Research Article

The Bacterial Profile and Antimicrobial Susceptibility Patterns of Urinary Tract Infection Patients at Pawe General Hospital, Northwest Ethiopia

Abayeneh Girma and Aleka Aemiro

Department of Biology, College of Natural and Computational Science, Mek dela Amba University, P.O. Box 32, Tuluawlia, Ethiopia

Correspondence should be addressed to Abayeneh Girma; gabayeneh2013@gmail.com

Received 3 November 2021; Revised 24 February 2022; Accepted 2 April 2022; Published 25 April 2022

Academic Editor: Joaquim Ruiz

Copyright © 2022 Abayeneh Girma and Aleka Aemiro. This is an open access article distributed under the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Urinary tract infection remains the most common infection widespread worldwide in both community and hospital settings. Rapidly increasing antibiotic resistance of uropathogens is resulting in limited treatment options. Thus, understanding the current uropathogens and their antimicrobial susceptibilities is essential for effective urinary tract infection treatment. The purpose of this study was to isolate, characterize, and determine the antimicrobial susceptibility patterns of bacterial pathogens associated with urinary tract infection at Pawe General Hospital in Northwest Ethiopia. A hospital-based cross-sectional study design was conducted from January to April, 2020, at Pawe General Hospital. Midstream urine specimens were collected from 141 individuals with suspected urinary tract infection for bacteriological identification and antimicrobial susceptibility testing. Among the 141 study participants, twenty-nine (20.6%) showed significant bacteriuria. Escherichia coli (42.6%) had the highest proportion of isolated uropathogen followed by Klebsiella spp. and Pseudomonas spp. each (10.7%); Proteus spp. (9.3%); coagulase negative staphylococci, Staphylococcus aureus, and Enterobacter spp. each (6.7%); Citrobacter spp. (4%); and Enterococcus faecalis and Streptococcus spp. each (1.3%). Outpatient isolates showed a resistance of 64% and 78.6% to amoxicillin-clavulanic acid and tetracycline, respectively. Inpatients showed 63.9% and 87.2% of resistance to cephalaxin and tetracycline. It was also observed that all the isolates have a multiple antimicrobial resistance index greater than 0.20 except Citrobacter spp. (0.142) in inpatients. Even though in this locality, most isolates were sensitive to ceftriaxone, gentamicin, ciprofloxacin, nitrofurantoin, and norfloxacin, they are considered appropriate antimicrobials for empirical treatment of urinary tract bacterial infections. Periodic monitoring of etiology and drug susceptibility is highly recommended, along with health education on the transmission and causes of urinary tract infection.

1. Introduction

Urinary tract infections (UTIs) are infections caused by infectious agents (bacteria, fungi, virus, and parasites) present and propagate in any part (bladder = cystitis, kidney = pyelonephritis, urethra = urethritis, ureters = urethritis, and urine = bacteriuria) of the urinary tract [1]. The infection of the urinary tract can either be asymptomatic or symptomatic and can occur in uncomplicated (UTIs that occur in a normal genitourinary tract with no prior instrumentation) or complicated (infections that diagnosed in genitourinary tracts that have structural or functional abnormalities, including instrumentation such as indwelling urethral catheters, and are frequently asymptomatic) individuals [2]. Annually, one hundred fifty million people are diagnosed with urinary tract infections across the world and subsequently spend around six billion dollars on health care [1, 2]. In low-income countries like Ethiopia, UTIs lead to treatment failures and long-term hospital complications, threaten our ability to perform modern medical procedures, impose a major economic burden on society, and finally result in too much morbidity and mortality [1–3].
Compared to other uropathogens, bacterial urinary tract infections are the most common and dangerous infections in humans and occur frequently in the community and hospital environments [1–4]. *Escherichia coli*, *Klebsiella* spp., *Enterobacter* spp., *Proteus* spp., *Pseudomonas* spp., *Acinetobacter* spp., *Serratia* spp., and *Citrobacter* spp. are Gram-negative bacteria with the most causative agents covering ninety percent of UTIs. Group B *streptococci*, *Enterococcus* spp., and *Staphylococcus* spp. are from the Gram-positive bacteria responsible for the remaining ten percent of UTI cases [3, 4]. Of all, *E. coli* are the most common and frequently isolated uropathogens accounting for sixty-five to ninety percent of the urinary tract bacterial infections [1–6]. Depending on the different factors like age, sex, catheterization, hospitalization, and previous exposure to antimicrobials; the relative frequency of both Gram-positive and Gram-negative bacterial pathogens may greatly vary.

Treatment and therapy for urinary tract infections is determined experimentally by the antimicrobial susceptibility testing. In Africa, however, it is observed that due to the high level of poverty, illiteracy, and poor hygienic practices, the easy availability and low cost of drugs, the high prevalence of fake and spurious drugs, the uncontrolled prescription and usage of antibiotics, and the lack of rapid laboratory facility for sensitivity test contributes to the emergence of resistant bacterial infections especially in uropathogens. The resistant strains of bacteria can be accelerated and spread by the transfer of resistant genes among species and genera through horizontal gene transfer (transformation, transduction, or/and conjugation) with mobile genetic elements (plasmids, transposons, or/and bacteriophages). This process results in the development and dissemination of new antimicrobial resistance varieties and novel resistance mechanisms among uropathogens due to the presence of R-plasmids that mediate resistance genes against various classes of commonly used antimicrobial agents. Since antibiotic resistance rates of pathogenic bacteria may vary from country to country, regionally and locally, and can also change rapidly with time, as such, they need to be monitored and managed closely because of their public health implications and impacts [5, 6].

Regarding the resistance rates in Ethiopia, different reports showed that a high incidence of resistance to the commonly used antimicrobial agents was observed [1, 2, 4–6], even though there are few published information available concerning the etiology and resistance patterns of urinary tract bacterial infections in some hospitals of Ethiopia. To the best of our knowledge, there is no previous study and published information on UTIs in the study area. Thus, this study was aimed to assess bacteriological profile and antimicrobial susceptibility patterns of symptomatic urinary tract infection among patients in Pawe General Hospital (PGH).

2. Materials and Methods

2.1. Study Setting, Design, and Period. Hospital-based cross-sectional study was conducted at Pawe General Hospital from January to April 2020. Pawe General Hospital is the mere public hospital found in Pawe town and provides various health services for routine cases. The hospital was chosen because it covers both rural and urban areas of the town. The town is found at a distance of 573 km from Addis Ababa which is the capital city of Ethiopia.

2.2. Sample Size Determination. Single population proportion formula was used to determine the sample size.

\[
 n = \frac{Z^2 \times P(1-P)}{d^2},
\]

where, \(Z = z\)-score for 95% confidence interval = 1.96. \(P = \) prevalence, and \(d = \) tolerable error = 5%. Since there was no data in Ethiopia, the prevalence of UTI among both inpatients and outpatients was taken from Chad (32.7%) which was done by Kengne et al. [7]

\[
 n = \frac{(1.96)^2 \times 0.327 \times (1 - 0.327)}{0.05^2} = 338 + 10\%\text{contingency}, 128 + 13 = 141.
\]

Therefore, a total of 141 UTI inpatient and outpatients were included in the study from the hospital.

2.3. Inclusion and Exclusion Criteria. One hundred forty-one patients to whom a cytobacteriological examination of urine was prescribed and who had not received antimicrobials within the previous two weeks were eligible for inclusion due to the fact that the antibiotic must have inhibited or destroyed the pathogens. UTI patients who were not willing to participate were excluded from this study.

2.4. Sample Collection. Clean catch mid-stream urine sample collection approach with aseptic measures was applied to minimize contamination of the sample [8]. A total of 141 fresh midstream urine samples were collected from both inpatient and outpatient UTI suspected individuals using sterile screw-capped universal container. The specimens were appropriately labeled and immediately processed after sampling.

2.5. Culturing and Identification of Isolates. The collected urine samples were spread on cysteine lactose electrolyte-deficient medium, MacConkey agar, and blood agar (Oxoid, UK) using L-shaped glass spreader and incubated aerobically at 37°C for 24 h. A significant bacteriuria was considered if urine culture yields ≥10⁶ CFU/mL. All positive
urine cultures with significant bacteriuria were further identified by their colony characteristics, Gram-staining reaction, and pattern of biochemical profiles using standard procedures. Enterobacteriaceae were identified by H₂S production and carbohydrate utilization tests in TSI agar, motility test, urease test, and IMViC (indole, methyl red, Voges-Proskauer, and citrate utilization) tests. Gram-positive bacteria were identified using catalase and coagulase tests [9].

2.6. Standardization of the Inoculum. 0.5 McFarland standard was prepared by mixing 0.50 mL of a (1.175% w/v) dehydrate barium chloride (BaCl₂·2H₂O) solution with 99.50 mL of (1% v/v) sulfuric acid (H₂SO₄) with constant stirring in a graduated cylinder. The turbidity standard solution was aliquoted into test tubes identical to those used to prepare the inoculum suspension. In addition, the absorbance of the prepared 0.5 McFarland standard solution was further confirmed to be 0.08 to 0.12 at 625 nm using spectrophotometry. To prevent evaporation, the tube containing a standard solution was tightly sealed and stored at room temperature. Before comparing with the bacterial suspension, the turbidity standard tube was vigorously mixed by the vortex mixer which makes a uniform turbid appearance [10].

2.7. Inoculum Preparation. From an overnight culture, 3–5 morphologically identical bacterial colonies were suspended in 5 mL of normal saline (0.85%; 8.5g/L NaCl) vigorously mixed by the vortex mixer and comparing to that of 0.5 McFarland standards which are approximately equivalent to 1.5 × 10⁸ CFU/mL. After adjusting the turbidity, a sterile cotton swab was dipped into the suspension and streaked over the entire surface of the prepared medium by rotating the plate in 60° to ensure the even distribution of the inoculum [10].

2.8. Antimicrobial Susceptibility Testing. Antimicrobial susceptibility testing was performed using Kirby-Bauer’s disk diffusion method [11]. The antimicrobial agents were selected due to the physicians prescribed for treatment of UTIs in the study setting. The standard commercially available (Oxoid, UK) antibiotic discs, namely, amoxicillin/clavulanic acid (AMC, 20/10 µg), cephalexin (CEPH, 30 µg), ceftriaxone (CRO, 30 µg), tetracycline (TE, 30 µg), gentamicin (CN, 10 µg), ciprofloxacin (CIP, 5 µg) nitrofurantoin (F, 300 µg), and norfloxacin (NOR, 10 µg) were used. These discs were aseptically laid with proper spacing on the surface of the inoculated agar plates and then pressed firmly onto the agar with sterile forceps and incubated at 35–37°C, for 18–24 hours. The diameter of inhibition around the discs was measured to the nearest millimeter and interpreted as sensitive (S), intermediate (I), or resistant (R) according to the annually published microbiological breakpoints of CLSI [12]. Bacterial isolates resistant to three or more antimicrobials belonging to the different structural classes were considered multidrug resistant (MDR).

2.9. Quality Control. All materials, equipment, and procedures required for the study were adequately controlled. All specimens were immediately processed after collection. Only specimens which produced ≥10⁵ CFU/mL of urine were considered significant for the study. E. coli (ATCC® 25922), and S. aureus (ATCC® 25923) standard reference strains were used for testing sterility and performance of culture media and antibiotic discs. Generally, CLSI 2020 guidelines were strictly followed.

2.10. MARI Determination. The multiple antimicrobial resistance index (MARI) is the ratio between the number of antibiotics resisted by the pathogen (a) and the total number of antibiotics used in this study (b).

2.11. Ethical Considerations. Ethical clearance was obtained from Pawe General Hospital Administration. A written informed consent was also obtained from each participant before collecting the data. All information obtained in the course of the study were kept confidential and used solely for the purpose of the study.

2.12. Data Analysis. Data were entered and analyzed using SPSS version 25.0 software. Discrete variables were

| Urinary tract bacterial isolates | Number of isolates (N) | Percentage (%) |
|---------------------------------|------------------------|----------------|
|                                 | Inpatient | Outpatient | Inpatient | Outpatient |
| E. coli                         | 21        | 11         | 33.60     | 32.50      |
| Klebsiella spp.                 | 5         | 3          | 15.81     | 15.00      |
| Proteus spp.                    | 4         | 3          | 13.84     | 13.50      |
| Pseudomonas spp.                | 5         | 3          | 9.88      | 11.00      |
| CNS                             | 3         | 2          | 7.91      | 9.00       |
| Staphylococcus aureus           | 3         | 2          | 6.72      | 6.50       |
| Enterobacter spp.               | 3         | 2          | 5.92      | 5.50       |
| Citrobacter spp.                | 2         | 1          | 3.95      | 3.50       |
| Enterococcus faecalis           | 1         | 0          | 2.37      | 2.00       |
| Streptococcus spp.              | 0         | 1          | 0.0       | 1.50       |
| Total                           | 47        | 28         | 100%      | 100%       |

CNS: coagulase negative staphylococci.

Table 1: Distribution of uropathogens in patients.
### Table 2: Antimicrobial susceptibility pattern of uropathogens isolated from urine specimens of inpatients.

| Bacterial pattern | Isolates | Amoxicillin/Cephalothin | Ceftriaxone | Tetracycline | Gentamicin | Ciprofloxacin | Norfloxacin | Nitrofurantoin |
|-------------------|----------|-------------------------|-------------|--------------|------------|---------------|-------------|--------------|
| **E. coli (N=21)** | S        | 5 (23.8)                | 8 (38.1)    | 1 (4.8)      | 19 (90.4)  | 21 (100)      | 21 (100)    | 21 (100)     |
|                   | I        | 1 (4.8)                 | 1 (4.8)     | 1 (4.8)      | 1 (4.8)    | 0 (0.0)       | 0 (0.0)     | 0 (0.0)      |
|                   | R        | 15 (71.4)               | 12 (57.1)   | 19 (90.4)    | 1 (4.8)    | 0 (0.0)       | 0 (0.0)     | 0 (0.0)      |
| **Klebsiella spp. (N=5)** | S        | 2 (40)                  | 3 (60)      | 0 (0.0)      | 4 (80)     | 5 (100)       | 5 (100)     | 5 (100)      |
|                   | I        | 1 (20)                  | 0 (0.0)     | 1 (20)       | 1 (20)    | 0 (0.0)       | 0 (0.0)     | 0 (0.0)      |
|                   | R        | 15 (71.4)               | 12 (57.1)   | 19 (90.4)    | 1 (4.8)    | 0 (0.0)       | 0 (0.0)     | 0 (0.0)      |
| **Proteus spp. (N=4)** | S        | 2 (50)                  | 2 (50)      | 0 (0.0)      | 3 (75)     | 4 (100)       | 4 (100)     | 4 (100)      |
|                   | I        | 1 (25)                  | 1 (25)      | 0 (0.0)      | 0 (0.0)    | 0 (0.0)       | 0 (0.0)     | 0 (0.0)      |
|                   | R        | 2 (50)                  | 2 (50)      | 0 (0.0)      | 3 (75)     | 4 (100)       | 4 (100)     | 4 (100)      |
| **Pseudomonas spp. (N=5)** | S        | 1 (20)                  | 0 (0.0)     | 1 (20)       | 0 (0.0)    | 0 (0.0)       | 0 (0.0)     | 0 (0.0)      |
|                   | I        | 0 (0.0)                 | 2 (40)      | 0 (0.0)      | 0 (0.0)    | 0 (0.0)       | 0 (0.0)     | 0 (0.0)      |
|                   | R        | 15 (71.4)               | 12 (57.1)   | 19 (90.4)    | 1 (4.8)    | 0 (0.0)       | 0 (0.0)     | 0 (0.0)      |
| **CNS (N=3)**     | S        | 1 (33.3)                | 2 (66.7)    | 0 (0.0)      | 3 (100)    | 3 (100)       | 3 (100)     | 3 (100)      |
|                   | I        | 0 (0.0)                 | 0 (0.0)     | 0 (0.0)      | 0 (0.0)    | 0 (0.0)       | 0 (0.0)     | 0 (0.0)      |
|                   | R        | 2 (66.7)                | 1 (33.3)    | 3 (100)      | 0 (0.0)    | 0 (0.0)       | 0 (0.0)     | 0 (0.0)      |
| **S. aureus (N=3)** | S        | 1 (33.3)                | 2 (66.7)    | 0 (0.0)      | 3 (100)    | 3 (100)       | 3 (100)     | 3 (100)      |
|                   | I        | 0 (0.0)                 | 0 (0.0)     | 0 (0.0)      | 0 (0.0)    | 0 (0.0)       | 0 (0.0)     | 0 (0.0)      |
|                   | R        | 2 (66.7)                | 1 (33.3)    | 3 (100)      | 0 (0.0)    | 0 (0.0)       | 0 (0.0)     | 0 (0.0)      |
| **Enterobacter spp. (N=3)** | S        | 1 (33.3)                | 2 (66.7)    | 0 (0.0)      | 3 (100)    | 3 (100)       | 3 (100)     | 3 (100)      |
|                   | I        | 0 (0.0)                 | 0 (0.0)     | 0 (0.0)      | 0 (0.0)    | 0 (0.0)       | 0 (0.0)     | 0 (0.0)      |
|                   | R        | 2 (66.7)                | 1 (33.3)    | 3 (100)      | 0 (0.0)    | 0 (0.0)       | 0 (0.0)     | 0 (0.0)      |
| **Citrobacter spp. (N=2)** | S        | 0 (0.0)                 | 0 (0.0)     | 0 (0.0)      | 1 (100)    | 1 (100)       | 1 (100)     | 1 (100)      |
|                   | I        | 2 (100)                 | 1 (50)      | 0 (0.0)      | 1 (100)    | 1 (100)       | 1 (100)     | 1 (100)      |
|                   | R        | 0 (0.0)                 | 1 (100)     | 1 (100)      | 0 (0.0)    | 0 (0.0)       | 0 (0.0)     | 0 (0.0)      |
| **E. faecalis (N=1)** | S        | 0 (0.0)                 | 0 (0.0)     | 0 (0.0)      | 1 (100)    | 1 (100)       | 1 (100)     | 1 (100)      |
|                   | I        | 0 (0.0)                 | 0 (0.0)     | 0 (0.0)      | 0 (0.0)    | 0 (0.0)       | 0 (0.0)     | 0 (0.0)      |
|                   | R        | 0 (0.0)                 | 1 (100)     | 1 (100)      | 0 (0.0)    | 0 (0.0)       | 0 (0.0)     | 0 (0.0)      |
| **Streptococcus spp. (N=0)** | S        | 0 (0.0)                 | 0 (0.0)     | 0 (0.0)      | 0 (0.0)    | 0 (0.0)       | 0 (0.0)     | 0 (0.0)      |
|                   | I        | 0 (0.0)                 | 0 (0.0)     | 0 (0.0)      | 0 (0.0)    | 0 (0.0)       | 0 (0.0)     | 0 (0.0)      |
|                   | R        | 0 (0.0)                 | 0 (0.0)     | 0 (0.0)      | 0 (0.0)    | 0 (0.0)       | 0 (0.0)     | 0 (0.0)      |
| **Total, n (%)**  | S        | 12 (25.5)               | 21 (44.7)   | 1 (2.2)      | 39 (83.0)  | 46 (97.9)     | 45 (95.8)   | 45 (95.8)    |
|                   | I        | 5 (10.6)                | 5 (10.6)    | 5 (10.6)     | 3 (6.4)    | 1 (2.1)       | 2 (4.2)     | 1 (2.1)      |
|                   | R        | 30 (63.9)               | 21 (44.7)   | 4 (8.2)      | 5 (10.6)   | 0 (0.0)       | 0 (0.0)     | 1 (2.1)      |

S: number of sensitive; I: number of intermediate; R: number of resistant isolates; -antibiotic was not used.
| Bacterial isolates      | Pattern | Antimicrobial susceptibility pattern, n (%) |
|-------------------------|---------|------------------------------------------|
|                         |         | Amoxicillin/C | Cephalothin | Ceftriaxone | Tetracycline | Gentamicin | Ciprofloxacin | Nitrofurantoin | Norfloxacin |
| **E. coli (N=11)**      |         | S 2 (18.2)   | 2 (18.2)   | 2 (18.2)   | 0 (0.0)     | 9 (81.8)   | 10 (90.9)    | 11 (100)      | 11 (100)    |
|                         |         | I 3 (27.3)   | 3 (27.3)   | 5 (45.4)   | 2 (18.2)    | 2 (18.2)   | 1 (9.1)      | 0 (0.0)       | 0 (0.0)     |
|                         |         | R 6 (54.5)   | 6 (54.5)   | 4 (36.4)   | 9 (81.8)    | 0 (0.0)    | 0 (0.0)      | 0 (0.0)       | 0 (0.0)     |
| **Klebsiella spp. (N=3)**|         | S 0 (0.0)    | 1 (33.3)   | 2 (66.7)   | 0 (0.0)     | 9 (66.7)   | 3 (100)      | 3 (100)       | 3 (100)     |
|                         |         | I 1 (33.3)   | 0 (0.0)    | 1 (33.3)   | 1 (33.3)    | 1 (33.3)   | 0 (0.0)      | 0 (0.0)       | 0 (0.0)     |
|                         |         | R 2 (66.7)   | 2 (66.7)   | 0 (0.0)    | 2 (66.7)    | 0 (0.0)    | 0 (0.0)      | 0 (0.0)       | 0 (0.0)     |
| **Proteus spp. (N=3)**  |         | S 0 (0.0)    | 2 (66.7)   | 2 (66.7)   | 0 (0.0)     | 2 (66.7)   | 3 (100)      | 3 (100)       | 3 (100)     |
|                         |         | I 0 (0.0)    | 0 (0.0)    | 0 (0.0)    | 1 (33.3)    | 1 (33.3)   | 0 (0.0)      | 0 (0.0)       | 0 (0.0)     |
|                         |         | R 3 (100)    | 1 (33.3)   | 1 (33.3)   | 2 (66.7)    | 0 (0.0)    | 0 (0.0)      | 0 (0.0)       | 0 (0.0)     |
| **Pseudomonas spp. (N=3)**|     | S —          | 0 (0.0)    | 1 (33.3)   | 0 (0.0)     | 2 (66.7)   | 3 (100)      | 3 (100)       | 3 (100)     |
|                         |         | I —          | 1 (33.3)   | 0 (0.0)    | 0 (0.0)     | 0 (0.0)    | 0 (0.0)      | 0 (0.0)       | 0 (0.0)     |
|                         |         | R —          | 2 (66.7)   | 2 (66.7)   | 3 (100)     | 1 (33.3)   | 0 (0.0)      | 0 (0.0)       | 1 (33.3)    |
| **CNS (N=2)**           |         | S 1 (50)     | 1 (50)     | 1 (50)     | 0 (0.0)     | 2 (100)    | 2 (100)      | 2 (100)       | 2 (100)     |
|                         |         | I 0 (0.0)    | 1 (50)     | 0 (0.0)    | 1 (50)      | 0 (0.0)    | 0 (0.0)      | 0 (0.0)       | 0 (0.0)     |
|                         |         | R 1 (50)     | 0 (0.0)    | 1 (50)     | 1 (50)      | 0 (0.0)    | 0 (0.0)      | 0 (0.0)       | 0 (0.0)     |
| **S. aureus (N=2)**     |         | S 1 (50)     | 0 (0.0)    | 2 (100)    | 0 (0.0)     | 2 (100)    | 2 (100)      | 2 (100)       | 2 (100)     |
|                         |         | I 0 (0.0)    | 1 (50)     | 0 (0.0)    | 1 (50)      | 0 (0.0)    | 0 (0.0)      | 0 (0.0)       | 0 (0.0)     |
|                         |         | R 1 (50)     | 1 (50)     | 0 (0.0)    | 1 (50)      | 0 (0.0)    | 0 (0.0)      | 0 (0.0)       | 0 (0.0)     |
| **Enterobacter spp. (N=2)**|     | S 0 (0.0)    | 1 (50)     | 2 (100)    | 0 (0.0)     | 2 (100)    | 2 (100)      | 2 (100)       | 2 (100)     |
|                         |         | I 1 (50)     | 1 (50)     | 0 (0.0)    | 0 (0.0)     | 0 (0.0)    | 0 (0.0)      | 0 (0.0)       | 0 (0.0)     |
|                         |         | R 1 (50)     | 0 (0.0)    | 0 (0.0)    | 2 (100)     | 0 (0.0)    | 0 (0.0)      | 0 (0.0)       | 0 (0.0)     |
| **Citrobacter spp. (N=1)**|     | S 0 (0.0)    | 0 (0.0)    | 1 (100)    | 0 (0.0)     | 1 (100)    | 1 (100)      | 1 (100)       | 1 (100)     |
|                         |         | I 0 (0.0)    | 0 (0.0)    | 0 (0.0)    | 0 (0.0)     | 0 (0.0)    | 0 (0.0)      | 0 (0.0)       | 0 (0.0)     |
|                         |         | R 1 (100)    | 0 (0.0)    | 0 (0.0)    | 1 (100)     | 0 (0.0)    | 0 (0.0)      | 0 (0.0)       | 0 (0.0)     |
| **E. faecalis (N=0)**   |         | S 0 (0.0)    | 0 (0.0)    | 0 (0.0)    | 0 (0.0)     | 0 (0.0)    | 0 (0.0)      | 0 (0.0)       | 0 (0.0)     |
|                         |         | I 0 (0.0)    | 0 (0.0)    | 0 (0.0)    | 0 (0.0)     | 0 (0.0)    | 0 (0.0)      | 0 (0.0)       | 0 (0.0)     |
|                         |         | R 0 (0.0)    | 0 (0.0)    | 0 (0.0)    | 0 (0.0)     | 0 (0.0)    | 0 (0.0)      | 0 (0.0)       | 0 (0.0)     |
| **Streptococcus spp. (N=1)**|     | S 0 (0.0)    | 0 (0.0)    | 0 (0.0)    | 0 (0.0)     | 1 (100)    | 1 (100)      | 1 (100)       | 1 (100)     |
|                         |         | I 0 (0.0)    | 0 (0.0)    | 0 (0.0)    | 0 (0.0)     | 0 (0.0)    | 0 (0.0)      | 0 (0.0)       | 0 (0.0)     |
|                         |         | R 1 (100)    | 1 (100)    | 1 (100)    | 1 (100)     | 0 (0.0)    | 0 (0.0)      | 0 (0.0)       | 0 (0.0)     |
| **Total, n (%)**        |         | S 4 (16)     | 7 (25.0)   | 13 (46.4)  | 0 (0.0)     | 23 (82.1)  | 27 (96.4)    | 28 (100)      | 27 (96.4)   |
|                         |         | I 5 (20)     | 8 (28.6)   | 6 (21.5)   | 6 (21.4)    | 4 (14.3)   | 1 (3.6)      | 0 (0.0)       | 0 (0.0)     |
|                         |         | R 16 (64)    | 13 (46.4)  | 9 (32.1)   | 22 (78.6)   | 1 (3.6)    | 0 (0.0)      | 0 (0.0)       | 1 (3.6)     |

S: number of sensitive; I: number of intermediate; R: number of resistant isolates; -antibiotic was not used.
expressed as frequencies and percentages. The results were presented by tables.

3. Results and Discussion

Urinary tract infections (UTIs) are one of the most common and serious infections of the human urinary system that occurred in the community and hospital environments. UTIs are most often treated empirically and the antimicrobial agent selection criteria are determined on the basis of the pathogen type and its expected antimicrobial resistance patterns. Also, the management of UTIs has been jeopardized by the increase in the incidence of antimicrobial drug resistance. Thus, there is a need for periodic monitoring of the pathogens of UTIs and their antimicrobial susceptibility pattern in the locality [13].

In the present study, the details of culture characterization are shown in Table 1. From 141 samples collected in inpatient and outpatient settings, 29/141 (20.6%) samples were positive urine cultures, from which 75 bacterial isolates were obtained. *E. coli* (42.6%) was the most predominant bacterium isolated from urine, followed by *Klebsiella* spp. and *Pseudomonas* spp. each (10.7%); *Proteus* spp. (9.3%); coagulase negative staphylococci (CNS), *S. aureus*, and *Enterobacter* spp. each (6.7%); *Citrobacter* spp. (4%); *E. faecalis* and *Streptococcus* spp. each (1.3%), and this study was similar to the previous studies of Kibret and Abera [13] and Alemu et al. [14]. However, the observed high proportion of *E. coli* was varied with previously published studies conducted in Nigeria by Ekwealor and his colleagues [15] where *Staphylococcus* spp. was found to be the predominant urinary tract pathogen. This might be due to the variation of UTI-causing bacterial pathogens, differences in sample size, specimen collection technique, and study settings.

In the current study, the frequency of inpatient 47/75 (62.7%) uropathogens was greater than outpatients 28/75 (37.3%) (Table 1). This is in line with the previous studies of Kengne et al. [7] that revealed bacteriuria was more present in inpatients (70.4%) compared to outpatients (29.6%). Tesfa et al. [16] also further confirmed that inpatients were two times more likely to have culture positive results than outpatients. This might be due to the hospitalization, comorbidity, long-term antibiotic treatment, and immunocompromised conditions. In this study, Gram-negative bacterial isolates were more prevalent (80%) than Gram-positives (20%). This finding is in agreement with studies done in Jimma, Jijiga, Dire Dawa, and Shashamane, where 80.9%, 76%, 73.1%, and 59.2% of the isolates were Gram-negatives [2, 17–19]. Differences in characterization and identification methods are known to influence the relative prevalence of bacteria, which makes comparison difficult. Bacterial etiologies of UTIs can also vary across regions and over time within a population.

Antimicrobial resistance is a major clinical problem in treating infections caused by different bacterial pathogens and has increased over time. In this study, antimicrobial susceptibility pattern of inpatients showed that most of the isolates were sensitive to nitrofurantoin (100%), ciprofloxacin (100%), norfloxacin (97.9%), gentamicin (89.4%), ceftriaxone (55.3%), cephalexin (36.1%), and tetracycline (12.8%). Among outpatients tested for the available drugs, the isolates respectively showed susceptibility of (100%), (96.4%), (67.9%), (53.6%), (36%), and (21.4%), to nitrofurantoin and ciprofloxacin, norfloxacin and gentamicin, ceftriaxone, cephalexin, amoxicillin-clavulanic acid, and tetracycline (Tables 2 and 3). Ceftriaxone, norfloxacin, gentamicin, ciprofloxacin, and nitrofurantoin showed greater than 55% activity against all the isolates. These could be an excellent choice for empirical therapy of UTI in the study setting. However, prescription of these antibiotics depends on the patient’s health status [15, 20–23]. Comparatively, the majority of the isolated uropathogens were resistant to amoxicillin-clavulanic acid and tetracycline [13, 15, 20–24]. This high level of resistance observed with amoxicillin-clavulanic acid and tetracycline might be due to the self-medication and irrational drug utilization habits of the communities for treating all kinds of bacterial infections.

MARI is a tool that indicates the spread of antimicrobial resistance in a given study population. In this study, 0.142–0.714 and 0.250–0.625 were the inpatient and outpatient MARI values of the isolates, respectively (Tables 4 and 5). Only *Citrobacter* spp. (0.142) gave MARI of <0.20 while others gave higher MARI. Similarly, [15] reported that only *Streptococcus* spp. (0.125) was <0.20 MARI value. Any MARI greater than 0.20 implies that the strains of such bacteria originate from an environment where several antibiotics are used or misused [25].

| Isolates            | A | B | MARI = (a/b) | Antibiotics to which the isolates are resistant |
|---------------------|---|---|-------------|-----------------------------------------------|
| *E. coli*           | 4 | 7 | 0.571       | CEPH, CRO, TE, and CN                          |
| *Klebsiella* spp.   | 3 | 7 | 0.428       | CEPH, CRO, and TE                             |
| *Proteus* spp.      | 4 | 7 | 0.571       | CEPH, CRO, TE, and CN                          |
| *Pseudomonas* spp.  | 5 | 7 | 0.714       | CEPH, CRO, TE, CN, and NOR                     |
| CNS                 | 3 | 7 | 0.428       | CEPH, CRO, and TE                             |
| *S. aureus*         | 4 | 7 | 0.571       | CEPH, CRO, TE, and CN                          |
| *Enterobacter* spp. | 2 | 7 | 0.285       | CEPH, and TE                                  |
| *Citrobacter* spp.  | 1 | 7 | 0.142       | TE                                             |
| *E. faecalis*       | 2 | 7 | 0.285       | CEPH, and TE                                  |
| *Streptococcus* spp.| ---|---|---|---|

Total number of antibiotics tested = 7; CEPH: cephalexin; CRO: ceftriaxone; TE: tetracycline; CN: gentamicin; CIP: ciprofloxacin; F: nitrofurantoin; NOR: norfloxacin.

Table 4: Multiple antimicrobial resistance indexes of uropathogens isolated from inpatients.
implies that a very large proportion of the bacterial isolates have been exposed to several antibiotics and thus have developed resistance to these antibiotics. Similar incidence was reported in the work of Ekwealor et al. [15] and Oli et al. [25] though not exactly with the same set of antibiotics.

3.1. Limitations of the Study. The study did not include the patients’ clinical data such as age, gender, and being catheterized and noncatheterized and other associated risk factors of the patients. Due to the COVID-19 pandemic, species level identification and the presence of genetic resistance determinants were not performed.

4. Conclusions

The overall prevalence of UTI in the study participants was 20.6% (29/141). In this study, E. coli, Klebsiella spp., Pseudomonas spp., and Proteus spp. were the most prevalent among the investigated uropathogens. Inpatients had a higher risk of developing bacterial infections compared to outpatients. Ceftriaxone, gentamicin, ciprofloxacin, nitrofurantoin, and norfloxacin are considered as appropriate antimicrobials for empirical treatment of UTIs in the study area. Greater than 0.2 MARI values of the uropathogens from urine samples of this study underscore the need for continuous monitoring of the etiology and antimicrobial susceptibility testing of bacteria, along with health education on the transmission and causes of urinary tract infection.

**Abbreviations**

CLSI: Clinical Laboratory Standards Institute  
CNS: Coagulase Negative Staphylococci  
MARI: Multiple Antimicrobial Resistance Index  
MHA: Muller-Hinton Agar  
PGH: Pawe General Hospital  
UTIs: Urinary Tract Infections.

**Data Availability**

The data used to support the findings of this study are included within this article.

**Conflicts of Interest**

The authors declare that they have no conflicts of interest.

**Authors’ Contributions**

AG and AA designed the project, carried out the experiments, analyzed the data, and drafted and edited the manuscript. Both authors have read and approved the final manuscript.

**Acknowledgments**

The authors are very grateful to Pawe General Hospital for providing the laboratory facilities and space excluding the media, reagents, and antibiotic discs. The authors also extend their deepest gratitude to all staff members of Pawe General Hospital.

**References**

[1] G. Gebremariam, H. Legese, Y. Woldu, T. Araya, K. Hagos, and A. GebreyesusWashihun, "Bacteriological profile, risk factors and antimicrobial susceptibility patterns of symptomatic urinary tract infection among students of Mekelle University, northern Ethiopia," BMC Infectious Diseases, vol. 19, no. 950, pp. 1–11, 2019.

[2] G. Beyene and W. Tsegaye, "Bacterial uropathogens in urinary tract infection and antibiotic susceptibility pattern in Jimma University Hospital, Ethiopia," Ethiopian Journal of Health Science, vol. 21, pp. 141–146, 2011.

[3] G. Dalela, S. Gupta, D. K. Jain, and P. Mehta, “Antibiotic resistance pattern in uropathogens at a tertiary care hospital at Jhalawar with special reference to Esbl, Ampc β-Lactamase and MRSA production,” Journal of Clinical and Diagnostic Research, vol. 6, pp. 645–651, 2012.

[4] M. B. Ashagrie, "Bacterial profile and ESBL screening of urinary tract infection among asymptomatic and symptomatic pregnant women attending antenatal care of northeastern Ethiopia region," Infection and Drug Resistance, vol. 13, pp. 2579–2592, 2020.

[5] G. Theodros, "Bacterial pathogens implicated in causing urinary tract infection (UTI) and their antimicrobial susceptibility pattern in Ethiopia," Revistas del Centro Nacional de Investigaciones Científicas, Ciencias Biológicas, vol. 41, pp. 1–6, 2010.
[6] T. Gutema, F. Weldegebreal, D. Marami, and Z. Teklemariam, "Prevalence, antimicrobial susceptibility pattern, and associated factors of urinary tract infections among adult diabetic patients at metu kari heinz referral hospital, southwest Ethiopia," *International Journal of Microbiology*, vol. 2018, Article ID 7991259, 7 pages, 2018.

[7] M. Kengne, A. T. Dounia, and J. M. Nwobegahay, "Bacteriological profile and antimicrobial susceptibility patterns of urine culture isolates from patients in Ndjamena, Chad," *The Pan African medical journal*, vol. 28, no. 1, p. 258, 2017.

[8] T. Demile, G. Beyene, S. Melaku, and W. Tsegaye, "Urinary bacterial profile and antibiotic susceptibility pattern among pregnant women in North West Ethiopia," *Ethiopian Journal of Health Science*, vol. 22, pp. 121–128, 2012.

[9] M. Cheesbrough, *District Laboratory Practice in Tropical Countries: Part 2*, Cambridge University Press, New York, NY, USA, 2006.

[10] Girma and A. Aemiro, "Antibacterial activity of lactic acid bacteria isolated from fermented Ethiopian traditional dairy products against food spoilage and pathogenic bacterial strains," *Journal of Food Quality*, vol. 2021, Article ID 9978561, 10 pages, 2021.

[11] A. W. Bauer, W. M. Kirby, J. C. Sherris, and M. Turck, "Antibiotic susceptibility testing by a standardized single disk method," *American Journal of Clinical Pathology*, vol. 45, no. 4, pp. 493–496, 1966.

[12] Clinical and Laboratory Standards Institute, *Performance Standards for Antimicrobial Susceptibility Testing. CLSI supplements M100*, Wayne, PA: USA, 2020.

[13] M. Kibret and B. Abera, "Prevalence and antibiogram of bacterial isolates from urinary tract infections at Dessie Health Research Laboratory, Ethiopia," *Asian Pacific Journal of Tropical Biomedicine*, vol. 4, no. 2, pp. 164–168, 2014.

[14] M. Alemu, M. A. Belete, S. Gebreselassie, A. Belay, and D. Gebretsadik, "Bacterial profiles and their associated factors of urinary tract infection and detection of extended spectrum beta-lactamase producing gram-negative uropathogens among patients with diabetes mellitus at dessie referral hospital, northeastern Ethiopia," *Diabetes, Metabolic Syndrome and Obesity: Targets and Therapy*, vol. 13, pp. 2935–2948, 2020.

[15] P. A. Ekwealor, M. C. Ugwu, I. Ezeobi et al., "Antimicrobial evaluation of bacterial isolates from urine specimen of patients with complaints of urinary tract infections in awka, Nigeria," *International Journal of Microbiology*, vol. 2016, Article ID 9740273, 6 pages, 2016.

[16] T. Tesfa, Y. Baye, M. Sisay, F. Amare, and T. Gashaw, "Bacterial uropathogens and susceptibility testing among patients diagnosed with urinary tract infections at Hiwot Fana Specialized University Hospital, Eastern Ethiopia," *SAGE Open Medicine*, vol. 9, pp. 1–10, 2021.

[17] S. W. Desta and G. A. Desalegn, "Prevalence and antibiotic susceptibility of Uropathogens from cases of urinary tract infections (UTI) in Shashemene referral hospital, Ethiopia," *BMC Infectious Diseases*, vol. 18, no. 30, pp. 1–9, 2018.

[18] B. Derese, H. Kedir, Z. Teklemariam, F. Weldegebreal, and S. Balakrishnan, "Bacterial profile of urinary tract infection and antimicrobial susceptibility pattern among pregnant women attending at antenatal clinic in Dil Chora Referral Hospital, Dire Dawa, Eastern Ethiopia," *Therapeutics and Clinical Risk Management*, vol. 12, pp. 251–260, 2016.

[19] A. Negussie, G. Worku, and E. Beyene, "Bacterial identification and drug susceptibility pattern of urinary tract infection in pregnant Women at Karamara Hospital Jigjiga, Eastern Ethiopia," *African Journal of Bacteriology Research*, vol. 10, no. 2, pp. 15–22, 2018.

[20] D. Marami, S. Balakrishnan, and B. Seyoum, "Prevalence, antimicrobial susceptibility pattern of bacterial isolates, and associated factors of urinary tract infections among HIV-positive patients at hiwot fana specialized university hospital, eastern Ethiopia," *The Canadian Journal of Infectious Diseases & Medical Microbiology*, vol. 2019, Article ID 6780354, 8 pages, 2019.

[21] K. C. Iregbu and P. I. Nwajobi-Princewill, "Urinary tract infections in a tertiary hospital in Abuja, Nigeria," *African Journal of Clinical and Experimental Microbiology*, vol. 14, pp. 169–173, 2013.

[22] D. S. Niladri and P. Kuhu, "Antimicrobial profile of urinary pathogens to determine empirical therapy for urinary tract infections in a rural teaching hospital of West Bengal," *Journal of Drug Delivery and Therapeutics*, vol. 3, pp. 16–19, 2013.

[23] R. Khoshbakht, A. Salim, S. H. Askii, and H. Keshavarzi, "Antibiotic susceptibility of bacterial strains isolated from urinary tract infections in Karaj, Iran," *Jundishapur Journal of Microbiology*, vol. 6, pp. 86–90, 2013.

[24] S. Taye, M. Getachew, Z. Desalegn, A. Biratu, and K. Mubashir, "Bacterial profile, antibiotic susceptibility pattern and associated factors among pregnant women with urinary tract infection in goba and sinana woredas, bale zone, southeast Ethiopia," *BMC Research Notes*, vol. 11, no. 799, pp. 1–7, 2018.

[25] N. Oli, R. A. Iyinagolu, U. J. Ichoku et al., "Antibiotic susceptibility profile of community isolates of *Staphylococcus aureus*," *Journal of Pharmaceutical Research and Opinion*, vol. 3, no. 7, pp. 42–47, 2013.