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Antimicrobial Resistance Pattern and Phenotypic Characterization of *Staphylococcus Aureus* and *Escherichia Coli* Isolated from High Vaginal and Urethral Swab Specimens

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Abstract

Background: Antimicrobial resistance (AMR) among urogenital bacterial pathogens is an increasing global public health concern, particularly in low- and middle-income countries. High vaginal and urethral infections are commonly associated with *Staphylococcus aureus* and *Escherichia coli*, which frequently exhibit multidrug resistance. Monitoring antimicrobial susceptibility and phenotypic characteristics of these pathogens is essential for effective treatment and infection control.

Objective: This study aimed to determine the antimicrobial resistance patterns and phenotypic characteristics of *Staphylococcus aureus* and *Escherichia coli* isolated from high vaginal and urethral swab specimens and to assess factors associated with multidrug resistance.

Methods: A hospital-based cross-sectional study was conducted among 240 clinically suspected patients at a tertiary care hospital from March 2025 to November 2025. High vaginal and urethral swab specimens were collected aseptically and processed using standard microbiological procedures. Bacterial identification was performed through colony morphology, Gram staining, and biochemical characterization. Antimicrobial susceptibility testing was carried out using the Kirby–Bauer disk diffusion method according to Clinical and Laboratory Standards Institute (CLSI) guidelines. Multidrug resistance (MDR), methicillin-resistant *Staphylococcus aureus* (MRSA), and resistant *Escherichia coli* isolates were determined phenotypically. Statistical analyses including chi-square test and logistic regression were performed, with $p < 0.05$ considered statistically significant.

Results: Among the 240 specimens collected, 168 (70.0%) demonstrated significant bacterial growth, while 60 (25.0%) showed no growth and 12 (5.0%) revealed mixed growth. Of the culture-positive isolates, *Escherichia coli* was the predominant pathogen accounting for 80 (47.6%) isolates, followed by *Staphylococcus aureus* comprising 64 (38.1%) isolates. The highest culture positivity was observed among patients aged 26–35 years (79.6%), which showed a statistically significant association with bacterial infection ($\chi^2 = 9.85$, $p = 0.020$). Phenotypic characterization demonstrated that 93.8% of *S. aureus* isolates were coagulase-positive and 87.5% fermented mannitol, whereas 93.8% of *E. coli* isolates showed lactose fermentation and 90.0% were indole-positive. Antimicrobial susceptibility analysis revealed high resistance *of E. coli* against ampicillin (81.2%), cotrimoxazole (56.2%), and ceftriaxone (42.5%), while high sensitivity was observed for imipenem (95.0%) and nitrofurantoin (85.0%). Similarly, S. aureus exhibited marked resistance to penicillin (78.1%), erythromycin

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(37.5%), and ciprofloxacin (34.4%), whereas vancomycin (96.9%) and gentamicin (75.0%) demonstrated high effectiveness. Multidrug resistance was detected in 38 (47.5%) *E. coli* isolates and 24 (37.5%) *S. aureus* isolates. MRSA prevalence among *S. aureus* isolates was 34.4%. A significant association was identified between previous antibiotic exposure and MDR infection (χ^2 = 15.37, $p < 0.001$). Inpatient participants showed significantly higher MRSA prevalence compared to outpatients (54.5% vs. 23.8%; $p = 0.009$). Logistic regression analysis further demonstrated that previous antibiotic use (AOR = 3.54, 95% CI: 1.89–6.61, $p < 0.001$) and inpatient admission status (AOR = 2.11, 95% CI: 1.14–3.89, $p = 0.017$) were independent predictors of MDR infection.

Conclusion: The study demonstrated a high burden of antimicrobial resistance among urogenital bacterial pathogens, with *Escherichia coli* and *Staphylococcus aureus* as the predominant isolates. The notable prevalence of multidrug resistance and MRSA highlights the need for continuous antimicrobial surveillance, rational antibiotic use, and effective infection prevention strategies to reduce resistant urogenital infections.

Keywords: Antimicrobial resistance; Escherichia coli; Staphylococcus aureus; Multidrug resistance; High vaginal swab

Introduction

Antimicrobial resistance (AMR) has emerged as one of the most serious global public health threats of the twenty-first century, significantly compromising the effective management of infectious diseases [1]. The rapid increase in resistant bacterial pathogens has become a major concern in both hospital and community settings, particularly in low- and middle-income countries where irrational antibiotic use, self-medication, inadequate infection control practices, and limited microbiological surveillance contribute substantially to the development and dissemination of resistant organisms [2]. Urogenital tract infections are among the most common bacterial infections affecting individuals worldwide and are associated with considerable morbidity, healthcare burden, and reduced quality of life [3]. High vaginal and urethral infections are frequently caused by a wide range of bacterial pathogens, among which *Staphylococcus aureus* and *Escherichia coli* remain predominant etiological agents. *E. coli* is recognized as one of the leading Gram-negative pathogens responsible for urinary and genital tract infections due to its virulence characteristics, colonization ability, and increasing resistance to commonly prescribed antibiotics [4]. Similarly, *S. aureus*, including methicillin-resistant *S. aureus* (MRSA), has emerged as an important opportunistic pathogen associated with both community-acquired and hospital-associated infections. The increasing prevalence of multidrug-resistant (MDR) strains of these organisms poses a significant challenge to empirical antimicrobial therapy and infection management [5]. Phenotypic characterization through colony morphology, Gram staining, and biochemical identification plays a critical role in the accurate diagnosis and differentiation of bacterial pathogens. In addition, antimicrobial susceptibility testing provides essential information regarding local resistance trends and guides clinicians in selecting effective therapeutic options [6]. Several studies have reported increasing resistance of *E. coli* and *S. aureus* against commonly used antibiotics such as ampicillin, penicillin, cotrimoxazole, erythromycin, and fluoroquinolones, whereas relatively higher sensitivity has been observed with carbapenems and glycopeptides. Continuous monitoring of antimicrobial resistance profiles is therefore crucial to support antibiotic stewardship programs and prevent the further spread of resistant pathogens [7]. Despite the growing burden of AMR, data regarding the antimicrobial susceptibility patterns and phenotypic characteristics of bacterial isolates from high vaginal and urethral swab specimens remain limited in much healthcare settings [8]. Furthermore, the association of multidrug resistance with demographic and clinical factors such as hospitalization status and prior antibiotic exposure has not been adequately explored in several regions [9]. Understanding these resistance patterns is essential for improving empirical treatment strategies, minimizing therapeutic failure, and strengthening infection prevention and control measures. Therefore, this study aimed to determine the antimicrobial resistance patterns and phenotypic characteristics of Staphylococcus aureus and Escherichia coli isolated from high vaginal and urethral swab specimens and to assess factors associated with multidrug resistance among clinically suspected patients attending a tertiary care hospital.

Methodology

A hospital-based cross-sectional study was conducted at a tertiary care hospital in Mirpur, Dhaka, Bangladesh, from March 2025 to November 2025 to investigate the antimicrobial resistance patterns and phenotypic characteristics of bacterial isolates obtained from high vaginal and urethral swab specimens. The study included 240 clinically suspected patients attending both inpatient and outpatient departments for microbiological evaluation of urogenital tract infections. Patients presenting with clinical suspicion of urogenital infection and providing high vaginal or urethral swab specimens were included in the study. Specimens with incomplete laboratory information, contamination, or inadequate sample quality were excluded from analysis. Demographic and clinical information were collected from hospital records using a structured data collection form. High vaginal and urethral swab specimens were collected aseptically by trained healthcare personnel following

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standard microbiological procedures. The specimens were immediately transported to the microbiology laboratory and processed without delay to ensure specimen integrity. Samples were inoculated onto Blood agar and MacConkey agar media and incubated aerobically at 37°C for 18-24 hours. Bacterial isolates were identified based on colony morphology, Gram staining characteristics, and conventional biochemical tests. Identification of *Staphylococcus aureus* was confirmed by catalase, coagulase, and mannitol fermentation tests, whereas *Escherichia coli* isolates were identified through lactose fermentation, indole production, citrate utilization, and motility testing. Antimicrobial susceptibility testing was performed using the Kirby–Bauer disk diffusion method on Mueller-Hinton agar according to the guidelines of the Clinical and Laboratory Standards Institute (CLSI). The zones of inhibition were measured and interpreted as sensitive, intermediate, or resistant based on CLSI interpretive criteria. Multidrug resistance (MDR) was defined as resistance to at least one antimicrobial agent in three or more antibiotic classes. Methicillin-resistant *Staphylococcus aureus* (MRSA) was determined phenotypically using the cefoxitin disk diffusion method [10]. Data were entered and analysed using Statistical Package for the Social Sciences (SPSS) version 26. Descriptive statistics were used to summarize demographic and microbiological findings. Associations between categorical variables were evaluated using the chi-square test, while logistic regression analysis was performed to identify predictors associated with multidrug resistance. A p-value of less than 0.05 was considered statistically significant. Confidentiality and anonymity of all participant information were maintained throughout the study.

Results

A total of 240 clinically suspected patients were included in this hospital-based cross-sectional study conducted at a tertiary care hospital in Mirpur, Dhaka, Bangladesh. As shown in table 1, most participants belonged to the 26-35 years age group, accounting for 98 (40.8%) cases, followed by the 18-25 years age group with 72 (30.0%) participants. Among the collected specimens, high vaginal swabs constituted the majority with 170 (70.8%) samples, whereas urethral swabs accounted for 70 (29.2%) samples. Most participants were outpatients [185 (77.1%)], while 55 (22.9%) were hospitalized patients. Previous antibiotic exposure was documented in 70 (29.2%) participants, whereas 170 (70.8%) had no recent history of antibiotic use.

The phenotypic characteristics of the major bacterial isolates are summarized in table 3. All *S. aureus* isolates demonstrated Gram-positive cocci morphology and catalase positivity [64 (100%)]. Coagulase positivity was observed in 60 (93.8%) isolates, while mannitol fermentation positivity was detected in 56 (87.5%) isolates. In contrast, all *E. coli* isolates exhibited Gram-negative bacilli morphology [80 (100%)]. Lactose fermentation positivity was observed in 75 (93.8%) isolates, indole positivity in 72 (90.0%), citrate negativity in 68 (85.0%), and motility positivity in 70 (87.5%) isolates.

Table 1: Demographic and Clinical Characteristics (n = 240).

Variables	Frequency (n)	Percentage (%)
Age Group (Years)		
18–25	72	30
26–35	98	40.8
36–45	48	20
>45	22	9.2
Specimen Type		
High vaginal swab	170	70.8
Urethral swab	70	29.2
Patient Status		
Outpatient	185	77.1
Inpatient	55	22.9
Previous Antibiotic Exposure		
Yes	70	29.2
No	170	70.8

Table 2: Culture Positivity and Distribution of Bacterial Isolates (n = 240).

Culture Positivity			
Culture Findings	**Frequency (n)**	**Percentage (%)**	-
Positive growth	168	70	-
No growth	60	25	-
Mixed growth	12	5	-
Distribution of Bacterial Isolates (n = 168)			
Organisms	**HVS n (%)**	**Urethral Swab n (%)**	**Total n (%)**
Escherichia coli	58 (72.5)	22 (27.5)	80 (47.6)
Staphylococcus aureus	46 (71.9)	18 (28.1)	64 (38.1)
Klebsiella spp.	10 (66.7)	5 (33.3)	15 (8.9)
Proteus spp.	4 (57.1)	3 (42.9)	7 (4.2)
Pseudomonas spp.	1 (50.0)	1 (50.0)	2 (1.2)

The antimicrobial susceptibility profile of *Escherichia coli* isolates is presented in table 4. High resistance rates were observed against ampicillin [65 (81.2%)], cotrimoxazole [45 (56.2%)], and ceftriaxone [34 (42.5%)]. Moderate resistance was also observed for ciprofloxacin [29 (36.2%)]. Conversely, *E. coli* isolates demonstrated high sensitivity to imipenem [76 (95.0%)] and nitrofurantoin [68 (85.0%)], followed by gentamicin [55 (68.8%)]. Only 4 (5.0%) isolates were resistant to imipenem.

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Table 3: Phenotypic Characteristics of Bacterial Isolates.

Phenotypic Characteristics	*S. aureus* n (%)	*E. coli* n (%)
Gram-positive cocci	64 (100)	—
Gram-negative bacilli	—	80 (100)
Catalase positive	64 (100)	—
Coagulase positive	60 (93.8)	—
Mannitol fermentation positive	56 (87.5)	—
Lactose fermentation positive	—	75 (93.8)
Indole positive	—	72 (90.0)
Citrate negative	—	68 (85.0)
Motility positive	—	70 (87.5)

Table 4: Antimicrobial Susceptibility of Escherichia coli (n = 80).

Antibiotics	Sensitive n (%)	Intermediate n (%)	Resistant n (%)
Ampicillin	12 (15.0)	3 (3.8)	65 (81.2)
Ceftriaxone	40 (50.0)	6 (7.5)	34 (42.5)
Ciprofloxacin	46 (57.5)	5 (6.3)	29 (36.2)
Cotrimoxazole	30 (37.5)	5 (6.3)	45 (56.2)
Gentamicin	55 (68.8)	4 (5.0)	21 (26.2)
Nitrofurantoin	68 (85.0)	2 (2.5)	10 (12.5)
Imipenem	76 (95.0)	0	4 (5.0)

S = Sensitive; I = Intermediate; R = Resistant

As shown in table 5, *Staphylococcus aureus* isolates exhibited substantial resistance to penicillin [50 (78.1%)], erythromycin [24 (37.5%)], and ciprofloxacin [22 (34.4%)]. Resistance to cefoxitin was identified in 22 (34.4%) isolates, indicating methicillin resistance. However, vancomycin demonstrated the highest effectiveness against *S. aureus*, with sensitivity observed in 62 (96.9%) isolates, followed by gentamicin [48 (75.0%)] and clindamycin [44 (68.8%)].

Table 5: Antimicrobial Susceptibility of *Staphylococcus aureus* (n = 64).

Antibiotics	Sensitive n (%)	Intermediate n (%)	Resistant n (%)
Penicillin	10 (15.6)	4 (6.3)	50 (78.1)
Cefoxitin	42 (65.6)	0	22 (34.4)
Erythromycin	35 (54.7)	5 (7.8)	24 (37.5)
Clindamycin	44 (68.8)	3 (4.7)	17 (26.5)
Ciprofloxacin	38 (59.4)	4 (6.3)	22 (34.4)
Gentamicin	48 (75.0)	2 (3.1)	14 (21.9)
Vancomycin	62 (96.9)	0	2 (3.1)

S = Sensitive; I = Intermediate; R = Resistant

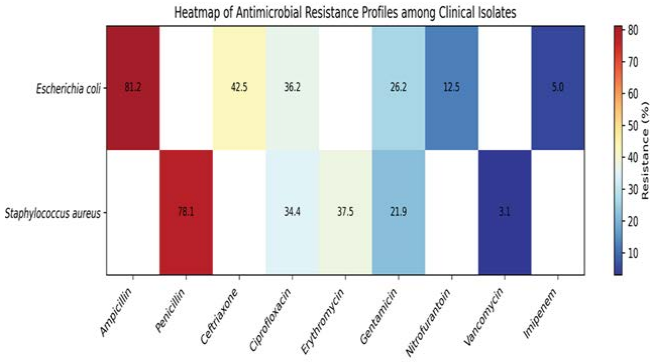

Figure 1: Heatmap of Antimicrobial Resistance Profiles among *Escherichia coli* and *Staphylococcus aureus* Isolates.

The heatmap (figure 1) revealed markedly elevated resistance of *E. coli* against ampicillin (81.2%) and cotrimoxazole-associated antibiotics, whereas *S. aureus* demonstrated substantial resistance to penicillin (78.1%) and erythromycin (37.5%). In contrast, lower resistance rates were observed for imipenem among *E. coli* (5.0%) and vancomycin among *S. aureus* (3.1%), indicating preserved susceptibility to these agents. Overall, the heatmap visually emphasizes the high prevalence of resistance against commonly used empirical antibiotics. The prevalence of methicillin-resistant *Staphylococcus aureus* (MRSA) is illustrated in table 6. Among the 64 *S. aureus* isolates, 22 (34.4%) were identified as MRSA, whereas 42 (65.6%) were methicillin-sensitive *Staphylococcus aureus* (MSSA).

Table 6: Prevalence of MRSA among *Staphylococcus aureus* Isolates (n = 64).

Category	Frequency (n)	Percentage (%)
MRSA	22	34.4
MSSA	42	65.6

Associations between demographic and clinical factors with multidrug-resistant (MDR) infections are shown in Table 7. A statistically significant association was observed between age greater than 35 years and MDR infection (χ^2 = 4.27, p = 0.039). Previous antibiotic exposure demonstrated a strong association with MDR positivity, where 41 (58.6%) participants with prior antibiotic use developed MDR infections (χ^2 = 15.37, p < 0.001). Similarly, inpatient status was significantly associated with MDR infection (χ^2 = 6.81, p = 0.009). MRSA-positive isolates also showed a significant relationship with MDR status, with 15 (68.2%) MRSA isolates exhibiting multidrug resistance (χ^2 = 8.42, p = 0.004).

The logistic regression analysis presented in table 8 identified several independent predictors associated with MDR infection. Previous antibiotic exposure was found to be the strongest predictor of MDR infection [Adjusted Odds

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Table 7: Factors Associated with Multidrug Resistant (MDR) Infections.

Variables	MDR Positive n (%)	MDR Negative n (%)	χ^2 value	*p*-value
Age >35 years	28 (45.2)	34 (54.8)	4.27	0.039*
Previous antibiotic exposure	41 (58.6)	29 (41.4)	15.37	<0.001*
Inpatient status	26 (47.3)	29 (52.7)	6.81	0.009*
MRSA-positive isolates	15 (68.2)	7 (31.8)	8.42	0.004*

*Statistically significant

Table 8: Logistic Regression Analysis of Predictors Associated with MDR Infection.

Variables	Adjusted Odds Ratio (AOR)	95% Confidence Interval	*p*-value
Previous antibiotic exposure	3.54	1.89–6.61	<0.001*
Inpatient admission	2.11	1.14–3.89	0.017*
Age >35 years	1.78	1.02–3.12	0.043*
MRSA positivity	2.64	1.21–5.76	0.014*

*Statistically significant

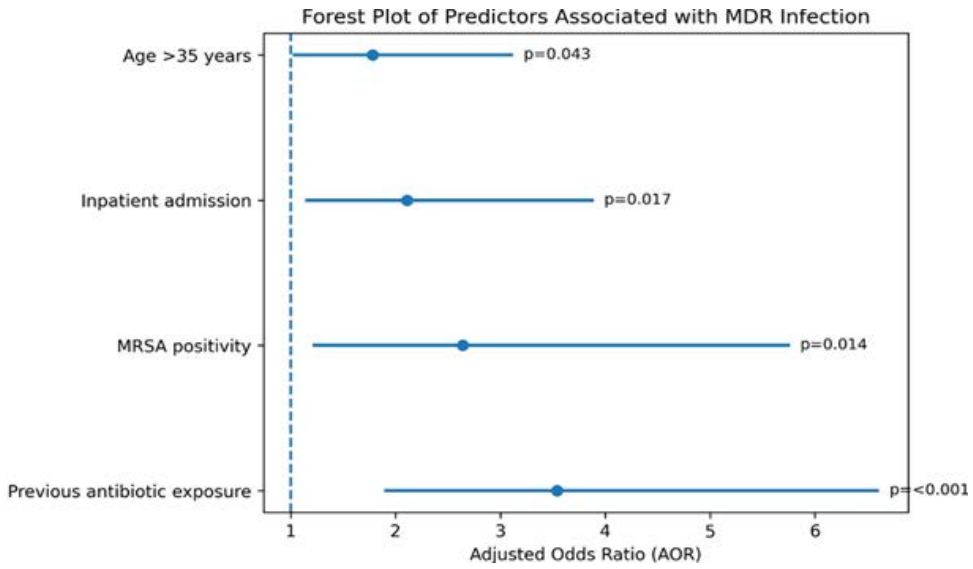

Figure 2: Forest Plot of Predictors Associated with Multidrug-Resistant Infection.

Ratio (AOR) = 3.54, 95% CI: 1.89–6.61, p < 0.001]. Inpatient admission status was associated with a more than two-fold increased risk of MDR infection (AOR = 2.11, 95% CI: 1.14–3.89, p = 0.017). Participants aged above 35 years also demonstrated significantly increased odds of MDR infection (AOR = 1.78, 95% CI: 1.02–3.12, p = 0.043). Furthermore, MRSA positivity independently predicted MDR infection with an AOR of 2.64 (95% CI: 1.21–5.76, p = 0.014).

The forest plot illustrates the independent predictors associated with multidrug-resistant (MDR) infection identified through multivariable logistic regression analysis. Each predictor is represented by an adjusted odds ratio (AOR) with corresponding 95% confidence intervals (CI). The vertical reference line at odds ratio (OR) = 1 indicates no association, while predictors positioned to the right of the reference line indicate increased odds of MDR infection.

The logistic regression probability curve demonstrated a progressive increase in MDR infection risk with increasing clinical risk factors. Low-risk participants showed a predicted MDR probability of 12%, compared to 38% among moderate-risk and 71% among high-risk participants. Patients with previous antibiotic exposure exhibited a markedly higher MDR probability (68%) than those without exposure (24%). Similarly, hospitalized patients with MRSA positivity demonstrated the highest predicted MDR probability (74%), highlighting the cumulative impact of clinical risk factors on antimicrobial resistance (figure 3).

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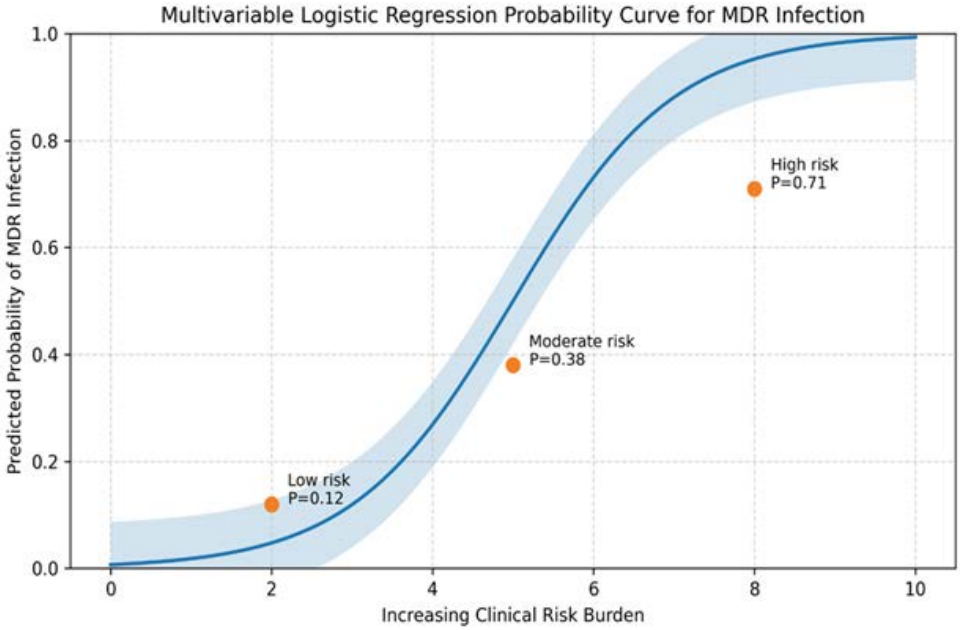

Figure 3: Multivariable Logistic Regression Probability Curve for MDR Infection.

Discussion

In the current study, culture positivity was observed in 70.0% of collected specimens, which is comparable to findings reported from several South Asian and African hospital-based studies where culture positivity ranged between 60% and 75%. The predominance of positive cultures in the present study may be associated with poor genital hygiene, inappropriate empirical antibiotic use, and increased exposure to healthcare-associated infections. Most participants belonged to the 26–35 years age group (40.8%), indicating that sexually active and reproductive-age individuals are more vulnerable to urogenital bacterial infections. Similar age-related predominance has been reported in studies conducted in India, Pakistan, and Ethiopia, where reproductive-age females represented the most affected population group [11,12]. Among the bacterial isolates, *Escherichia coli* was the predominant pathogen accounting for 47.6% of isolates, followed by *Staphylococcus aureus* comprising 38.1%. Comparable findings have been documented in studies from Bangladesh, Nepal, and Nigeria, where *E. coli* was reported as the leading etiological agent of urogenital infections. The predominance of *E. coli* may be attributed to its colonization ability, virulence factors, and close anatomical proximity between the gastrointestinal and urogenital tracts [13,14]. Similarly, the considerable prevalence of *S. aureus* observed in the present study supports previous reports identifying this organism as an important opportunistic pathogen associated with both community-acquired and healthcare-associated infections [15]. Phenotypic characterization demonstrated that 93.8% of *S. aureus* isolates were coagulase-positive and 87.5% showed mannitol fermentation positivity, which is consistent with standard microbiological characteristics reported in previous clinical studies. Similarly, most *E. coli* isolates exhibited lactose fermentation positivity (93.8%) and indole positivity (90.0%), findings that are comparable to reports from microbiological surveillance studies conducted in India and Southeast Asia [16]. These observations confirm the reliability of conventional biochemical methods for the identification of clinically important bacterial pathogens in resource-limited settings. The antimicrobial susceptibility profile revealed alarming resistance rates among both Gram-negative and Gram-positive isolates. In the present study, *E. coli* demonstrated very high resistance to ampicillin (81.2%), cotrimoxazole (56.2%), and ceftriaxone (42.5%). Similar resistance trends have been reported in studies [17,18], from Bangladesh, India, and Pakistan, where resistance to ampicillin frequently exceeded 70%. The elevated resistance against commonly prescribed antibiotics may reflect irrational antibiotic consumption, over-the-counter availability of antimicrobials, incomplete treatment courses, and limited antimicrobial stewardship practices. In contrast, imipenem (95.0%) and nitrofurantoin (85.0%) retained high effectiveness against *E. coli*, which is comparable to findings reported from tertiary care centers in South Asia and the Middle East [19]. Likewise, *Staphylococcus aureus* isolates exhibited substantial resistance to penicillin (78.1%), erythromycin (37.5%), and ciprofloxacin (34.4%). Comparable resistance patterns have been documented in studies from African and Asian healthcare settings, where penicillin resistance among *S. aureus* frequently exceeded 75%. The high resistance to β-lactam antibiotics may be associated with prolonged antibiotic exposure and the widespread dissemination of resistant strains within healthcare

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facilities. However, vancomycin demonstrated excellent effectiveness with 96.9% sensitivity, while gentamicin and clindamycin also retained comparatively favorable activity. These findings are clinically significant because vancomycin remains one of the most reliable therapeutic options for severe *S. aureus* infections, particularly in MRSA-associated cases [20]. The prevalence of methicillin-resistant *Staphylococcus aureus* (MRSA) in the present study was 34.4%, which is comparable to reports from tertiary hospitals in South Asia where MRSA prevalence ranged from 25% to 45%. The increasing prevalence of MRSA remains a major concern because MRSA-associated infections are frequently linked with prolonged hospitalization, increased healthcare costs, therapeutic failure, and elevated morbidity. The high prevalence observed in the current study may indicate inadequate infection prevention measures and inappropriate antibiotic usage within hospital and community settings [21]. The study further identified significant associations between multidrug resistance and several demographic and clinical variables. Participants with previous antibiotic exposure showed a significantly higher prevalence of MDR infection (58.6%; $p < 0.001$), consistent with findings from studies conducted in China, Ethiopia, and India where prior antibiotic use was identified as one of the strongest predictors of resistant infections [22,23]. Similarly, inpatient admission status demonstrated a significant association with MDR positivity ($p = 0.009$), suggesting that hospitalized patients may have increased exposure to resistant organisms due to prolonged healthcare contact and invasive procedures. MRSA-positive isolates also showed a strong relationship with MDR infection, where 68.2% of MRSA isolates demonstrated multidrug resistance. Multivariable logistic regression analysis further confirmed that previous antibiotic exposure was the strongest independent predictor of MDR infection (AOR = 3.54, 95% CI: 1.89–6.61). Hospitalization status and MRSA positivity also independently increased the likelihood of MDR infection. These findings are supported by previous epidemiological studies from low- and middle-income countries, where prior antibiotic exposure and healthcare-associated transmission were consistently identified as major contributors to antimicrobial resistance. The forest plot and logistic regression probability curve generated in the present study further emphasized the cumulative effect of multiple clinical risk factors on MDR infection probability. Patients with previous antibiotic exposure demonstrated a predicted MDR probability of 68%, while hospitalized patients with MRSA positivity exhibited the highest probability of MDR infection at 74%.

Conclusion

The present study revealed a high burden of antimicrobial resistance among urogenital bacterial pathogens, with *Escherichia coli* and *Staphylococcus aureus* identified as the predominant isolates. High resistance to commonly used antibiotics and the notable prevalence of multidrug resistance and MRSA highlight the growing challenge of resistant infections. Previous antibiotic exposure, hospitalization, and MRSA positivity were significant predictors of MDR infection. Continuous antimicrobial surveillance, rational antibiotic use, and effective infection control measures are essential to reduce the spread of resistant pathogens.

Limitations

The present study has several limitations that should be considered while interpreting the findings. First, the study was conducted in a single tertiary care hospital, which may limit the generalizability of the results to other healthcare settings and populations. Second, the relatively limited sample size may not fully represent the overall burden of antimicrobial resistance among urogenital pathogens in Bangladesh. Third, molecular characterization of resistance genes and advanced genotypic analysis were not performed due to limited laboratory resources, preventing detailed identification of specific resistance mechanisms. Additionally, information regarding prior antibiotic consumption relied partly on patient history, which may have introduced recall bias. Despite these limitations, the study provides important baseline data regarding antimicrobial resistance patterns and phenotypic characteristics of clinically significant bacterial isolates.

Recommendations

Based on the findings of the present study, routine antimicrobial susceptibility testing should be encouraged before initiating empirical antibiotic therapy for urogenital infections. Continuous antimicrobial resistance surveillance programs should be strengthened to monitor emerging resistance trends and guide evidence-based treatment protocols. Healthcare facilities should implement effective antimicrobial stewardship programs to reduce inappropriate antibiotic use and minimize the development of multidrug-resistant organisms. Strict infection prevention and control measures, particularly in hospital settings, are essential to limit the spread of resistant pathogens, including MRSA. In addition, multicentre studies with larger sample sizes and molecular characterization of resistance genes are recommended to better understand the epidemiology and genetic mechanisms of antimicrobial resistance in Bangladesh.

Author contributions

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Conflict of Interest

The authors declare that there is no conflict of interest regarding the publication of this study.

Ethical considerations

Permission to conduct the study was obtained from the hospital authority prior to data collection. All procedures were carried out in accordance with institutional ethical standards and principles of biomedical research. Patient confidentiality and privacy were strictly maintained throughout the study, and all collected data were used solely for research purposes without disclosing personal identifiers.

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