Original Research Article

STUDY OF MICROBIOLOGICAL PROFILE AND ANTIBIOTIC SUSCEPTIBILITY PATTERN OF DIABETIC FOOT IN A TERTIARY CARE HOSPITAL

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ABSTRACT

Background: Diabetes mellitus can cause diabetic foot ulcers (DFUs), which is the most prevalent complication and often progress to secondary infections. If untreated, they may require limb amputation, severely affecting quality of life. Various bacteria and fungi can cause these infections. Early detection and knowledge of antibiotic resistance are crucial for effective treatment. This study aims to identify the bacteria involved in DFUs and evaluate their antibiotic resistance.

Materials and Methods: This prospective observational study was conducted in the Department of Microbiology. Samples from diabetic foot ulcers were collected using sterile swabs, and pus samples were taken with sterile needles. Bacterial identification was done using standard microbiological techniques, including culture, Gram staining, and biochemical tests. Antibiotic susceptibility testing was performed using the Kirby-Bauer disk diffusion method following CLSI guidelines.

Results: Out of 138 patients (aged 20–81 years), 72 bacterial isolates were recovered. Gram-negative bacteria made up 94.5% of the isolates, while Gram-positive bacteria accounted for 5.5%. The most common bacteria were Pseudomonas aeruginosa (12.85%), E. coli (10%), and Acinetobacter baumannii (7.85%). Staphylococcus aureus was the main Gram-positive isolate (2.86%). About 48.57% of samples showed no bacterial growth. Gram-negative organisms were more sensitive to third-generation cephalosporins, carbapenems, and aminoglycosides. Vancomycin, linezolid, and cefoxitin were most effective against Gram-positive organisms.

Conclusion: Multidrug-resistant bacteria pose a serious challenge in diabetic foot infections. Early microbiological testing and antibiotic sensitivity analysis are essential for proper treatment.

Keywords: Gram-positive bacteria, gram-negative bacteria, resistance, diabetic foot infections, multidrug drug resistance.

INTRODUCTION

Diabetic foot infections (DFIs) are a significant cause of morbidity among individuals with diabetes, often leading to prolonged hospitalizations and, in severe cases, amputations.[1]

Approximately 10-25% of diabetic patients may develop foot ulcers during their lifetime, with a substantial risk of these ulcers becoming infected. Notably, Polymicrobial infections are common, occurring in up to 69.6% of cases, and the prevalence of multidrug-resistant organisms poses significant treatment challenges.[2] Understanding the regional microbiological landscape and antibiotic susceptibility patterns is crucial for the effective management of DFIs. This study aims to explore the microbiological profile and antibiotic susceptibility patterns of diabetic foot infections in a tertiary care hospital of south Gujarat to inform empirical therapy and improve patient outcomes. This study will also help clinicians make better-informed decisions, ultimately improving care for diabetic patients with foot infections to prevent complications.

MATERIALS AND METHODS

A prospective, hospital-based study was conducted over a six-month duration in the Department of Microbiology at a tertiary care center, following formal approval from the institution's ethics committee. The study enrolled a total of 138 patients aged above 18 years who were clinically evaluated and diagnosed with diabetic foot infections by the surgical department. Patients under the age of 18 and repeat samples from the same individual were excluded to maintain data integrity.

Clinical specimens, including pus or wound swabs, were aseptically collected by the surgical team from diabetic foot lesions and promptly transported to the microbiology laboratory for further analysis. Each sample underwent direct Gram staining to provide preliminary microscopic evaluation and was simultaneously inoculated onto MacConkey agar and Blood agar media. These culture plates were incubated at 37°C under aerobic conditions to facilitate the growth of pathogenic organisms.

Isolated bacterial colonies were identified based on Gram staining characteristics, motility testing, and a series of standardized biochemical reactions to confirm species-level identification. Antimicrobial susceptibility testing of aerobic isolates was performed using the Kirby-Bauer disk diffusion technique. Antibiotic-impregnated discs were placed on Mueller-Hinton agar plates inoculated with standardized bacterial suspensions and incubated at 37°C for 24 hours. The diameters of the zones of inhibition were then measured and interpreted according to the Clinical and Laboratory Standards Institute (CLSI) guidelines, 2023 edition.[3]

Statistical Analysis

In the present analysis, categorical variables were evaluated by analyzing the data in terms of frequencies and percentages, while continuous variables were presented as mean values with corresponding standard deviations. All statistical analyses were performed using SPSS software, version 20.

RESULTS

An observational cross-sectional study was conducted in the department of microbiology from January to June 2024 in a tertiary care hospital. A total 138 patients with diabetic foot were included in this study. Out of 138 patients, 103 patients (75%) were male, and 35 patients (25%) were female. Most of the patients in this study belong to age group 41-60 years (46%) followed by 20-40years (31%) & 61-80 years (23%). (Graph 1, Table 1)

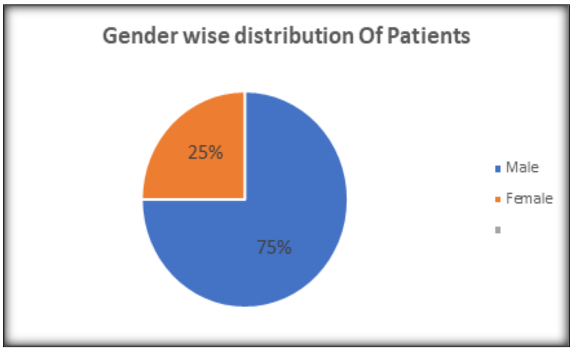

Figure 1: Patient 's distribution according to sex

Table 1: Distribution according to age

Age group wise distribution of all patients		
Age group (Years)	**No. of patients**	**Percentage (%)**
20-40	43	31
41-60	63	46
61-80	32	23
Total	138	100%
Mean ± SD	48.41 ± 14.66	

In this study total number of patients showing culture positivity were 70 (50.72%), out of which there were 68 (97%) monomicrobial and 2(3%) polymicrobial cases.A total of 72 organisms were isolated in this study; 68 organisms (94.5%) were Gram-negative, and 4(5.5%) were Gram-positive.

Most common isolated organism was Psedomonas aerguniosa (12.85%), followed by E. coli (10%) Acinetobacter baumanni(7.85 %), P.mirabilis (6.42%) Klebsiella pneumoniae (5.71%), , S.aureus (2.86%), Klebsiella aerogenes(1.42%), Morganella Morgagni (1.42%), Providentia rettegeri(0.7%), Pseudomonas spp.(0.7%), Providentia stuartii(0.7%), and P.vulgaris (0.7%) in swab and Pus sample. 48.57 % of samples were culture-negative. (Table 2)

Table 2: Distribution according to isolated organism of all patients

Finding	No. of organism isolated from patients	Percentage (%)
Sterile cultures	68	48.57
Pseudomonas aeruginosa	18	12.85
E. coli	14	10
Acinetobacter baumanni	11	7.85
P.mirabilis	9	6.42
Klebseilla pneumoniae	8	5.71

S.aureus	4	2.86
Klebsiella aerogenes	2	1.42
Morganella morgagni	2	1.42
Providentia rettegeri	1	0.7
Providentia stuartii	1	0.7
Pseudomonas spp.	1	0.7
P.vulgaris	1	0.7
Total	**140**	**100%**

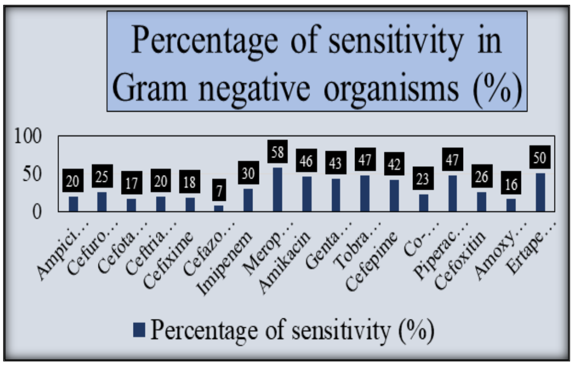

Figure 2A: Percentage of antibiotic sensitivity of gram -ve organisms

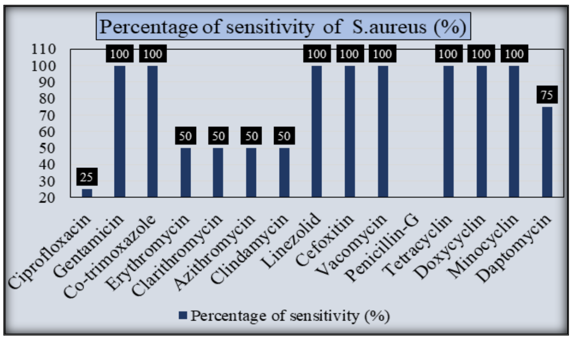

Figure 2B: Percentage of antibiotic sensitivity of S. Aureus

The most sensitive antibiotic for gram-negative organisms is carbapenems, followed by aminoglycosides and 4th generation cephalosporins. The most sensitive antibiotics for gram positive organisms were vancomycin and linezolid. (Graph 3A and 3B, Table 3)

Table 3: Percentage of antibiotic sensitivity of aerobic organisms

Name of Organism	PERCENTAGE OF ANTIBIOTIC SENSITIVITY OF AEROBIC ORGANISMS																						
	AMP	AMC	PIT	A/S	CPM	CTX	CTR	CAZ	CX	CZ	IPM	MRP	AK	GEN	CIP	LE	E	CD	Va	COT	TE	DO	MI
	%	%	%	%	%	%	%	%	%	%	%	%	%	%	%	%	%	%	%	%	%	%	%
Pseudomonas aeruginosa	-	-	73	-	83	-	-	64	-	-	41	78	80	78	72	70	-	-	-	-	-	-	-
E.coli	0	7	23	14	15	7	7		0	0	29	58	58	36	0	0	-	-	-	29	14	22	-
Acinetobacter baumanni	-	-	0	0	0	0	0	0	-	-	0	0	0	0	0	0	-	-	-	0	-	-	55
P.mirabilis	22	45	100	45	55	44	56	33	88	27	45	89	43	43	33	22	-	-	-	44	-	-	-
Klebseilla pneumoniae	-	0	13	13	13	14	12		0	0	25	25	25	12	0	13	-	-	-	13	13	38	-
S.aureus	-	-	-	-	-	-	-	-	-	-	-	-	-	100	25		50	50	100	100	100	100	100
K.aerogenes	-	-	50		50	0	0	-	100		50	50	0	50	0	0	-	-	-	0	0	0	-
Morganella morgagni	-	-	100	50	100	0	50	100	0	-	50	100	100	100	50	50	-	-	-	0	-	-	-
Providentia rettegeri	-	-	100	0	100	100	100	100	100	-	0	100	100	-	100	100	-	-	-	100	-	-	-
Providentia stuartii	-	-	100	100	100	100	100	0	0	-	0	100	100	-	100	100	-	-	-	100	-	-	-
Pseudomonas spp.	-	-	0	-	0	-	-	0	-	-	0	100	100	-	0	0	-	-	-		-	-	-
P.vulgaris	0	0	100	0	0	0	0	0		0	100	100	0	0	0	0	-	-	-	0	-	-	-

DISCUSSION

One of the most common and serious complications of DM is the development of foot ulcers. Key contributing factors include peripheral arterial disease (PAD), foot deformities, diabetic neuropathy, unnoticed trauma, and increased peak plantar pressure. Although infection is not usually the primary cause, diabetic foot ulcers become highly susceptible to infection once structural deformities occur.[4-5] These infections often remain inadequately treated due to limited understanding of the causative pathogens and their antimicrobial sensitivity patterns. In this study, 138 patients were evaluated, with the majority aged 41–60 years (46%), followed by 20–40 years (31%) and 61–80 years (23%). The mean age was 48.41 ± 14.66 years. Among them, 70 patients (50.72%) showed culture positivity, with 97% (n=68) being monomicrobial and 3% (n=2) polymicrobial infections. A total of 72 organisms were isolated, of which 94.5% were Gram-negative and 5.5% were Gram-positive.[5-6]

The most commonly isolated organism was Pseudomonas aeruginosa (12.85%), followed by E. coli (10%), Acinetobacter baumannii (7.85%), Proteus mirabilis (6.42%), and Klebsiella pneumoniae (5.71%). Less frequent isolates included S. aureus (2.86%), Klebsiella aerogenes, Morganella morganii, Providencia rettgeri, Providencia stuartii, Pseudomonas spp., and Proteus vulgaris. Culture-negative samples accounted for 48.57%.[7] Regarding antibiotic sensitivity, Gram-negative organisms showed the highest sensitivity to carbapenems, followed by aminoglycosides and 4th-generation cephalosporins. Gram-positive organisms demonstrated the highest sensitivity to vancomycin and linezolid.[8]

In the study by Taki E et al., Gram-positive bacteria, particularly Staphylococcus spp., accounted for the majority (64.2%) of isolates, consistent with findings from other populations including the UK (63%), Portugal (60%), and a previous study in Iran (62.1%). In contrast to the previous analysis the present investigation demonstrates the predominance of Pseudomonas aeruginosa. This indicates a notable shift in the microbial profile, with Pseudomonas aeruginosa emerging as the predominant pathogen, suggesting possible regional or temporal variations in infection patterns.[7,9,10]

The present study highlights the predominance of Gram-negative organisms, particularly Pseudomonas aeruginosa and E. coli, in diabetic foot infections, in contrast to previous studies such as that by Taki et al., which reported a higher prevalence of Gram-positive bacteria like Staphylococcus spp. This variation may reflect regional microbial patterns and underscores the need for localized microbiological surveillance. The study also reinforces the association between increasing wound severity and the shift from Gram-positive to mixed or predominantly Gram-negative infections, aligning with existing literature. A notable gap in previous research has been the limited focus on antimicrobial sensitivity patterns in polymicrobial and Gram-negative dominant infections. The current analysis addresses this by providing detailed sensitivity data, thereby aiding more targeted empirical therapy and contributing valuable region-specific insights to the existing literature.

CONCLUSION

This study underscores the high prevalence of Gram-negative organisms, particularly Pseudomonas aeruginosa, in diabetic foot infections, with notable antimicrobial resistance patterns. Early microbiological evaluation and targeted antibiotic therapy based on local susceptibility data are essential for effective management. Emphasis on patient education, foot care, and the implementation of hospital-based antibiotic policies and stewardship programs is critical to improving outcomes and combating the rise of multidrug-resistant pathogens.

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