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Original Research Paper

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A STUDY ON ANTIMICROBIAL RESISTANCE PATTERN IN DIABETIC FOOT ULCER AT TERTIARY CARE HOSPITAL

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ABSTRACT

Aim: The study was conducted with the objective of identifying bacterial profiles associated with infected diabetic foot ulcers (DFUs) and examining the patterns of antibiotic prescription utilized in their management. **Methods:** A prospective observational cross-sectional study was conducted at Government Cuddalore Medical College and Hospital (GCMCH), enrolling 80 patients with type 2 diabetes and DFUs. Clinical data and microbiology culture results were analyzed using Microsoft Excel to characterize bacterial profiles and assess antimicrobial resistance patterns. **Results:** Pseudomonas aeruginosa was the predominant pathogen (55%), followed by Klebsiella pneumoniae (25%), Staphylococcus aureus (10%), Escherichia coli, and Proteus sp. Detailed resistance analysis revealed varying susceptibility among pathogens, with P. aeruginosa displaying resistance primarily to cephalosporins, while K. pneumoniae showed higher susceptibility to aminoglycosides. E. coli exhibited resistance to aminoglycosides but susceptibility to penicillin/beta-lactamase inhibitors and cephalosporins. S. aureus was resistant to macrolides but susceptible to linezolid and chloramphenicol. Proteus sp. Demonstrated resistance to aminoglycosides and cephalosporins but susceptibility to fluoroquinolones. **Conclusion:** This study underscores the importance of antimicrobial stewardship in DFU management. Tailored antibiotic regimens, guided by local resistance patterns, are essential for optimizing treatment outcomes and minimizing AMR emergence. Understanding resistance profiles facilitates evidence-based antibiotic selection, thereby enhancing patient care and addressing the global challenge of AMR.

KEYWORDS : Diabetic foot ulcers, antimicrobial resistance, bacterial profiles, susceptibility patterns, antimicrobial stewardship.

INTRODUCTION

Diabetes poses a significant global health threat, ranking as the ninth leading cause of death worldwide and claiming 1.6 million lives in 2019. Among its complications, diabetic foot ulcers (DFUs) stand out, affecting 12–25% of diabetic individuals and often leading to hospitalization due to severe infections like osteomyelitis, which can result in amputation. Despite treatment efforts with antibiotics and other modalities, antimicrobial resistance (AMR) presents a formidable barrier to DFU management. In India, with high diabetes prevalence and limited healthcare access, AMR in DFUs is particularly challenging. Factors include inappropriate antibiotic use, suboptimal wound care, and difficulty implementing stewardship programs. ESBL-producing bacteria and carbapenem-resistant organisms compound the issue, limiting treatment options. Biofilm-forming bacteria in DFUs worsen infections and complicate therapy. Understanding resistance patterns is crucial for guiding treatment and implementing stewardship programs. A comprehensive analysis of AMR in DFUs is vital for evidence-based guidelines and combating AMR in this vulnerable population.

Methodology

Study site: Department of surgery, Government Cuddalore Medical College and Hospital (GCMCH), a tertiary care hospital. Study period: September 2023 - February 2024 (6 months)

Study tool: Proforma, Source of study: The case sheets of inpatients in GCMCH.

Study design: Prospective observational cross- sectional study.

Study recruitment: Recruited based on the inclusion and exclusion criteria. Inclusion Criteria are patients diagnosed with diabetic foot ulcers, Age 18 years and above, both male and female. Patient's case sheets with microbiology culture and sensitivity data. Exclusion Criteria are Patients with DM but no diabetic foot ulcers. Patients with psychological disorders. Study procedure: The study will involve selecting subjects based on predefined inclusion and exclusion criteria. Demographic information such as patient name, age, disease duration, and antimicrobial management details will be gathered from the case sheets. Additionally, data on culture and sensitivity investigations will be recorded. Information regarding the identified organisms, their resistance patterns, and susceptibility to antimicrobial agents will also be collected. The collected data will then be analyzed using appropriate descriptive statistical tools, with Microsoft Excel being utilized for this purpose. Following analysis, the results will be interpreted based on the data collected, providing insights into antimicrobial resistance patterns in diabetic foot ulcers.

RESULT

A total of 80 diabetic foot ulcer cases (type 2 diabetes) were collected. Out of which 85% (68) are male and 15% (12) are female patients

Bacterial Isolates Obtained From Microbiology Data

In this study, it reveals *Pseudomonas aeruginosa* as the prevailing gram-negative bacterium in diabetic foot ulcers, constituting approximately 55% of all identified organisms. *Klebsiella pneumoniae*, another gram-negative bacterium, accounts for around 25% of infections in diabetic foot ulcers, followed by *Staphylococcus aureus* at approximately 10%. *Escherichia coli* and *Proteus species* are each implicated in approximately 10% and 5% of diabetic foot ulcer cases,

respectively.

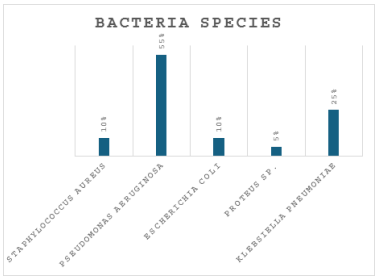

Figure 1 Type of bacterial species

Antimicrobial Resistance Pattern Of Bacterial Isolates

Pseudomonas aeruginosa shows varying resistance to antibiotics, highest for ceftazidime (19%), followed by cefixime and cefotaxime (11%), and lowest for ceftriaxone (1%). Aminoglycoside resistance is 13% for gentamicin, 11% for ofloxacin, and 7% for piperacillin-tazobactam and amikacin, while resistance to polymyxin B is 3%, tobramycin 5%, and co-trimoxazole, chloramphenicol, and norfloxacin each 1%. *Klebsiella pneumoniae* exhibits notable resistance to cephalosporins: 16% to cefotaxime, 12% to cefixime, and 9% to ceftazidime. Resistance to ofloxacin is 12%, to piperacillin-tazobactam 9%, and to co-trimoxazole, ampicillin, and polymyxin B also 9%. Gentamicin and amikacin show lower resistance rates of 6% and 3%, respectively. *Escherichia coli* shows high resistance to aminoglycosides: 40% to amikacin and 20% to gentamicin, and 20% to cefixime. Ofloxacin and polymyxin B resistance is 10%. *Staphylococcus aureus* is significantly resistant to macrolides, with 37% to erythromycin, 25% to gentamicin and piperacillin-tazobactam, and 12.5% to ofloxacin. *Proteus sp.* shows resistance to aminoglycosides and cephalosporins: 22% to amikacin and cefotaxime, 11% to gentamicin, cefixime, ofloxacin, and co-trimoxazole.

Table 1 Antimicrobial pattern of bacterial isolates.

Bacterial species	Type of species	Antimicrobial resistance pattern of bacterial isolates
Staphylococcus aureus	Gram positive	Erythromycin (E) – 37.5% Gentamycin (GEN) – 25% Piperacillin tazobactam (PIT) – 25% Ofloxacin (OF) – 12.5%
Pseudomonas aeruginosa	Gram negative	Ceftazidime (CAZ) – 19% Gentamycin (GEN) – 13% Ofloxacin (OF) – 11% Cefotaxime (CTX) – 11% Cefixime - 11% Amikacin (AK) – 7% Piperacillin tazobactam (PIT) – 7% Polymyxin (B) – 3% Norfloxacin (NX) – 1% Ceftriaxone (CTR) – 1% Chloramphenicol (C) – 1% Co trimoxazole (COT) – 1%
Escherichia coli	Gram negative	Amikacin (AK) – 40% Gentamycin (GEN) – 20% Ofloxacin (OF) – 10% Polymyxin (B) – 10% Cefixime – 20%
Proteus sp.	Gram negative	Amikacin (AK) – 22% Gentamycin (GEN) – 11% Piperacillin tazobactam (PIT) – 11% Ofloxacin (OF) – 11% Cefotaxime (CTX) – 22% Cefixime – 11% Co trimoxazole (COT) – 11%
Klebsiella	Gram negative	Ampicillin (AMP) – 9% Amikacin (AK) – 3% Gentamycin (GEN) – 6% Piperacillin Tazobactam (PIT) – 9% Ofloxacin (OF) – 12% Cefotaxime (CTX) – 16% Ceftazidime (CAZ) – 9% Polymyxin (B) – 9% Cefixime – 12% Co trimoxazole (COT) – 9%

Antimicrobial Susceptibility Pattern Of Bacterial Isolates

Pseudomonas aeruginosa demonstrates susceptibility to certain polypeptide antibiotics. Polymyxin B exhibits a sensitivity rate of 26%, while amikacin (an aminoglycoside) shows a sensitivity of 20%. Piperacillin-tazobactam and ofloxacin have a susceptibility rate of 16%. Gentamicin and cefixime exhibit a sensitivity of 10%, while cefotaxime, tobramycin, and co-trimoxazole show lower sensitivity rates at 3%. Gram-negative bacteria *Klebsiella pneumoniae* shows higher susceptibility to aminoglycoside antibiotics, with amikacin exhibiting a sensitivity of 29% and gentamicin at 17%. Additionally, piperacillin-tazobactam shows a high sensitivity of 26%. However, sensitivity to ofloxacin is only 11%, while cefotaxime, polymyxin, and chloramphenicol exhibit sensitivities of 5%. Gram-negative bacteria *Escherichia coli* is predominantly susceptible to penicillin/beta-lactamase inhibitor antibiotics. *E. coli* shows a 75% sensitivity to piperacillin-tazobactam and a 25% sensitivity to cefotaxime (cephalosporin). The gram-positive bacteria *staphylococcus aureus* is mostly susceptible to oxazolidinones antibiotics, Sensitivity to linezolid is 75%. Sensitivity to chloramphenicol is 25%. *Proteus sp.* is predominantly susceptible to fluoroquinolone antibiotics, with a sensitivity rate of 50% to ofloxacin, 33% to gentamicin (GEN), and 16% to piperacillin-tazobactam.

Table 2 Antimicrobial sensitivity pattern of bacterial isolates.

Bacterial species	Type of species	Antimicrobial sensitivity pattern of bacterial isolates
Staphylococcus aureus	Gram positive	Linezolid (LZ) – 75% Chloramphenicol (C) -25%
Pseudomonas aeruginosa	Gram negative	Amikacin (AK) – 20% Gentamycin (GEN) – 10% Piperacillin tazobactam (PIT) – 16% Ofloxacin (OF) – 16% Cefotaxime (CTX) – 3% Tobramycin (TOB) – 3% Polymyxin (B) – 26% Cefixime – 10% Co trimoxazole (COT) – 3%
Escherichia coli	Gram negative	Piperacillin Tazobactam (PIT) – 75% Cefotaxime (CTX) – 25%
Proteus sp.	Gram negative	Gentamycin (GEN) – 33% Piperacillin Tazobactam (PIT) – 16% Ofloxacin (OF) – 50%
Klebsiella	Gram negative	Amikacin (AK) – 29% Gentamycin (GEN) – 17% Piperacillin tazobactam (PIT) – 23% Ofloxacin (OF) – 11% Cefotaxime (CTX) – 5% Chloramphenicol (C) – 5% Polymyxin (B) – 5%

DISCUSSION

80 cases of diabetic foot ulcers (DFUs) among type 2 diabetes patients were analyzed.85% (68) were male patients, while 15% (12) were female patients. **Predominant Bacteria:** *Pseudomonas aeruginosa*: 55% of all identified organisms. *Klebsiella pneumoniae:* 25%. *Staphylococcus aureus:* 10%. *Escherichia coli:* 10%. *Proteus sp.*: 5%. *Pseudomonas aeruginosa:* Resistance mainly to cephalosporin antibiotics; susceptibility to polypeptide bacterial antibiotics. *Klebsiella pneumoniae*: Resistance primarily to cephalosporin

antibiotics; susceptibility to aminoglycoside antibiotics. *Escherichia coli:* Resistance mainly to aminoglycoside antibiotics; susceptibility to penicillin/beta-lactamase inhibitors and cephalosporin antibiotics. *Staphylococcus aureus*: Resistance primarily to macrolide antibiotics; susceptibility to linezolid and chloramphenicol. *Proteus sp.:* Resistance mainly to aminoglycoside and cephalosporin antibiotics; susceptibility to fluoroquinolone antibiotics. Emphasizes the need for judicious antibiotic use in DFU management based on local epidemiological data and antimicrobial susceptibility patterns. Insights into antimicrobial resistance patterns aid in optimizing antibiotic therapy and improving patient outcomes.

CONCLUSION

The study involved 80 cases of diabetic foot ulcers (DFUs) in patients with type 2 diabetes, predominantly male (85%). *Pseudomonas aeruginosa* was the most common bacterium isolated (55%), followed by *Klebsiella pneumoniae* (25%), *Staphylococcus aureus* (10%), *Escherichia coli*, and *Proteus sp*. Detailed analysis of antimicrobial resistance patterns revealed *Pseudomonas Aeruginosa's* resistance primarily to cephalosporin antibiotics, while *Klebsiella pneumoniae* exhibited resistance mainly to cephalosporins but higher susceptibility to aminoglycosides. *Escherichia coli* displayed resistance to aminoglycosides but susceptibility to penicillin/beta-lactamase inhibitors and cephalosporins. *Staphylococcus aureus* was resistant to macrolide antibiotics but susceptible to linezolid and chloramphenicol. *Proteus sp*. showed resistance to aminoglycosides and cephalosporins but susceptibility to fluoroquinolones. Understanding resistance patterns enables healthcare providers to customize antibiotic regimens, enhancing patient care and potentially mitigating the rise of drug-resistant bacteria. Overall, this study contributes to the development of more effective treatment strategies.

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