multidrug-Resistant *Escherichia coli* Associated with Urinary Tract Infections. *Infection Epidemiology and Microbiology*. 2026;12(2): 109-120.

Article History

Received: February 26, 2026

Accepted: June 20, 2026

Published: July 27, 2026

ABSTRACT

Background: This study aimed to investigate the antimicrobial resistance profile and the occurrence of multidrug resistance (MDR) among *Escherichia coli* isolates recovered from urine cultures of outpatients attending a public teaching hospital in Brazil and to assess the association of sex and age with MDR.

Materials & Methods: This cross-sectional study was conducted based on a retrospective analysis of urine cultures collected from outpatients between January and December 2024. Descriptive statistics were applied, and univariate and multivariate logistic regression analyses were performed to identify factors associated with MDR.

Findings: Among 1955 urine cultures analyzed, 418 (21.4%) demonstrated significant bacterial growth, with *E. coli* accounting for 48.3% (n=202) of the positive cultures. The highest resistance rates were to ampicillin (56.9%), ciprofloxacin (37.6%), and trimethoprim-sulfamethoxazole (35.0%), whereas the lowest resistance rates were observed to nitrofurantoin (8.3%) and fosfomycin (3.1%). MDR was identified in 71 (35.1%) *E. coli* isolates, among which 24 (33.8%) exhibited an extended-spectrum β -lactamase phenotype, and three (4.2%) produced carbapenemases. In the multivariate analysis, above-median age was independently associated with MDR (adjusted OR = 2.27; 95% CI: 1.24–4.14).

Conclusion: A substantial proportion of *E. coli* isolates from community-acquired urinary tract infections presented multidrug resistance, particularly among older patients. These findings emphasize the importance of local surveillance of antimicrobial resistance and periodic review of empirical treatment protocols in outpatient settings.

Keywords: Urinary tract infections, *Escherichia coli*, Microbial drug resistance, Multiple drug resistance, Drug resistance surveillance

CITATION LINKS

[1] Al Lawati H, Blair BM, Larnard J. Urinary... [2] Flores-Mireles AL, Walker JN, Caparon M, Hultgren SJ. Urinary... [3] Foxman B. Urinary tract... [4] Kot B. Antibiotic... [5] Mohammed OA, et al. Microbial... [6] Mazzariol A, Bazaj A, Cornaglia G. Multidrug... [7] Poirel L, et al. Antimicrobial... [8] Walker MM, et al. Current and... [9] da Silva CE, et al. Profile of ... [10] Terlizzi ME, Griboaldo G, Maffei ME. Uropathogenic... [11] Leber AL, editor. Clinical... [12] Tille PM. Bailey &... [13] The European Committee on... [14] The European Committee on... [15] Magiorakos AP, et al. Multidrug... [16] Razaq L, Uddin F, Alhilfi WA, Alorabi M, Sohail M. Molecular... [17] Demir C, Metin S. Microorganisms... [18] Yang X, Chen H, Zheng Y, Qu S, Wang H, Yi F. Disease... [19] Thapa TB, et al. Prevalence and... [20] Alós JI. Epidemiology and... [21] Aggarwal N, Leslie SW. Recurrent... [22] McLellan LK, Hunstad DA. Urinary... [23] Gasparin AP, Lovison OVA, Dalzochio T. Prevalence... [24] Reolom RP, Klafke A. Antimicrobial... [25] Moreira da Silva RC, et al. Ciprofloxacin... [26] Reis AC, et al. Ciprofloxacin... [27] Al-Mayahie SM, et al. Prevalence of... [28] Krause KM, et al. Aminoglycosides... [29] Squadrio FJ, Del Portal D. Nitrofurantoin... [30] Guclu E, et al. Risk factors of... [31] Chaudhary R, et al. Multidrug... [32] Belay WY, et al. Mechanism of... [33] Ahanjan M, Salehian M, Gholami M. Prevalence and... [34] Naziri Z, et al. Treatment... [35] Evins CW, et al. Community... [36] World Health Organization... [37] Sati H, et al. The WHO... [38] O'Neill J. Tackling... [39] World Health Organization... [40] Chen YH, Ko WC, Hsueh PR. Emerging...

Introduction

Urinary tract infections (UTIs) are among the most common infectious diseases in clinical practice and represent one of the leading causes of healthcare utilization and antimicrobial prescription worldwide. It is estimated that a substantial proportion of the population, particularly women, will experience at least one episode of UTIs during their lifetime, highlighting the epidemiological relevance of these infections and their significant impact on healthcare systems [1-3].

Although UTIs occur in both hospital and community settings, community-acquired infections have received increasing attention owing to the frequent use of empirical therapy and limited availability of systematically organized data on local antimicrobial resistance patterns. In this context, uropathogenic *Escherichia coli* (UPEC) is recognized as the primary etiological agent of community-acquired UTIs, accounting for the majority of uncomplicated cases and a substantial proportion of complicated infections [4,5].

In recent decades, the management of UTIs has been increasingly challenged by the rise in antimicrobial resistance among uropathogens, with growing resistance rates to drugs traditionally used for empirical treatment, such as penicillins, cephalosporins, and fluoroquinolones. The spread of multidrug-resistant (MDR) strains, including those producing extended-spectrum β -lactamases (ESBLs) and, more recently, carbapenemases, represents a major public health concern, as it compromises therapeutic effectiveness and increases the risk of clinical failure [6-8]. Antimicrobial resistance among community-acquired uropathogens is strongly associated with inappropriate antimicrobial use, empirical prescribing without microbiological support, and lack of systematic surveillance in outpatient settings. Despite the importance of this issue, much of the avail-

able evidence is derived from hospital-based data, thereby limiting our understanding of MDR circulation in the community and hindering the development of effective antimicrobial stewardship strategies [3,4].

In this context, it is crucial to provide evidence to support antimicrobial resistance surveillance in highly prevalent community-acquired infections, such as UTIs, particularly in reference services within the Brazilian Unified Health System (SUS). Analysis of the epidemiological profile and resistance patterns of *E. coli* isolates from outpatient urine cultures could help review therapeutic protocols, strengthen microbiological surveillance strategies, and enhance public health measures aimed at controlling antimicrobial resistance [9,10].

Objectives: Therefore, this study aimed to evaluate the antimicrobial resistance profile of *E. coli* isolates from outpatient urine cultures at a teaching hospital in Juiz de Fora, Minas Gerais, Brazil, in 2024. To this end, this study sought to: (i) describe resistance patterns to commonly-prescribed antimicrobials; (ii) determine the prevalence and distribution of multidrug-resistant (MDR) isolates; (iii) identify phenotypes associated with ESBL and carbapenemase production; and (iv) analyze demographic factors associated with the occurrence of MDR.

Materials and Methods

Study design, setting, and period: This observational, cross-sectional study involved a retrospective analysis of urine culture data from outpatients attending a high-complexity teaching hospital in Juiz de Fora, Minas Gerais, Brazil. The institution is affiliated with the Brazilian Hospital Services Company (EBSERH) and is integrated into the Brazilian Unified Health System (SUS). Data from all microbiological examinations performed between January and December 2024 were included.

Study population and eligibility criteria:

The study population consisted of outpatients who underwent urine culture during the study period. Monomicrobial cultures with significant bacterial growth ($\geq 100,000$ colony-forming units per milliliter [CFU/mL]), consistent with the conventional criterion for significant bacteriuria, adopted in clinical microbiology laboratories, were included [1]. Conversely, samples from hospitalized patients, polymicrobial cultures, those with bacterial growth below this threshold, and records with incomplete data were excluded.

Laboratory procedures and resistance phenotype definition:

Urine sample collection, processing, bacterial identification, and antimicrobial susceptibility testing were performed according to routine laboratory protocols, following national and international guidelines [11,12]. *E. coli* identification was performed using standardized phenotypic laboratory methods [11,12]. Antimicrobial susceptibility was determined by the disk diffusion method and interpreted according to the European Committee on Antimicrobial Susceptibility Testing (EUCAST) guidelines (Version 2024), which were in force during the study period [13]. Fifteen antimicrobials were tested: amikacin

(30 µg), gentamicin (10 µg), ciprofloxacin (5 µg), amoxicillin/clavulanate (20/10 µg), ampicillin (10 µg), ceftazidime (30 µg), cefotaxime (5 µg), ceftriaxone (30 µg), cefepime (30 µg), ertapenem (10 µg), imipenem (10 µg), fosfomycin (200 µg), nitrofurantoin (100 µg), and trimethoprim-sulfamethoxazole (1.25/23.75 µg) [13].

As this was a retrospective study based on routine laboratory records, susceptibility results to all antimicrobials were not available for each isolate. Therefore, the number of isolates tested varied according to the antimicrobial agent.

Phenotypic detection of β -lactam resistance mechanisms, including ESBL, AmpC, and carbapenemase production, was performed according to BrCAST recommendations. ESBL production was investigated using the disk approximation (double-disk synergy) test with third-generation cephalosporins and amoxicillin/clavulanate. AmpC production was assessed based on the phenotypic resistance profile and BrCAST interpretive criteria. Carbapenemase production was screened in isolates showing reduced susceptibility to carbapenems and confirmed using the modified carbapenem inactivation method (mCIM) and the

Table 1) Categories and antimicrobial agents tested for uropathogenic *Escherichia coli* isolates from outpatients

Categories	Antimicrobial Agents
Penicillins	Ampicillin
Penicillin + β -lactamase inhibitor	Amoxicillin + clavulanic acid
Cephameycin	Cefoxitin
Third- and fourth-generation cephalosporins	Ceftriaxone, cefotaxime, ceftazidime, cefepime
Carbapenems	Ertapenem, imipenem
Aminoglycosides	Amikacin, gentamicin
Fluoroquinolones	Ciprofloxacin
Sulfonamides	Trimethoprim-sulfamethoxazole
Nitrofurans	Nitrofurantoin
Phosphonates	Fosfomycin

Note: Categories were defined according to antimicrobial classes used for multidrug resistance (MDR) classification, based on Magiorakos et al. (2012).

EDTA-modified carbapenem inactivation method (eCIM) according to EUCAST recommendations, which were in force during the study period [14]. Quality control of antimicrobial susceptibility testing was performed using *E. coli* ATCC 25922 in accordance with EUCAST recommendations.

Definition of multidrug resistance: *E. coli* isolates were classified according to the multidrug resistance criteria proposed by Magiorakos et al. (2012), whereby strains were considered MDR when they exhibited resistance to at least one agent in three or more antimicrobial categories [15]. This definition was adopted to ensure standardization and comparability with national and international epidemiological studies. Table 1 presents the categories and examples of antimicrobial drugs tested.

Data collection and analysis: Microbiological and demographic data were extracted from electronic records available in the computerized hospital information system called “Management Application for University Hospitals” (AGHU - Aplicativo de Gestão para Hospitais Universitários). Variables of interest included the total number of positive urine cultures, the frequency of *E. coli* isolates, patients’ sex and age group, antimicrobial susceptibility profiles, and the proportion of isolates classified as multidrug-resistant.

Data were organized in electronic spreadsheets and analyzed using descriptive and analytical statistics. Categorical variables were presented as absolute and relative frequencies, while age was described using the median (62 years), which was subsequently used as the cutoff point for age-group stratification in regression analyses. This approach was adopted to characterize the epidemiological profile and antimicrobial resistance patterns of the study population. Resistance data were presented by antimicrobial agent, individually or

in combination (including MDR), as absolute frequencies and percentages with corresponding 95% confidence intervals (95% CI).

The outcome of the inferential analysis was the occurrence of multidrug resistance (MDR), defined as a dichotomous variable (yes/no). Univariate and multivariate logistic regression analyses were performed to assess factors associated with MDR among *E. coli* isolates, with sex and age group (defined by the median cutoff) as the main explanatory variables. Variables with a p -value $\leq .20$ in univariate analysis were included in the multivariate model. Statistical significance was set at 0.05, and the magnitude of associations was expressed as odds ratios (OR) with corresponding 95% confidence intervals.

Ethical aspects: This study used secondary data without nominal identification of participants, ensuring confidentiality of information. The project involving human subjects was approved by the Research Ethics Committee of the University Hospital of the Federal University of Juiz de Fora, under Certificate of Presentation for Ethical Consideration no. 51147021.9.0000.5133 and approval opinion no. 7,316,549.

Findings

A total of 1,955 urine cultures from outpatients were analyzed between January and December 2024. Of these, 418 (21.38%) yielded significant bacterial growth ($\geq 100,000$ CFU/mL), 203 (10.38%) were classified as mixed cultures or presented bacterial counts below the established cutoff, and 1,334 (68.24%) showed no bacterial growth.

Among the isolated uropathogens, *E. coli* was the most prevalent, accounting for 202 of the 418 positive isolates (48.3%), followed by *Klebsiella pneumoniae* (16.0%). The remaining species each accounted for

Table 2) Frequency of antimicrobial resistance among *Escherichia coli* isolates from outpatient urine cultures

Antimicrobials Tested	Isolates Tested (n)	Number of Resistant Isolates	% (95% CI)
Amikacin	201	3	1.5 (0.3-4.3)
Gentamicin	163	20	12.3 (7.7-18.3)
Ciprofloxacin	202	76	37.6 (30.9-44.7)
Amoxicillin + clavulanic acid	200	19	9.5 (5.8-14.4)
Ampicillin	188	107	56.9 (49.5-64.1)
Cefoxitin	153	12	7.8 (4.1-13.3)
Cefotaxime	197	32	16.2 (11.4-22.2)
Ceftazidime	187	31	16.6 (11.6-22.7)
Ceftriaxone	135	23	17.0 (11.1-24.5)
Cefepime	193	27	14.0 (9.4-19.7)
Ertapenem	202	3	1.5 (0.3-4.3)
Imipenem	191	2	1.0 (0.1-3.7)
Fosfomycin	127	4	3.1 (0.9-7.9)
Nitrofurantoin	192	16	8.3 (4.8-13.2)
Trimethoprim-sulfamethoxazole	200	70	35.0 (28.4-42.0)

Note: n = the number of isolates tested for each antimicrobial, CI = confidence interval. The number of isolates tested varied among antimicrobial agents because susceptibility results were obtained retrospectively from routine laboratory records.

Table 3) Distribution of *Escherichia coli* strains (n = 202) according to antimicrobial susceptibility and number of antimicrobial categories with resistance among the isolates

Antimicrobial Susceptibility Category	Absolute Frequency	% (95% CI)
Susceptible to all antimicrobials tested	70	34.7 (28.1-41.7)
Resistant to one antimicrobial	36	17.8 (12.8-23.8)
Resistant to two antimicrobials	25	12.4 (8.2-17.7)
Resistant to at least one antimicrobial in three or more therapeutic categories (MDR)	71	35.1 (28.6-42.2)
Number of Antimicrobial Categories with Resistance among MDR Isolates (n = 71)	Absolute Frequency	% (95% CI)
Resistant to 3 categories	31	43.7 (31.9-56.0)
Resistant to 4 categories	15	21.1 (12.3-32.4)
Resistant to 5 categories	14	19.7 (11.2-30.9)
Resistant to 6 categories	5	7.0 (2.3-15.7)
Resistant to 7 categories	3	4.2 (0.9-11.9)
Resistant to 8 categories	1	1.4 (0.0-7.6)
Resistant to 9 categories	1	1.4 (0.0-7.6)
Resistant to 10 categories	1	1.4 (0.0-7.6)

Note: n = total number of strains; MDR = multidrug-resistance, defined as resistance to at least one antimicrobial agent in three or more antimicrobial categories according to Magiorakos et al. (2012); CI = confidence interval. The categories correspond to antimicrobial classes presented in Table 1.

Table 4) Distribution of multidrug-resistant *Escherichia coli* isolates according to sex and age groups

Characteristics	Total(n)	MDR n (%)	P-Value	OR (95%CI)
Sex				
Male	26	13 (50.0)	.13	-
Female	176	58 (33.0)		
Age group				
≤ 62 years	102	26 (25.5)	.0058	1.00
>62 years	100	45 (45.0)		2.39 (1.31-4.33)

Note: MDR = multidrug resistance, OR = odds ratio, CI = confidence interval. Odds ratios were calculated using logistic regression. The reference category for age group was ≤ 62 years.

less than 10% of the isolates and included coagulase-negative *Staphylococcus* spp., *Enterococcus* spp., *Streptococcus* spp., and other Gram-negative bacilli such as *Proteus* spp., *Enterobacter* spp., and *Pseudomonas* spp. Among *E. coli* isolates, the highest resistance rates were observed to ampicillin (56.9%), ciprofloxacin (37.6%), and trimethoprim-sulfamethoxazole (35.0%). Intermediate resistance rates (14.0–17.0%) were against third- and fourth-generation cephalosporins. In contrast, low resistance rates were observed to aminoglycosides, nitrofurantoin, fosfomycin, and carbapenems (Table 2). Of the 202 *E. coli* strains analyzed, 70 (34.7%) isolates were susceptible to all antimicrobials tested. Resistance to one antimicrobial was observed in 36 isolates (17.8%), while 25 (12.4%) isolates exhibited resistance to two antimicrobials belonging to distinct categories. Additionally, 71 (35.1%) isolates showed resistance to at least one antimicrobial in three or more therapeutic categories and were classified as multidrug-resistant (MDR).

Within the MDR group, 31 (43.7%) isolates showed resistance to three antimicrobial categories. Resistance to four categories was observed in 15 isolates (21.1%), to five categories in 14 (19.7%) isolates, to six categories in five (7.0%) isolates, and to seven categories in three (4.2%) isolates. Furthermore, three isolates exhibited extensive resistance profiles: one isolate was resistant to

eight therapeutic categories, and the other two were resistant to nine and ten therapeutic categories, respectively (Table 3).

Among the 71 *E. coli* strains classified as multidrug-resistant, 24 (33.8%) exhibited an extended-spectrum β -lactamase (ESBL)-producing phenotype, and three (4.2%) were identified as carbapenemase producers. No isolate showed a profile compatible with AmpC β -lactamase production.

Regarding demographic characteristics, 76.8% (321 of 418) of the positive urine cultures were from female patients. Among *E. coli* and MDR *E. coli* isolates, 87.1% (176 of 202) and 81.6% (58 of 71) occurred in women, respectively. The median age of patients with *E. coli*-positive urine cultures was 62 years (range: 17–89 years), and this value was used as the cutoff for age-group stratification in the regression analyses (Table 4). MDR occurrence was not significantly associated with sex ($p = .13$) but was significantly associated with age group ($p = .0058$). In univariate analysis, patients above the median age had higher odds of MDR compared with those at or below the median age (crude OR = 2.39; 95% CI: 1.31–4.33). In the multivariate logistic regression model, age remained independently associated with this resistance profile (adjusted OR = 2.27; 95% CI: 1.24–4.14; $p = .0075$), whereas the association of sex was not statistically significant.

Discussion

Urinary tract infections (UTIs) rank among the most frequent bacterial infections in clinical practice, representing an important cause of morbidity worldwide and a growing challenge for public health, particularly with regard to antimicrobial resistance among uropathogens in the outpatient setting ^[1]. In the present study, the positivity rate of urine cultures was 21.38%, with a predominance of women among positive cases and *E. coli* as the most frequent pathogen. Additionally, the frequency of resistance to antimicrobials widely used in empirical therapy was high, and the proportion of MDR isolates was substantial, including those with phenotypes associated with ESBL and carbapenemase production.

The positivity rate observed in the present study was lower than those reported among patients with community and hospital-acquired UTIs ^[16] and among adult patients admitted to the intensive care units of a tertiary hospital ^[17]. These differences may reflect variations in the study populations and clinical settings, while reinforcing that UTIs remain frequent across different levels of healthcare. In hospital settings, these infections are associated with significant clinical and economic impacts, including increased attributable mortality rates and healthcare costs ^[18].

The predominance of positive urine cultures among women (76.8%) is consistent with the established epidemiology of UTIs, in which female sex is recognized as a major risk factor ^[1]. Older age is also an important epidemiological factor, with significantly higher culture positivity reported among patients with chronic kidney disease aged over 75 years ^[19,20]. In the present study, women also accounted for most *E. coli* isolates (87.1%) and multidrug-resistant isolates (81.6%), indicating that the female predominance extended to these clinically

relevant subgroups.

Anatomical and behavioral factors, such as a shorter urethra, proximity of the urethral meatus to the perineal region, and certain hygiene habits, contribute to a greater risk of bacterial colonization and ascension in women ^[21]. Conversely, anatomical mechanisms in men tend to exert a protective effect, although prostatic alterations associated with aging may increase susceptibility to UTIs ^[22].

Although no statistically significant association was observed between sex and the occurrence of multidrug resistance, age demonstrated an independent association with MDR, with patients above the median age presenting approximately 2.3-fold higher odds of harboring multidrug-resistant *E. coli*. This finding may be related to greater prior exposure to antimicrobials, hospitalizations, and comorbidities among older individuals, factors recognized to be associated with the development of resistant strains.

Regarding etiology, *E. coli* accounted for 48.3% of the isolates in the present study, corroborating evidence that this species is the principal etiological agent of UTIs in both outpatient and hospital settings ^[2,5,9]. Previous studies have indicated that *E. coli* may be responsible for up to 80–90% of uncomplicated UTIs and a significant proportion of complicated infections ^[2, 3]. Regarding the antimicrobial resistance profile, high resistance rates were observed against ampicillin (56.9%), ciprofloxacin (37.6%), and trimethoprim–sulfamethoxazole (35.0%), antimicrobials historically used in the empirical treatment of community-acquired UTIs ^[1]. Similar results have been described in studies conducted in different outpatient settings in Brazil ^[23, 24] as well as in a recent investigation carried out at the same institution on patients with chronic kidney disease ^[19], indicating the persistence of high resistance rates to first-line agents.

In the present study, resistance to ciprofloxacin was substantial (37.6%), approaching findings reported in other national settings and reinforcing the need for continuous monitoring of this antimicrobial in outpatient settings [25,26]. Furthermore, resistance to fluoroquinolones has often been reported to be associated with resistance to other antimicrobial classes, contributing to multidrug-resistance profiles [26].

Among aminoglycosides, higher resistance was observed to gentamicin (12.3%) than to amikacin (1.5%), a pattern consistent with scientific literature [24,27]. This difference may reflect distinct resistance mechanisms, including enzymatic modification, alterations in the target site, reduced permeability, and efflux pump activity, in addition to differentiated clinical use patterns of these agents [27,28].

Conversely, low resistance rates were observed for fosfomycin and nitrofurantoin (3.1% and 8.3%, respectively), both of which are recommended as first-line options for uncomplicated cystitis and generally retain good activity against uropathogenic *E. coli* [4]. The preserved activity of nitrofurantoin is also consistent with previous findings involving urinary isolates from patients with chronic kidney disease [19]. Its sustained effectiveness may be related to its high urinary concentrations, minimal impact on the intestinal microbiota, and multiple bacterial targets, which may limit the emergence of acquired resistance [29].

The proportion of MDR isolates observed (35.1%) in this outpatient setting is of particular importance from a clinical and epidemiological perspective. This percentage indicates that more than one-third of *E. coli* isolates obtained from outpatients attending this teaching hospital exhibited resistance to multiple antimicrobial classes, which may significantly limit effective empirical treatment options [4,30].

Among the MDR isolates in the present study, 33.8% exhibited an ESBL-producing phenotype, and 4.2% were identified as carbapenemase producers. The detection of these resistance mechanisms among outpatients reinforces the hypothesis of community circulation of resistance determinants traditionally associated with the hospital environment [31]. Previous studies have demonstrated marked differences in the resistance profiles of *E. coli* isolates from urine cultures between developed and developing countries, with substantially higher ciprofloxacin resistance rates reported in developing countries [4]. Such variations have been linked to differences in antimicrobial prescribing patterns as well as to social, economic, and organizational factors within healthcare services, which influence the dynamics of antimicrobial resistance at the community level [4,32].

ESBL production stands out for its clinical relevance, as it compromises the efficacy of penicillins and broad-spectrum cephalosporins, classes widely used in the treatment of UTIs. Although less frequent, the detection of phenotypes associated with carbapenemase production in outpatients is a relevant finding that has been highlighted as a matter of concern in different epidemiological contexts, indicating the possible expansion of these resistance mechanisms into the community setting [33,34].

Clinical reports reinforce the potential impact of these phenotypes; for example, Evins et al. (2021) documented a case of severe community-acquired pyelonephritis caused by ESBL-producing *E. coli* with an extensively drug-resistant (XDR) profile, even in the absence of evident predisposing factors [35]. Furthermore, the literature highlights *E. coli* as an important reservoir and disseminator of genetic resistance determinants, including ESBLs and carbapenemases, which may

favor the amplification of MDR phenotypes in different niches, including community settings [7]. Considering that carbapenems are frequently used as a therapeutic option for infections caused by ESBL-producing bacteria, the emergence of uropathogenic strains resistant to these antimicrobials is a relevant public health concern, although studies have indicated that there is variation in the frequency of resistance and enzyme production among different countries and populations [31,33].

The findings demonstrated that a significant proportion of *E. coli* isolates were MDR, a phenomenon already described as an emerging phenomenon in the community [2,4,26]. This scenario is consistent with the findings of the 2022 World Health Organization (WHO) report titled “Global Antimicrobial Resistance and Use Surveillance System” (GLASS) [36], documenting increasing resistance patterns globally in clinically important pathogens, including enterobacteria. Furthermore, the WHO has classified *Enterobacterales* resistant to third-generation cephalosporins and carbapenems as a critical public health priority on its list of priority bacterial pathogens [37].

In this context, the report coordinated by O'Neill (2016) is particularly noteworthy, estimating that in the absence of effective interventions, infections caused by resistant microorganisms may account for up to 10 million deaths annually by 2050, with significant repercussions for health systems and the global economy [38]. This scenario reinforces the need for continuous strengthening of microbiological surveillance, periodic updating of therapeutic protocols, and implementation of consistent strategies for the rational use of antimicrobials [39,40].

This study has some limitations that should be acknowledged. Due to the retrospective nature of the study and the use of second-

ary laboratory data, information regarding previous antimicrobial use, prior hospitalizations, comorbidities, urinary catheterization, and previous urinary tract infections was unavailable for analysis. Consequently, the multivariate model was restricted to the demographic variables available in the database. Future studies incorporating clinical variables may provide a more comprehensive assessment of factors associated with multidrug resistance in community-acquired urinary tract infections.

Conclusion

The present study confirmed *E. coli* as the principal uropathogen isolated from urine cultures of outpatients, which was predominant among women and demonstrated elevated resistance rates to antimicrobials widely used in the empirical treatment of community-acquired urinary tract infections, such as ampicillin, ciprofloxacin, and trimethoprim-sulfamethoxazole. In contrast, agents recommended for the treatment of uncomplicated UTIs, such as nitrofurantoin and fosfomycin, showed efficacy with low resistance rates, reinforcing their importance as first-line therapeutic options in the outpatient setting.

The substantial proportion of MDR strains, including ESBL-producing isolates and, although less frequently, carbapenemase producers, indicated community circulation of *E. coli* with complex resistance profiles. These findings underscore the need for continuous microbiological surveillance at the outpatient level as well as periodic review of empirical treatment protocols based on local susceptibility data. Furthermore, the findings highlight the importance of rational antimicrobial use and the consolidation of public health surveillance strategies aimed at controlling antimicrobial resistance in the community.

Acknowledgments

The authors gratefully acknowledge the professionals of the Microbiology Laboratory of the University Hospital of the Federal University of Juiz de Fora, Minas Gerais, Brazil, for their excellence in microbiological diagnostics and their contribution to data generation for this study.

Ethical approval: This study was conducted in accordance with the ethical principles of the Declaration of Helsinki. The research protocol was reviewed and approved by the Research Ethics Committee of the Federal University of Juiz de Fora (UFJF), under Certificate of Presentation for Ethical Consideration (CAAE) no. 51147021.9.0000.5133 and approval opinion no. 7,316,549.

Authors' contributions: All authors contributed to the conception and design of the study. Data collection was conducted by Patrícia Guedes Garcia, Bianca Silva Soares, and Janita Soraia de Oliveira da Silva. Data analysis and statistical analysis were performed by Patrícia Guedes Garcia and Marcio Roberto Silva. The original draft of the manuscript was prepared by Patrícia Guedes Garcia, with contributions from Luzia Miranda da Silva. Critical review of the manuscript was undertaken by Luciana Debortoli de Carvalho and Marcelo Silva Silvério. All authors reviewed and approved the final version of the manuscript. Natália Maria da Silva Fernandes contributed to investigation, formal analysis, and writing – review & editing.

Conflicts of interest: The authors declare no conflicts of interest.

Funding: This research received no external funding.

Declaration of Artificial Intelligence (AI)

Use: ChatGPT (OpenAI) was used only to assist with reference checking and minor textual revisions. The final English version was reviewed by a professional language editor. All content was reviewed and verified

by the authors.

Consent to participate: Due to the retrospective nature of the study and the use of anonymized secondary data, the requirement for informed consent was waived by the Research Ethics Committee.

References

1. Al Lawati H, Blair BM, Larnard J. Urinary tract infections: Core curriculum 2024. *Am J Kidney Dis.* 2024;83(1):90-100.
2. Flores-Mireles AL, Walker JN, Caparon M, Hultgren SJ. Urinary tract infections: Epidemiology, mechanisms of infection, and treatment options. *Nat Rev Microbiol.* 2015;13(5):269-84.
3. Foxman B. Urinary tract infection syndromes: Occurrence, recurrence, bacteriology, risk factors, and disease burden. *Infect Dis Clin North Am.* 2014;28(1):1-13.
4. Kot B. Antibiotic resistance among uropathogenic *Escherichia coli*. *Pol J Microbiol.* 2019;68(4):403-15.
5. Mohammed OA, Abubakr KT, Yaghoobi A, Khedhir HH, Ali DH, Abdalrahman PK, et al. Microbial prevalence and antimicrobial susceptibility in urinary tract infections at a teaching hospital (2018–2022). *BMC Res Notes.* 2025;18(1):329.
6. Mazzariol A, Bazaj A, Cornaglia G. Multidrug-resistant Gram-negative bacteria causing urinary tract infections: A review. *J Chemother.* 2017;29(Suppl 1):2-9.
7. Poirel L, Madec JY, Lupo A, Schink AK, Kieffer N, Nordmann P, et al. Antimicrobial resistance in *Escherichia coli*. *Microbiol Spectr.* 2018;6(4):10-128.
8. Walker MM, Roberts JA, Rogers BA, Harris PNA, Sime FB. Current and Emerging Treatment Options for Multidrug Resistant *Escherichia coli* Urosepsis: A Review. *Antibiotics (Basel).* 2022 Dec 15;11(12):1821.
9. da Silva CE, Carvalho PHS, Capretz GCG, Ciriaco YS, de Souza WHM, Alves MEFS, et al. Profile of antimicrobial resistance of uropathogens in urinary tract infections: An analysis of 1117 hospitalized patients in Brazil. *IJID Reg.* 2025 Aug 7;16:100724.
10. Terlizzi ME, Griboaldo G, Maffei ME. Uropathogenic *Escherichia coli* (UPEC) infections: Virulence factors, bladder responses, antibiotic and non-antibiotic antimicrobial strategies. *Front Microbiol.* 2017;8:1566.
11. Leber AL, editor. Clinical microbiology procedures handbook. 4th ed. Washington (DC): ASM Press; 2016.
12. Tille PM. Bailey & Scott's diagnostic microbiology.

- 15th ed. St. Louis: Elsevier; 2021.
13. The European Committee on Antimicrobial Susceptibility Testing (EUCAST). EUCAST disk diffusion method for antimicrobial susceptibility testing. Version 12.0 [Internet]. EUCAST; 2024 [cited 2026 Jul 30].
14. The European Committee on Antimicrobial Susceptibility Testing (EUCAST). EUCAST guidelines for detection of resistance mechanisms and specific resistances of clinical and/or epidemiological importance. Version 2.0 [Internet]. EUCAST; 2017 [cited 2026 Jul 30].
15. Magiorakos AP, Srinivasan A, Carey RB, Carmeli Y, Falagas ME, Giske CG, et al. Multidrug-resistant, extensively drug-resistant, and pandrug-resistant bacteria: An international expert proposal for interim standard definitions for acquired resistance. *Clin Microbiol Infect.* 2012;18(3):268-81.
16. Razaq L, Uddin F, Alhilfi WA, Alorabi M, Sohail M. Molecular characterization of bla_{NDM} and other carbapenemases genes among carbapenem-resistant Enterobacterales from community-and hospital- acquired urinary tract infections. *BMC Infect Dis.* 2025 Oct 9;25(1):1260.
17. Demir C, Metin S. Microorganisms grown in urine cultures and antimicrobial resistance patterns: A randomised retrospective analysis from a tertiary hospital. *J Infect Dev Ctries.* 2023 Mar 31;17(3):337-344. doi: 10.3855/jidc.17483. PMID: 37023421.
18. Yang X, Chen H, Zheng Y, Qu S, Wang H, Yi F. Disease burden and long-term trends of urinary tract infections: A worldwide report. *Front Public Health.* 2022;10:888205.
19. Thapa TB, Pokhrel S, Lamichhane A, Singh VK, Shrestha O, Sapkota M, Khanal PR. Prevalence and antibiogram of bacteria causing urinary tract infection among patients with chronic kidney disease. *Open Med (Wars).* 2023 Oct 19;18(1):20230824.
20. Alós JI. Epidemiology and etiology of urinary tract infections in the community: antimicrobial susceptibility of the main pathogens and clinical significance of resistance [article in Spanish]. *Enferm Infecc Microbiol Clin.* 2005 Dec;23 Suppl 4:3-8.
21. Aggarwal N, Leslie SW. Recurrent urinary tract infections. *Treasure Island (FL): StatPearls Publishing;* 2025.
22. McLellan LK, Hunstad DA. Urinary tract infection: Pathogenesis and outlook. *Trends Mol Med.* 2016;22(11):946-57.
23. Gasparin AP, Lovison OVA, Dalzochio T. Prevalence of urinary tract infections and antimicrobial susceptibility profile among patients admitted to a clinical analysis laboratory. *Arch Health Sci.* 2022;29(1):21-25.
24. Reolom RP, Klafke A. Antimicrobial resistance in urine cultures of residents of the North and Northeast Areas of Porto Alegre. *Rev Bras Med Fam Comunidade.* 2022;17(44):3067.
25. Moreira da Silva RC, Oliveira Martins Júnior P, Gonçalves LF, Paulo Martins V, Melo AB, Pitondo-Silva A, et al. Ciprofloxacin resistance in uropathogenic *Escherichia coli* isolates causing community-acquired urinary infections in Brasília, Brazil. *J Glob Antimicrob Resist.* 2017;9:61-7.
26. Reis AC, Santos SR, Souza SC, Saldanha MG, Pitanga TN, Oliveira RR, et al. Ciprofloxacin resistance pattern among bacteria isolated from patients with community-acquired urinary tract infection. *Rev Inst Med Trop Sao Paulo.* 2016;58:e53.
27. Al-Mayahie SM, Al-Guranie DR, Hussein AA, Bachai ZA. Prevalence of common carbapenemase genes and multidrug resistance among uropathogenic *Escherichia coli* phylogroup B2 isolates from outpatients in Wasit province, Iraq. *PLoS One.* 2022;17(1):e0262984.
28. Krause KM, Serio AW, Kane TR, Connolly LE. Aminoglycosides: An overview. *Cold Spring Harb Perspect Med.* 2016;6(6):a027029.
29. Squadrio FJ, Del Portal D. Nitrofurantoin. *Treasure Island (FL): StatPearls Publishing;* 2023.
30. Guclu E, Halis F, Kose E, Ogutlu A, Karabay O. Risk factors of multidrug-resistant bacteria in community-acquired urinary tract infections. *Afr Health Sci.* 2021;21(1):214-9.
31. Chaudhary R, Pradhan M, Bhatta S, Shrestha S, Adhikari N, Singh YI. Multidrug resistant *Escherichia coli* among urinary samples of patients with urinary tract infection in a tertiary care center: A descriptive cross-sectional study. *JNMA J Nepal Med Assoc.* 2023;61(261):437-41.
32. Belay WY, Getachew M, Tegegne BA, Teffera ZH, Dagne A, Zeleke TK, et al. Mechanism of antibacterial resistance, strategies and next-generation antimicrobials to contain antimicrobial resistance: a review. *Front Pharmacol.* 2024;15:1444781.
33. Ahanjan M, Salehian M, Gholami M. Prevalence and resistance pattern of extended-spectrum β -lactamase-producing *Escherichia coli* isolated from patients with urinary tract infection. *Arch Med Lab Sci.* 2020;6(1):e13.
34. Naziri Z, Derakhshandeh A, Borchaloe AS, Poormaleknia M, Azimzadeh N. Treatment failure in urinary tract infections: A warning witness for virulent multidrug-resistant ESBL-producing *Escherichia coli*. *Infect Drug Resist.* 2020;13:1839-50.
35. Evins CW, Sutton CM, Withers ST, Grier JT, Schammel CM, Fiester SE. Community-acquired,

- extended-spectrum β -lactamase-producing and extensively drug-resistant *Escherichia coli* in a 28-year-old pyelonephritis patient lacking risk factors. *Antibiotics*. 2021;10(5):533.
36. World Health Organization. Global antimicrobial resistance and use surveillance system (GLASS) report: 2022. Geneva: WHO; 2022.
37. Sati H, Carrara E, Savoldi A, Hansen P, Garlasco J, Campagnaro E, et al. The WHO bacterial priority pathogens list 2024: A prioritisation study to guide research, development, and public health strategies against antimicrobial resistance. *Lancet Infect Dis*. 2025;25(9):1033-43.
38. O'Neill J. Tackling drug-resistant infections globally: Final report and recommendations. London: Review on Antimicrobial Resistance; 2016.
39. World Health Organization. Global action plan on antimicrobial resistance. Geneva: WHO; 2015.
40. Chen YH, Ko WC, Hsueh PR. Emerging resistance problems and future perspectives in pharmacotherapy for complicated urinary tract infections. *Expert Opin Pharmacother*. 2013;14(5):587-96.