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Common Isolates and Antibiotic Susceptibility Pattern of Urine Samples among Patients Attending a Tertiary Health Institution in South Nigeria

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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Original Research Article

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ABSTRACT

Aim: To identify the main isolates in Urinary Tract Infection (UTI) and their antibiotic susceptibility patterns in Federal Medical Centre Asaba as a guide to developing corresponding antibiogram to support empirical treatment of these infections.

Study Design: A three - year retrospective cross-sectional study.

Place and Duration of Study: Federal Medical Centre, Asaba, Delta State, Nigeria between 1st of January 2019 to 31st December 2022.

Methodology: A three - year retrospective cross-sectional study carried out by reviewing laboratory records with a focus on identifying bacterial pathogens causing UTI as well as evaluating their antibiotics susceptibility in Federal Medical Centre, Asaba, Delta State, Nigeria. All Urine microscopy, culture and sensitivity results from the 1st of January 2019 to 31st December, 2022 were collected and reviewed.

Results: A total number of 2113 results of subjects, 683 males and 1430 females, that attended the tertiary hospital from the 1st of January 2019 to 31st December 2022 were reviewed. The bacterial strains identified/isolated among the population studied were *Staphylococcus aureus* 907 (42.9%), *Escherichia coli* 866 (41.9%), *Klebsiella spp* 232 (11.0%), *Pseudomonas aeruginosa* 54 (2.6%), *Proteus spp* 31 (1.4%), *Streptococcus spp* 2 (0.1%) and *Pantoea spp* 1.The records revealed that the organisms were isolated more in female subjects (66.7%) than male subjects (33.3%), *Staphylococcus aureus* 285 males, 622 females, *Escherichia coli* 294 males, 592 females, *Klebsiella spp* 62 males, 170 females, *Pseudomonas aeruginosa* 29 males 25 females, *Proteus spp* 13 males, 18 females, *Streptococcus spp* 2 females. *Pantoea spp* 1 female as well. The highest percentages of resistance have been observed against tested antibiotics.

Conclusion: Most of the isolates were extended spectrum β-lactamase producers and multidrug-resistant. We observed that Gram-negative bacteria were the main cause of UTIs where the predominant microorganism was *E. coli.*

Keywords: Urinary tract infection (UTI); antibiotics susceptibility; bacterial infection; kidney failure.

1. INTRODUCTION

Urinary tract infections cause significant morbidity and mortality. Globally, UTIs are the second most frequently seen bacterial infection in individuals of different ages (Najafabadi, et al., 2018). Approximately 50% of women have UTIs at least once in their lifetime worldwide. UTIs occur more commonly in individuals aged 16–64 years (Tandogdu & Wagenlehner, 2016) with very low prevalence among boys. However, UTIs can be seen in the first year of life mostly in those with anatomical or functional abnormalities. Additionally, UTIs recur very often in most individuals, majorly due to disruption in or cessation of treatment leading to reinfection with the same or different microorganisms (Muhammad, et al., 2020). UTIs are most of the time caused by bacteria accounting for over 95% of cases, nonetheless, microorganisms such as fungi, parasites and viruses can also cause UTIs (Arjunan, et al., 2010). Furthermore, UTIs have been classified as uncomplicated and complicated. Uncomplicated UTIs occur most of the time in healthy non gravid adult women, whereas complicated UTIs can be seen in different age and sex groups. Kidney failure, transplantation and calculi, indwelling catheters, compromised immunity and pregnancy have been implicated as risk factors to complicated UTI (Tandogdu & Wagenlehner, 2016, Lichtenberger & Hooton, 2008).

It has been reported that the most common Gram-positive bacteria incriminated in UTIs are *Staphylococcus aureus*, *Staphylococcus saprophyticus* and *Enterococcus species* (Mireles, et al., 2015). About 75%–95% of bacteria related UTIs are caused by *E. coli* (Muhammad, et al., 2020). Various antibiotics have been used effectively in the management of UTIs, however, a rising degree of frequently changing and alarming multidrug – resistant (MDR) UTI causing agents has been recorded globally over the past years due to indiscriminate use of antibiotics and their availability over the counter (Prah, et al., 2019, Spellberg, et al., 2013). This increase in MDR bacterial strain has been the cause of UTI related morbidity and mortality. Therefore, it is very crucial to overcome the indiscriminate use of antibiotics, in order to prevent multidrug resistance. Varied patterns of bacterial antibiotic susceptibility have been observed among different hospitals within different geographical zones (Muhammad, et al., 2020). Generally, broad-spectrum antibiotics are used for empirical treatment, nonetheless, the infectious Disease Society of America recommends a regular regional study to identify variations in antibiotic susceptibility patterns, (Muhammad, et al., 2020) in order to inform appropriate antibiotic selection for empirical treatment in each region. This practice will support prevention of the emergence of antimicrobial resistance. There is no report on the common uropathogens isolated and their antibiotics susceptibility profile at Federal Medical Centre, Asaba. Hence, this study aimed to determine the incidence of UTI – Causing agents and their antibiotics susceptibility pattern among subjects who attended FMC, Asaba for a selected period.

2. MATERIALS AND METHODS

2.1 Study Area

The study site for this work is Federal Medical Centre (FMC), Asaba Delta State. Federal Medical Centre, Asaba is situated in the central Area of Asaba metropolis, the capital city of Delta State. The hospital is a tertiary health institution, a research and referral centre for the whole of the state capital territory and neighboring towns like Ibusa, Iseleukwu, Ogwashiuku, Onicha – Ugbo, onicha – olona, Agbor etc. Federal Medical centre Asaba also serve parts of some neighboring states like Edo and Anambra states including the largest commercial city of South-Eastern Nigeria, Onitsha with the largest market in West Africa. The hospital is in the South-South Geo-political zone of Nigeria. It was established on 12th August 1998 because of the Federal Government of Nigeria policy to setup a Federal Medical Centre in states where a Federal Teaching Hospital is non-existent. The institution took over its current site from the central hospital. Asaba was established in 1991 (after the creation of Delta State) which metamorphosed itself from the colonial cottage \hospital of the Mid-Western region established in March, 1962 with a thirty bed complement. FMC, Asaba has since grown tremendously with bed capacity of about two hundred and seventy, over twenty clinical departments including Obstetrics and Gynaecology, Medicine, Surgery, Ophthalmology, Paediatrics, Medical laboratory Services etc.

2.2 Study Population

All the individuals tested for urine microscopy, culture and sensitivity from 1st January 2019 to 31st December 2022.

2.3 Sample Size Determination

Sample size (N) will be calculated using the formula described by Cochran, (Cochran, 1977).

N = Z2PQ
      D2
N= Sample size
Z= the confidence interval usually set at 1.96
P= Expected prevalence using the prevalence rate of 12.3% in Abakaliki, South-Eastern, Nigeria (John-Onwe, et al., 2022)
Q= 1- P (1- 0.123)
D= Desired level of significance usually set at 0.05.
Therefore: N = (1.96)2 X 0.123 X 0.877
                              (0.05)2
N= 166

2.4 Data Collection

All the urine microscopy, culture and sensitivity results for the years under review from the records of Medical Laboratory Service department of Federal Medical Centre Asaba were collected.

2.5 Data Analysis

SPSS version 26 was used in analyzing the data. Data was analyzed using Frequency tables, Chi-Square test and t-test. The statistical significance was set at $p < 0.05$.

3. RESULTS AND DISCUSSION

As shown in Table 1, results of a total of 2113 subjects were reviewed over the period studied. Organisms isolated from these individuals include *Staphlococcccus aureus* 907 (42.9%), *E. coli* 866 (41.9%), *Klebsiella spp* 232 (11.0%), *P. aeruginosa* 54 (2.6%), *Proteus spp* 31 (1.4%), *Streptococcus. Spp* 2 (0.1%), and *Pantoea spp* 1.

As shown in Table 2 and Fig 1, majority of the organisms isolated were significantly.

Table 1. Data of bacterial species isolated from urine culture

Bacteria	Frequency (n= 2113)	Percentage (%)
S. aureus	907	42.9
E.coli	866	41.9
Klebsiella spp	232	11.0
Pseudomonas aeruginosa	54	2.6
Proteus.spp	31	1.5
Strep.spp	2	0.1
Pantoea spp	1	0
Total	**2113**	**100**

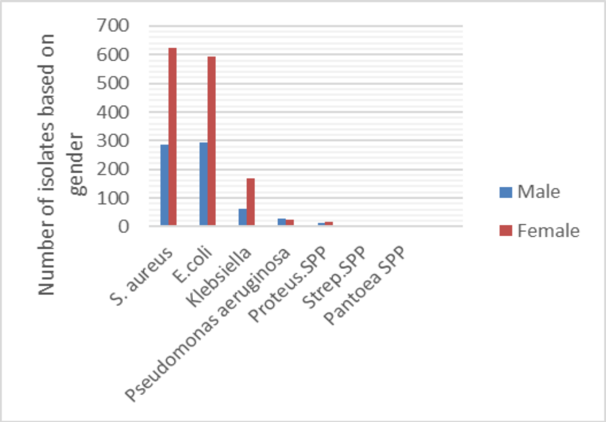

Fig. 1. Distribution of bacteria species based on gender

Table 2. Distribution of bacteria Species according to age

Bacteria	≤18years	19years-59years	60years &above	Total	X²	p-value
S. aureus	108 (11.9%)	653 (72%)	146(16.1%)	907	75.6	< 0.001
E. coli	78(8.8%)	553 (62.4%)	255(28.8%)	886		
Klebsiella spp	35(15.1%)	131(56.5%)	66(28.4%)	232		
Pseudomonas aeruginosa	7(13%)	22(40.7%)	25(46.3%)	54		
Proteus.spp	4(13.3)	18(53.7%)	9(23.7)	31		
Strep.spp	1(50%)	0(0%)	1(50%)	2		
Pantoea spp	0(0%)	1(0%)	0(0%)	1		
Total	233(11%)	1378(65.2%)	502(23.7%)	2113		

Higher in females (P = 0.009) than in males. *S. aureus* was isolated in 622 females and 285 males, *E, coli* 592 females, 294 males, *Klebsiella spp* 170 females, 62 males, *P. aeruginosa* 25 females, 29 males, *Proteus spp* 18 females, 13 males*, Streptococcus spp* 2 females, and *Pantoea spp* 1 female each.

As outlined in Table 2, there was a significant difference in the organisms identified in different age groups with the highest number of majority of the isolated organisms seen in subjects between 19 to 59 years and the least seen in subjects that are less than 18 years.

Surprisingly, very high levels of resistance to different antibiotics was observed with many of the isolates. Out of the 907 samples with growth of *S, aureus*, 530, 463, 608, 499, 552 and 456 were resistant to ciprofloxacin, Augmentin, Ofloxacin, gentamicin, Ceftazidime and cefixime respectively. Similarly, 528, 610, 526, 509, 484 and 453 samples with *E. coli* were resistant to Ciprofloxacin, Augmentin, Ofl0xacin, Gentamicin, Ceftazidime and Cefixime respectively. Additionally, 128, 140, 120, 156, 123 and 105 samples that yielded growth of *Klebsiella Spp* were resistant to the same antibiotics in the same order. All the other isolates include *Pseudomonas aeruginosa, Proteus Spp, Streptococcus Spp* and *Pantoea Spp* exhibited greater levels of resistance than susceptibility.

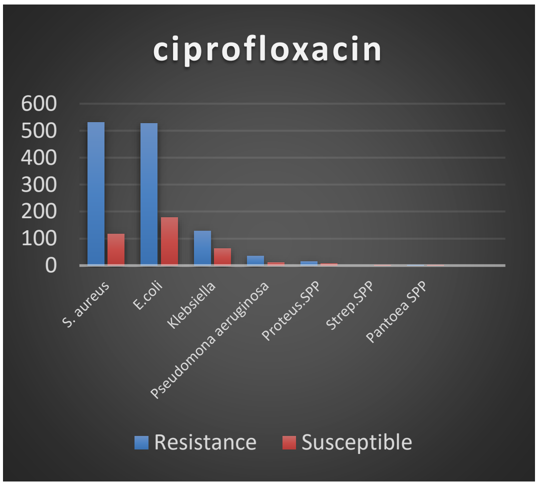

Fig. 2. Antimicrobial susceptibility profile of bacteria to Ciprofloxacin

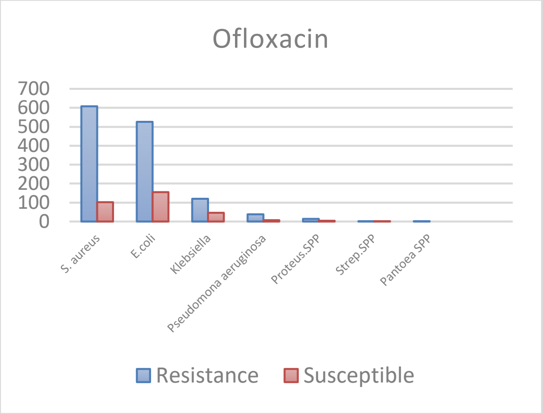

Fig. 3. Antimicrobial susceptibility profile of bacteria to Ofloxacin

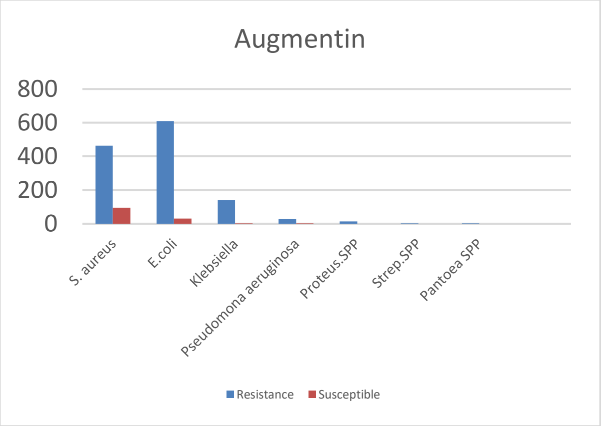

Fig. 4. Antimicrobial susceptibility profile of bacteria to Augmentin

UTIs are a common health concern affecting individuals of both genders and all ages. Over 90% of UTI are caused by normal body flora bacteria that contaminate the genital area and the urinary tract (Ekwealor, et al., 2024). Studies have shown that the pathogenic bacteria associated with UTI are mostly *Staphylococcus saprophyticus, Escherichia coli, Klebsiella pneumonia, Staphylococcus aureus, Proteus spp., Pseudomonas auroginosa* and Enterococci (Thakur & Nepal, 2020, (Thakur & Nepal, 2020) with the most frequently isolated gram negative and gram-positive bacteria being *E. coli* and *Staphylococcus aureus* respectively (Ekwealor, et al., 2021). Generally, among bacteria, 75%–95% of cases of UTI are caused by *E. coli* (Kashef, et al., 2010).

In this study, Gram-negative organisms accounted for 1204 (57%) of the isolates with *E. coli* 866 (41.9%) as the most prevalent while *Pontoea spp* (0%) was the least. High prevalence of Gram-negative organisms in UTI has also been reported by Johnson et al., (2021), Ali et al., (2022), and Ekwealor et al., (2024), who recorded 76.45%, 71% and (55.6%) gram negative bacteria respectively. Furthermore, in line with our study, *E. coli* has also been reported by several researchers as the most common Gram-negative bacteria involved in UTI (Onyango, et al., 2018, Muhammad, et al., 2020, Vicar, et al., 2023, Ekwealor, et al., 2024). It is noteworthy that approximately 80% of uropathogenic *E. coli* express *P. fimbriae,* a virulent factor that assists it to anchor to the glycolipid of the outer membrane of urothelial cells in the kidney thereby causing inflammation (Onyango, et al., 2018).

Interestingly, in our study, most of the uropathogens were recovered from female patients (1430; 67.7%). This is consistent with the report of Muhammed et al., (2020). who found uropathogens in females (50.7%) more than males. This increased incidence of *E. coli* in UTI has been alluded to its presence in the vaginal and rectal area as well as the shortness of female urethra (Muhammad, et al., 2020).

Contrary to our observation, Johnson et al., (2021) isolated *Klebsiella pneumonia* (37.41%) as the most frequent Gram-negative organism. *Klebsiella spp.* is now known to emerge as a dominant community acquired uropathogen (Kaduma, et al., 2019, Taye, et al., 2018) although observed as the second most prevalent bacteria 10 (18.5%) isolated in this study. Its emergence has also been linked to the presence of inherent factors like siderophore, types 1 and 3 fimbrae, biofilm formation and capsules (Johnson, et al., 2021). Other Gram-negative bacteria are isolated were *Proteus mirabilis* 4 (7.4%) and *Pseudomonas spp*. 3 (5.6%). Their involvement in UTI among pregnant women had also been reported (Ali, et al., 2022, Johnson, et al., 2021).

Staphylococcus aureus was the most common Gram-positive bacteria 24 (44.4%) isolated. This finding is supported by the reports of Johnson et al., (2021) and Muhammed et al., (2020) who recorded *S. aureus* as the only Gram-positive bacteria isolated in their work. As suggested by Top et al., (2012) the high incidence of *S. aureus* may be attributed to the rate of vaginal carriage of *S. aureus,* which has been reported to be 4% - 22% of the vaginal microbiota in pregnant women (Muhammad, et al., 2020).

Frankly speaking, antimicrobial resistance (MDR) currently constitutes a continuous global health challenge with a world concern. According to the study carried out by the European survey of antibiotic consumption, MDR bacterial strains in complicated UTIs are responsible for the mortality rate of approximately 25 000 Europeans/year. In our study there was a very high level of antibiotic resistance by the isolated bacteria. Ciprofloxacin was the most susceptible antibiotics by both gram positive and Gram-negative bacteria hence is recommended for empirical use in case of suspected UTI. Knowledge of the microorganism involves and antibiograms are important for the empirical treatment of UTIs (Muhammad, et al., 2020).

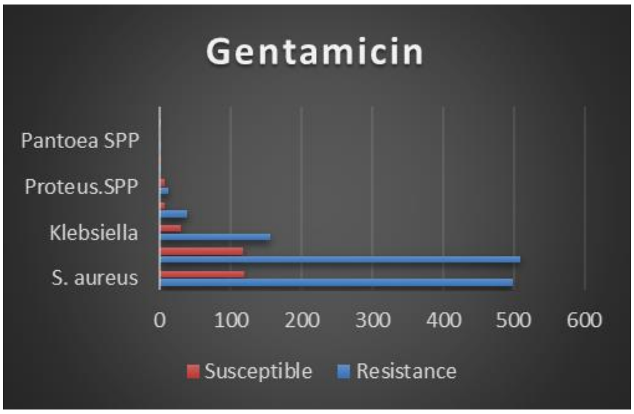

Fig. 5. Antimicrobial susceptibility profile of bacteria to Gentamicin

4. CONCLUSION

In our study, the most common isolated pathogens among outpatients were Gram-positive *Staphylococcus aureus* followed by Gram-negative E. coli. Furthermore, there was very high level of antibiotic resistance by the bacteria isolated. Ciprofloxacin was the most susceptible antibiotics by both gram positive and Gram-negative bacteria hence is recommended for empirical use in case of suspected UTI prior to release of urine microscopy culture and sensitivity result. The emergence of MDR organisms, which we reported in our study, threatens the management of patients with UTIs. This study will help physicians in prescribing appropriate antibiotics for the treatment of UTIs.

ETHICAL APPROVAL

As per international standards or university standards written ethical approval has been collected and preserved by the author(s).

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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