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Bacteriological Profile and Antibiotic Susceptibility Pattern of Clinical Isolates from A Tertiary Care Hospital in Dhaka, Bangladesh

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Abstract

Antimicrobial resistance (AMR) has emerged as one of the most significant public health challenges worldwide, posing a serious threat to the effective treatment of infectious diseases. This study aimed to identify bacterial isolates among various clinical samples and to determine their antimicrobial susceptibility profile. This observational study was carried out from January to December, 2022 in the Department of Microbiology at Uttara Adhunik Medical College Hospital (UAMCH). Clinical samples such as urine, sputum, blood and wound swabs were collected from different body site infections that occurred among patients who visited the hospital within the study period. These samples were sent to the microbiology laboratory for processing, identification and antimicrobial susceptibility testing (AST). Standard microbiological protocols were followed. Among 12,337 clinical samples only 1,679 (13.60%) yielded bacterial growth. Rate of bacterial growth was highest in wound swab (46.36%). Out of culture-positive cases, *Escherichia coli* was the most predominant one which accounted for 565 (37.16%) of all the bacterial isolates, followed by *Salmonella* Typhi 408 (24.30%) and *Klebsiella* species 208 (12.40%). In case of *Escherichia coli* increased level of susceptibility were observed in case of meropenem (99.75%), amikacin (90.78%), nitrofurantoin (85.79%), gentamicin (83.99%) and piperacillin/tazobactam (71.13%). Increased susceptibility of *Klebsiella* species were observed for meropenem (93.50%), amikacin (89.17%) and gentamicin (88.64%). All the 2nd, 3rd and 4th generation of cephalosporins showed reduce level of susceptibility towards *Escherichia coli* and *Klebsiella* species. All the isolates of *Salmonella* Typhi and Paratyphi A were susceptible to ceftriaxone and meropenem and almost all the strains of *Salmonella* Typhi and Paratyphi A were resistant to ciprofloxacin. All the isolates of Gram positive organisms were susceptible towards linezolid and vancomycin. In conclusion, the study highlights the concerning trends in antimicrobial susceptibility among bacterial isolates, emphasizing the need for continuous surveillance, antibiogram, rational antibiotic use and the implementation of effective infection control measures to combat this growing public health threat.

Keywords: Antibiogram, Antimicrobial susceptibility pattern, Antimicrobial resistance

Introduction

Antimicrobial resistance (AMR) occurs when pathogenic microorganisms develop resistance to the drugs used to control these microorganisms, made treatments less effective or ineffective [1]. The global spread of antimicrobial

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resistance (AMR) poses a serious threat to public health. Antibiotic resistance not only increases morbidity and mortality but also leads to a growing economic burden on health care. The World Health Organization (WHO) ranked AMR among the top 10 threats to global health in 2019 and evaluated that AMR could cause 10 million deaths annually by 2050 in the world. WHO recently reported that around 700,000 people die each year out of drug-resistant infections [2]. In spite of various agencies working towards the cause of rationalizing antibiotic usage and promoting safe prescription practices, a lot of knowledge, attitude and practice gap remains amongst the healthcare professionals especially in underdeveloped or developing nations. Lack of dynamic data's of antibiogram at global, nationwide and regional levels often force clinicians to choose regimens based on their wisdom and prevalent local practices. The South-East Asia is considered to have the highest risk of AMR among all the WHO regions [3].

AMR is a growing threat for Bangladesh, therefore high levels of resistance to commonly used antimicrobials is observed in the country. Antimicrobials are widely available over-the-counter (OTC) in Bangladesh [4]. The overuse of antimicrobials, increased exposure to hospital and invasive procedures such as mechanical ventilation and central venous catheterization alongside disruption and breach of routine infection prevention and control (IPC) activities, including screening and isolation, may have intensified the emergence and transmission of resistant pathogens [5,6].

Escherichia coli, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Streptococcus pneumoniae* and *Salmonella* spp. are the commonly isolated organisms from infections in the clinical and community settings [7] and they are also the current most serious antibiotic-resistant organisms [8]. The present study aimed to determine the bacterial profile and antimicrobial susceptibility patterns of bacterial isolates from different body site infections that occurred among patients of Uttara Adhunik Medical College Hospital (UAMCH).

Materials and Methods

This observational study was carried out from January to December, 2022 in the Department of Microbiology at Uttara Adhunik Medical College Hospital (UAMCH), Dhaka, Bangladesh. All laboratory procedures were performed in the Department of Microbiology, UAMCH. Total 12,337 clinical samples from patients with different diseases were collected, among which 1,679 bacteria were isolated from urine, blood, sputum and wound swabs specimen. All clinical samples were collected following standard microbiological techniques. Clinical specimens were transported to the microbiology laboratory within 2 hours. Based on sample type, the specimens were plated onto appropriate media following laboratory SOP. After an overnight incubation at 37°C for 24 hours, isolates were processed for further analysis. Bacterial species were identified using Gram staining and biochemical tests which include indole, urease, oxidase, triple sugar iron agar, citrate utilization and motility tests for Gram negative bacteria, while Gram positive bacteria were identified by Gram staining, hemolysis, catalase and coagulase tests following standard microbiological protocols [9,10]. Determination of antimicrobial susceptibility was done by disk diffusion method. Pure culture from different clinical samples were selected for determining antibiotic susceptibility pattern against different groups of antibiotics such as Ampicillin(10µg), Amikacin(30µg), Amoxicillin/Clavulanicacid(30µg), Azithromycin(15µg), Aztreonam(30µg), Cefepime(30µg), Cefixime(5µg), Ceftazidime(30µg), Ciprofloxacin(5µg), Ceftriaxone(30µg), Cefuroxime(30µg), Cotrimoxazole(25µg), Doxycycline(30µg), Gentamicin(10µg), Levofloxacin(5µg), Linezolid(30µg), Meropenem(10µg), Netilmicin(30µg), Nitrofurantoin(300µg), Oxacillin(01mcg), Penicillin(10µg), Piperacillin/Tazobactum (100/10µg), Tetracycline(30µg), Tobramycin(10µg) and Vancomycin(30µg) by Kirby Bauer disc diffusion method [11]. The plates were then inverted and incubated at 37°C for 24 hours. After incubation, the plates were examined and the zone of inhibition was measured in mm of diameter according to Clinical and Laboratory Standards Institute (CLSI) guideline, 2021 [12]. For antimicrobial susceptibility test Mueller Hinton agar media and antimicrobial discs were procured from Oxoid Ltd.,UK. Quality control was ensured using reference strains, including *Pseudomonas aeruginosa* ATCC 27853, *Escherichia coli* ATCC 25922 and *Staphylococcus aureus* ATCC 25923.

Results

Table 1: Distribution of bacterial growth pattern

Bacteria	Total samples (N=12337)	%
Growth	1679	13.6
No growth	10658	86.4

Total 12,337 clinical specimens were processed of which 1,679 yielded positive culture and the growth rate of bacteria was 13.60% (Table 1).

Distribution of bacterial growth in different specimens were showed in Table 2. Among 1,679 bacterial isolates highest numbers (919) were isolated from urine where total urine samples were 7,768. Rate of growth was highest in case of wound swab (46.36%) where among total 302 samples, 140 yielded positive growth.

Table 3 observed the most common isolated bacteria was *Escherichia coli* 624 (37.16%) followed by *Salmonella* Typhi

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408 (24.30%) and *Klebsiella* species 208 (12.40%). The least isolated organisms were *Salmonella* Paratyphi A 110 (6.55%), *Staphylococcus aureus* 95 (5.66%), *Enterococcus* species 59 (3.51%), *Enterobacter* species 66 (3.93%), *Pseudomonas aeruginosa* 39 (2.32%) and *Acinetobacter* species 38 (2.26%) respectively.

Table 2: Distribution of bacterial growth in different specimens

Specimens	Total samples (N=12337)	Total growth (N=1679)	%
Urine	7768	919	11.83
Blood	4045	603	14.91
Wound swab	302	140	46.36
Sputum	222	17	7.66

Antibiotic susceptibility test of all the isolated bacteria were done by using different antibiotics. Among Gram positive pathogens in case of *Enterococcus* species all the strains were susceptible towards vancomycin and linezolid (100%). *Staphylococcus aureus* was found 100% sensitive towards linezolid (Table 4).

Table 5 presented that increased level of susceptibility was observed in case of *Escherichia coli* for meropenem (99.75%), amikacin (90.78%), nitrofurantoin (85.79%), gentamicin (83.99%) and piperacillin/tazobactam (71.13%). In case of *Klebsiella* species elevated level of susceptibility were seen in case of meropenem (93.50%), amikacin (89.17%) and gentamicin (88.64%). All the isolates of *Salmonella* Typhi and *Salmonella* Paratyphi A were susceptible to ceftriaxone and meropenem. Susceptibility percentage of cefixime, cotrimoxazole and ampicillin

Table 3: Distribution of isolated organisms and specimens

Organisms	Urine (N=931)	Blood (N=599)	Wound swab (N=133)	Sputum (N=16)	Total (N=1679)	%
Escherichia coli	565	19	36	4	624	37.16
Salmonella Typhi	-	408	-	-	408	24.3
Klebsiella sp.	165	12	25	6	208	12.4
Salmonella Paratyphi A	-	110	-	-	110	6.55
S. aureus	22	30	41	2	95	5.66
Enterococcus sp.	59	-	-	-	59	3.51
Enterobacter sp.	59	-	6	1	66	3.93
Acinetobacter sp.	20	16	-	2	38	2.26
P.aeruginosa	16	4	18	1	39	2.32
Citrobacter freundii	19	-	-	-	19	1.13
Proteus sp.	6	-	7	-	13	0.78

Table 4: Antibiotic susceptibility pattern of major Gram-positive organisms

Antibiotics	*Staphylococcus aureus* (N=95) %	*Enterococcus* sp. (N=59) %
Ampicillin	-	97.3
Azithromycin	41.95	-
Ciprofloxacin	63.83	42.11
Doxycycline	90	-
Linezolid	100	100
Nitrofurantoin	80	85
Oxacillin	81.67	-
Penicillin	27.91	72.78
Cotrimoxazole	70.83	-
Vancomycin	-	100

Note: (-) = not tested

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Table 5: Antibiotic susceptibility pattern of major Gram-negative organisms

Antibiotics	*E. coli (N=624)* %	*Klebsiella sp. (N=208)* %	*S.* Typhi *(N=408)* %	*S.*Paratyphi A *(N=110)* %	*Acinetobacter* sp. *(N=38)* %	*Enterobacter sp. (N=66)* %	*P.aeruginosa (N=39)* %
Amoxicillin/ Clavulanic acid	28.14	39.13	-	-	-	-	-
Amikacin	90.78	89.17	-	-	80.97	71.63	75
Ampicillin	15.29	-	89.04	97.62	-	-	-
Azithromycin	-	-	78.57	-	-	-	-
Aztreonam	31.7	57.14	-	-	-	35.29	67.57
Cefepime	47.06	58.82	-	-	24.58	41.94	71.05
Cefixime	29.45	57.58	98.81	100	-	16.67	-
Ceftazidime	33.94	57.14	-	-	38.71	35.61	75.61
Ceftriaxone	39.58	65.44	100	100	26.39	36.11	-
Cefuroxime	16.67	38.06	-	-	-	-	-
Ciprofloxacin	35.71	58.21	1.22	2	52.5	42.86	67.5
Gentamicin	83.99	88.64	-	-	78.69	59.46	-
Levofloxacin	35.32	55.14	57.14	58.97	71.35	96	95
Meropenem	99.75	93.5	100	100	85.71	97.22	71.79
Nitrofurantoin	85.79	45.13	-	-	-	52.5	-
Netilmicin	-	-	-	-	-	-	72
Piperacillin /Tazobactam	71.13	67.2	-	-	72	72	75
Tetracycline	-	-	-	-	75	-	-
Tobramycin	-	-	-	-	-	-	76
Cotrimoxazole	51.56	60.74	90.53	87.5	71	51	-

Note: (-) = not tested

were 98.81%, 90.53% and 89.04% respectively in case of *Salmonella* Typhi and 100%, 87.50% and 97.62% respectively in *Salmonella* Paratyphi A. In *Salmonella* Typhi 1.22% strains and *Salmonella* Paratyphi A 2% strains were susceptible to ciprofloxacin. In case of *Acinetobacter* species meropenem, amikacin and gentamicin exhibited raised level of susceptibility and the percentages were 85.71%, 80.97% and 78.69% respectively. Susceptibility rate was higher for meropenem (97.22%), piperacillin/tazobactam (72%) and amikacin (71.63%) in case of *Enterobacter* species. All the 2nd, 3rd and 4th generation of cephalosporins showed reduce level of susceptibility in case of *Escherichia coli*, *Klebsiella* and *Enterobacter* species. In case of *Pseudomonas aeruginosa* both meropenem and piperacillin/tazobactam exhibited 71.79% and 75% susceptibility individually and 72% susceptibility was observed in case of netilmicin.

Discussion

Increased antimicrobial resistance has made it necessary in recent time to an up-to- date information on antibiotic susceptibility and resistance patterns of bacterial isolates through antibiogram in order to determine appropriate empirical therapy. Antibiograms served as invaluable tools for guiding empirical therapy decisions, informing hospital infection control policies and supporting broader antimicrobial resistance surveillance efforts. In current study, the frequency of bacterial growth rate among various clinical samples were 13.60% (Table 1). Similar findings (11%) were found by Nasrin et al. [13] but in contrary to our finding, higher growth rate was observed in a study done in Northwest Ethiopia by Yitayeh et al. and the rate was 18.7% [14]. In our study, the rate of bacterial growth was relatively low in comparison to study by Yitayeh et al. [14] and the reason might be due to prior antibiotic therapy before submitting the clinical samples. The isolated bacteria were highest (919) in urine samples which correspond proportionally to the number of urine samples tested and which is a common finding in any diagnostic laboratory. Even though blood culture was performed in higher frequency compared to wound swab, the bacterial isolation rate from blood (14.91%) was relatively lower than the latter (46.36%) (Table 2). In general, the blood culture positivity rate among clinically suspected sepsis

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patients would be low when the patient was on antibiotic therapy. It is important that these observations are reported and interpreted by an expert and that high quality standards of the data generated are maintained for further use of these data as evidence for policy making. An absence of standard protocol for reporting a pathogen may lead to over-reporting or false positive results from bacterial contaminants/normal flora and these factors have a direct effect on patient management as well as the development of guidelines and policies.

In present study among the culture-positive cases, Gram negative organisms were mostly isolated in comparison to Gram positive one (Table 3). The great majority of UTIs are caused by Gram negative bacteria, most commonly by *Escherichia coli* and this observation is similar to another study [15]. In conflict with current study, Aika and Enato of Nigeria [16] observed *Staphylococcus aureus* and Coliforms as predominant organisms in their study. The difference in the pattern of bacterial isolates might be due to difference in study subjects, study design, identification method, geographic variation and variation within a study population. In our study *Salmonella* Typhi, *Salmonella* Paratyphi A, *Escherichia coli*, *Staphylococcus aureus* and *Acinetobacter* species were the top 5 isolates from blood cultures (Table 3). A relatively high number of *Salmonella* species in blood indicating a high burden of the disease in Bangladesh. Similar study was found in Chittagong, Bangladesh [17]. In this study, in case of *Escherichia coli* increased level of susceptibility was observed in case of meropenem (99.75%), nitrofurantoin (85.79%), amikacin (90.78%), gentamicin (83.99%) and piperacillin/tazobactam (71.13%) and decreased level of sensitivity was marked in case of 2nd, 3rd and 4th generation of cephalosporins and ciprofloxacin (Table 5). Our findings are in line with those reported in other studies where they found that *Escherichia coli* was highly susceptible to amikacin, meropenem, nitrofurantoin, gentamicin and ceftolozane/tazobactam [18-22]. Diminished level of sensitivity towards ciprofloxacin and 2nd, 3rd and 4th generation of cephalosporins might be due to irrational use of these drugs by clinicians, paramedics and other personnel in hospitals and other clinical settings.

In current study, *Klebsiella* species showed elevated level of susceptibility against meropenem (93.50%), amikacin (89.17%) and gentamicin (88.64%) and these observations were almost similar with other study where susceptibility of *Klebsiella pneumoniae* for antibiotics was 100% for amikacin, 82.8% for meropenem [23] but decreased level of sensitivity was marked in case of 2nd, 3rd and 4th generation of cephalosporins, ciprofloxacin, levofloxacin, nitrofurantoin and amoxicillin/clavulanate. Due to the high prevalence of resistance in *Klebsiella* species there is a need for strict measures in the administration of antibiotics. In opposite to current study, diminished level of susceptibility was marked in a study done by Dikkatwar et al. where in case of meropenem (10%), gentamicin (27%) and amikacin (18%) susceptibility was noted [24]. All the isolates of *Salmonella* Typhi and Paratyphi A were susceptible to ceftriaxone and meropenem. Similar results were observed in a study by Nasrin et al. [13] and Nazia et al. [25]. In identical with present study, lower level of ceftriaxone (38.7%) susceptibility in case of *Salmonella* Typhi was noted in another study [26]. In case of ciprofloxacin our study showed sensitivity of *Salmonella* Typhi *and* Paratyphi were 1.22% and 2% respectively. Similar findings were found in a study where ciprofloxacin susceptibility were 2.1% in *Salmonella* Typhi and 1.1% in *Salmonella* Paratyphi [27]. In this study, the susceptibility rate of *Enterobacter* species was higher in case of meropenem (97.22%), amikacin (71.63%), and piperacillin/tazobactam (72%). Reduced level of Susceptibility was marked in 3rd and 4th generation of cephalosporins (Table 5). Similar observations were found in a study where 73%, 68% and 64% susceptibility was noted in case of meropenem, amikacin and piperacillin/tazobactam respectively [28].

In case of *Pseudomonas aeruginosa* in present study, meropenem and piperacillin/tazobactam exhibited 71.79% and 75% susceptibility respectively (Table 5). A similar study where in case of meropenem (93%) and piperacillin/tazobactam (85%) susceptibility was observed by R et al. [29] but in contrast to present study, 51% susceptibility was observed in case of meropenem done by Iftikhar et al [30]. In our study it is showed that *Acinetobacter* species were 85.71% susceptible in case of meropenem and almost similar rate of susceptibility was observed in a study done in Pakistan [30]. All the isolates of *Staphylococcus aureus* were 100% susceptible to linezolid and increased level of susceptibility were observed in case doxycycline (90%), oxacillin (81.67%), nitrofurantoin (80%) and cotrimoxazole (70.83%) (Table 4). Like present study, Theos et al. observed *Staphylococuus aureus* were 100% susceptible to Linezolid [31]. This study showed all the isolates of *Enterococcus* species were 100% susceptible to vancomycin and linezolid and elevated level of susceptibility was marked in case of ampicillin (97.30%) and nitrofurantoin (85%) (Table 4). Like present study, another study observed higher level of susceptibility towards vancomycin (87.5%) and linezolid (93.8%) [32].

Conclusion

Bacterial antimicrobial resistance (AMR) is a significant global health challenge. This study highlights the prevalent bacterial isolates and their resistance patterns against commonly used antibiotics. The findings provide valuable insights that can support healthcare professionals in making informed, evidence-based treatment decisions and improving

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patient care. As the distribution of bacterial pathogens and their resistance profiles can vary across different settings, it is crucial to perform culture and sensitivity testing whenever possible before initiating antibiotic therapy. Empirical treatment should be guided by the most recent local antibiogram data. Adopting appropriate, evidence-based antibiotic policies is essential to ensure effective treatment outcomes and to combat the growing threat of antimicrobial resistance in both developed and developing countries.

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Data Availability Statement

The dataset will be shared upon request

Conflicts of Interest

Authors declared that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Author's Contribution

NN and MFB drafted the manuscript. MN, FR, RK, MSA, MMB and MJS validated the results and revised the manuscript.

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