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Original Research Article

MAPPING THE ANTIBIOTIC SUSCEPTIBILITY PATTERNS OF COMMONLY ISOLATED PATHOGENIC BACTERIAL ISOLATES FROM CLINICAL SPECIMENS – A MEGHALAYA PERSPECTIVE

Robertson Sawian[1], H. Larikyrpang Kharchandy[2], Olisha Sumer[3]

[1]Senior Resident, Microbiology Department, Shillong Medical College, Pasteur Hills, Shillong, Meghalaya, India
[2]Assistant Professor, Microbiology Department, Shillong Medical College, Pasteur Hills, Shillong, Meghalaya, India
[3]Senior Resident, Microbiology Department, Shillong Medical College, Pasteur Hills, Shillong, Meghalaya, India

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Corresponding Author:
Dr. Robertson Sawian,
Senior Resident, Microbiology Department, Shillong Medical College, Pasteur Hills, Shillong, Meghalaya, India.
Email: sawianrobertson@gmail.com

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ABSTRACT

Background: Antimicrobial resistance (AMR) is a major global health threat with devastating outcomes if not acted upon efficiently. Data on AMR in the state of Meghalaya, India, is limited. The objective is to map the antibiotic susceptibility patterns of the commonly isolated pathogenic bacterial isolates from clinical specimens received from several hospitals across four regions of the State.

Materials and Methods: Clinical specimens were collected from both outpatients and inpatients from several hospitals in four regions of Meghalaya for Culture and Antibiotic Susceptibility testing (AST). Identification and AST were performed using the Vitek-2 Compact Automated system (Biomerieux), and data were analysed using Microsoft Excel.

Results: Out of 3053 isolates, Gram-negative bacilli were more frequently isolated than Gram-positive bacteria. Urine yielded the majority of bacterial isolates. Variable susceptibility pattern is exhibited by various isolates, notably among which is very low susceptibility to Fluoroquinolones among Escherichia coli and Klebsiella species, but high susceptibility among Pseudomonas species and Acinetobacter species. Carbapenems and Aminoglycosides have good susceptibility patterns against most gram-negative isolates. The Methicillin-Resistant Staphylococcus aureus (MRSA) rate is 35.26%, only slightly lower than the National prevalence rate of 37%. Among the Enterococcus species, Enterococcus faecium predominates over other species.

Conclusion: Implementation of the Antimicrobial Stewardship Programme across the State, coupled with a robust AMR surveillance system, is imperative to further the prevention and containment of Antimicrobial Resistance.

Keywords: Antibiotic, Susceptibility, Meghalaya, AMR.

INTRODUCTION

Antimicrobial resistance (AMR) has emerged as a serious global health threat, posing even greater challenges in resource-limited settings.[1] Common infections, such as pneumonia, diarrhoea, sexually transmitted diseases, postoperative complications, and tuberculosis, are becoming increasingly difficult to treat. Recent data indicate that AMR infections account for approximately 700,000 deaths annually, with projections suggesting a staggering increase to 10 million per year by 2050 if current trends persist.[2]

Clinically, AMR arises primarily due to the misuse, overuse, and non-compliance with prescribed antimicrobial therapies, fostering spontaneous mutations in chromosomes or control genes. These mutations, under selective pressure from antimicrobial exposure, generate new resistant strains. As these mutations accumulate, multidrug-resistant pathogens evolve, necessitating the use of broad-spectrum antibiotics as a last resort.[3]

Particularly concerning is the rapid emergence and spread of multidrug-resistant bacteria, which are increasingly difficult to treat with existing antibiotics.

This includes extended-spectrum beta-lactamases (ESBL), AmpC beta-lactamases, and carbapenemase-producing Gram-negative bacteria, such as carbapenem-resistant Enterobacteriaceae (CRE) - along with methicillin-resistant Staphylococcus aureus (MRSA), all of which are proliferating globally at an alarming rate.[4]

Meghalaya, one of the states in the North-Eastern Region of India, lacks statewide AMR data from a human health perspective, and no statewide studies have been conducted to date that encompass all regions of the state. This study aims to highlight the common bacterial infections in Meghalaya and map the susceptibility patterns of the clinically important bacterial species commonly isolated.

MATERIALS AND METHODS

Study Design and Setting: We conducted a hospital-based observational study between April 2024 and April 2025 involving ten (10) district hospitals and all urban health centres (e.g., dispensaries and urban PHCs) from four different regions in Meghalaya, namely, Khasi, Jaintia, Ri-Bhoi, and Garo regions. Such hospitals are listed in [Table 1].

Data Collection: Clinical specimens were collected from both outpatients and inpatients as part of each hospital's routine clinical care. Thus, specimens were requested based on clinicians' assessment and then submitted for microbiological tests. Specimens were transported as per standard guidelines to the Microbiology Laboratory, Pasteur Institute, Shillong.

Laboratory Procedure: Specimen processing, identification of organisms to the genus and/or species level, and in vitro antibiotic susceptibility testing were performed per the standard microbiological procedures and the CLSI guidelines. Pathogenic bacteria were identified using standard microbiological methods such as morphology on culture media, Gram staining, and using the Vitek-2 Compact automated system (Biomerieux). In vitro antibiotic susceptibility testing was performed using the Vitek-2 Compact automated system (Biomerieux). Isolates with intermediate or resistant results on antibiotic susceptibility were classified as resistant strains during data analysis.

Quality Control: Stenotrophomonas maltophilia ATCC 17666 and Staphylococcus saprophyticus ATCC BAA 750 are used as Quality control strains for the identification of Gram-negative and Gram-positive bacteria using the Vitek-2 system (Biomerieux), respectively. For Antibiotic Susceptibility of Gram-negative bacilli, Escherichia coli ATCC 25922 for Lactose fermenting colonies and Pseudomonas aeruginosa ATCC 27853 for Non-lactose fermenting colonies are used. Whereas for the Antibiotic susceptibility of Gram-positive, Staphylococcus aureus ATCC 29213 is used.

Data Management and Analysis: Demographic information (i.e., age, sex, and patient location) for patients from whom bacterial pathogens were isolated was entered into the Vitek-2 system during identification and antibiotic susceptibility testing. Data analysis was performed using Microsoft Excel. Only the first isolate of a particular bacterial species during the analysis period was included from each patient. Variables (i.e., bacterial isolates, antibiotic susceptibility, and demographic characteristics) were summarised as frequencies, percentages, medians, and inter-quartile ranges as deemed appropriate.

RESULTS

Patient Demographic Characteristics: We isolated a total of 3053 bacterial isolates from clinical specimens. The patients' median (IQR) age was 25.2 years, and 2079 (68.09%) isolates were from females [Table 1]. Ganesh Das Government Maternal & Child Health Hospital, Shillong (GDH), contributed the majority of clinical specimens [Table 2].

Culture Results: Most of the isolates were isolated from urine (56.14%), sputum (13.10%), wound pus (12.05%), blood (6.35%), high vaginal swab (5.43%) and respiratory samples (other than sputum) (3.7%). The majority of S. aureus was highly recovered from pus, sputum, and urine [Figure 1].

The most frequent isolate recovered was Escherichia coli (30.55%), followed by Coagulase-negative Staphylococcus species (14.73%), Klebsiella species (11.23%), Enterococcus faecium (11.19%), Enterococcus faecalis (9.58%), and Staphylococcus aureus (6.5%). Other genera belonging to the order Enterobacterales (except Escherichia coli, Klebsiella, Salmonella, and Shigella) constitute 5.18% of all isolates. Acinetobacter spp. and Pseudomonas spp. comprised 3.43% and 4%, respectively. [Figure 1].

Antibiotic Susceptibility Pattern of the Bacterial Isolates Identified: [Table 3 and 4] report the antibiotic susceptibility patterns of Gram-negative and Gram-positive bacterial isolates to commonly used antibiotics, respectively. Gram-negative bacteria were the predominant isolates in this study, demonstrating variable susceptibility patterns to commonly used antibiotics. Both gram-negative and gram-positive bacteria exhibited diverse resistance profiles.

DISCUSSION

Antimicrobial resistance (AMR) is one of the top public health and development challenges worldwide. In this study, we evaluated the in vitro susceptibility patterns of frequently isolated bacterial pathogens to commonly prescribed antibiotics. The analysis of antimicrobial susceptibility patterns provides crucial insight into the evolving resistance trends among commonly isolated bacterial pathogens. The predominance of Gram-negative bacterial isolates over Gram-positive bacteria underscores their significant role in infectious diseases, particularly in healthcare-associated infections.[5]

Sample Distribution and Pathogen Isolation: Urine samples yielded the highest number of isolates, followed by sputum, pus, blood, high vaginal swabs, and respiratory aspirates. This pattern potentially underscores the burden of urinary tract infections (UTIs) caused by resistant pathogens, necessitating vigilant monitoring and the implementation of appropriate therapeutic strategies.[6] Respiratory and wound infections also significantly contributed to the bacterial load, underscoring the need for targeted antimicrobial approaches.

Antimicrobial Susceptibility Trends: The study revealed a decreased susceptibility to fluoroquinolones, particularly among Escherichia coli, Klebsiella pneumoniae, and even among Staphylococcus aureus, Coagulase-negative Staphylococci (CoNS), and Enterococcus species, raising concerns about the continued efficacy of these agents in empirical therapy. Very high resistance (>80%) to fluoroquinolones among Escherichia coli and Klebsiella Pneumoniae was also reported among adult and paediatric intensive care unit patients in a tertiary hospital in Kolkata, India.[7] However, in contrast to previous studies in India (Nandlal Kumar, 2023; Rajeev Ranjan, 2024), their susceptibility among Pseudomonas aeruginosa and Acinetobacter baumannii is higher in this study.[8,9] Therefore, they can be considered viable therapeutic options for infections caused by these bacterial species. As far as Meghalaya is concerned, a previous study also reported higher susceptibility of Acinetobacter baumannii to fluoroquinolones and aminoglycosides.[10]

The MRSA rate of 35.26%, close to the overall MRSA prevalence rate in India (37%), underscores the need for alternative treatment options for Staphylococcus aureus-related infections. The same study reported MRSA prevalence of 40% for the North-East Zone, higher than in the present study.[11] The study highlights the predominance of Enterococcus faecium over Enterococcus faecalis. Contrastingly, other studies report Enterococcus faecalis as the predominant species within the genus.[12] In this study, 17.61% of Enterococcus faecium isolates and 4.32% of Enterococcus faecalis isolates are Vancomycin-Resistant (VRE), highlighting the growing resistance of Enterococcus species, limiting treatment choices for severe infections, similar to findings in a systematic and meta-analysis by Shrestha et al.[13] VRE prevalence was estimated at 4.8% between 2000 and 2010 and 14.1% between 2011 and 2020. Interestingly, Enterococcus faecalis exhibited high susceptibility (96.76%) to benzyl penicillin (used as a surrogate for ampicillin, amoxicillin, ampicillin-sulbactam, amoxicillin-clavulanate, and piperacillin-tazobactam), whereas Enterococcus faecium showed significantly lower susceptibility (15%), indicating species-specific resistance mechanisms that warrant further investigation.[14]

Further examination demonstrated reduced susceptibility of Nitrofurantoin against Klebsiella spp. and Enterococcus faecium, raising questions about its effectiveness in urinary tract infections involving these pathogens.[15] However, nitrofurantoin demonstrated high susceptibility when evaluated for Escherichia coli, S. aureus, S. saprophyticus, and Enterococcus faecalis, comparable to a 2020 study by Chavan et al for isolates collected from various Indian Tertiary Care Hospitals.[16]

β-Lactam Resistance and Alternative Therapeutic Options: Escherichia coli and Klebsiella pneumoniae exhibited excellent susceptibility to Carbapenems, as also observed by Vandana Verma in a multicentric and retrospective study among ICU patients in 2024.[17] We also observed excellent susceptibility to Carbapenems among Pseudomonas aeruginosa isolates, which is in contrast to the findings (53.42% for Imipenem & 51.83% for Meropenem) in the above study. However, reduced susceptibility to carbapenems is seen among the Acinetobacter baumannii isolates (39.68% for Imipenem), also observed by Dash et al in a five-year trend analytic study, whereby a decrease in resistance to carbapenems from 88% to 81.5% is reported.[18] Susceptibility of Escherichia coli and Klebsiella spp. to Piperacillin-tazobactam and Amoxicillin-clavulanate is also good, a contrasting finding to a pharmaco-epidemiological study involving multiple teaching hospitals.[19] Piperacillin-tazobactam, Cefepime, and Ceftazidime have good in vitro susceptibility to Pseudomonas aeruginosa, higher than in the previous study conducted in Italy.[20] Ceftriaxone, one of the most widely used antibiotics, exhibited low susceptibility to Acinetobacter baumannii as well as to Escherichia coli and Klebsiella pneumoniae. Similarly, cefuroxime (2nd generation) and Cefixime (3rd generation, oral) show low susceptibilities, limiting their use against infections caused by Escherichia coli and Klebsiella pneumoniae.[21] Cefepime, a 4th-generation cephalosporin, similarly exhibited low susceptibility in our study, comparable to a study conducted in some states in India, reporting high prevalence of Cefepime resistance by Escherichia coli isolates.[22] Some studies reported high susceptibility of Escherichia coli and Klebsiella spp. to Cefepime.[23,24]

Aminoglycosides, notably Gentamicin and Amikacin, have very good susceptibility against Escherichia coli and Klebsiella spp. in our study. Lower per cent susceptibilities were reported in a previous study in a tertiary centre.[25] A susceptibility rate of 68.8% is observed against Acinetobacter baumannii. While some studies report low susceptibilities of A. baumannii to Amikacin. [26,27] Another 2004 study observed a susceptibility of 60%, which is slightly lower than the one reported in this study.[28] Amikacin, recommended as an option for treating UTI caused by Pseudomonas aeruginosa, shows excellent susceptibility. Other Indian studies also reported a high susceptibility profile of Pseudomonas aeruginosa to Amikacin. [29,30]

Limitation: The current study elaborates only on phenotypic resistance among bacterial isolates. Genotypic resistance typing would have complemented this study to a greater extent. However, findings from this study can be useful for operational purposes, considering the limited published data for the state of Meghalaya.

CONCLUSION

Depending on the genus and species, clinical isolates exhibited variable susceptibilities to the commonly used antibiotics. This emphasizes the need to implement and strengthen antimicrobial stewardship programs in various hospitals across the state, coupled with a robust AMR Surveillance System that encompasses human, animal, and plant health.

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