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Microbiological Profile of Diabetic Foot Infections in a Tertiary Care Hospital in Navi Mumbai

Dr. Rahila Khan, Dr. Shrikrishna A Joshi*, Dr. Abhay Chowdhary

Department of Microbiology, DY Patil University, School of Medicine, Nerul, Navi Mumbai-400706, India

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***Corresponding author:** Dr. Shrikrishna A Joshi

Abstract **Original Research Article**

Diabetic foot ulcers are most common serious consequences of diabetes. The proper management of diabetic foot infection (DFI) requires a detailed knowledge about the microbial spectrum and their antibiogram. In this study, 123 cases with DFI were studied. Pus swabs and deep tissue/ bone samples were collected. We observed 74.8% & 16.2% cases were monomicrobial and polymicrobial in nature, respectively. Pseudomonas aeruginosa (29.5%) was the most commonly isolated organism followed by *Staphylococcus aureus* (16.6%) and *Escherichia coli* (12.8%). We observed 27.27% strains of Methicillin Resistant Staphylococcus aureus (MRSA) & 100% Extended Spectrum Beta Lactamases (ESBLs) strains of enterobacteriacae. All the gram positive organisms, *Staphylococcus aureus, Enterococcus faecalis* and *Coagulase negative Staphylococcus* were sensitive to vancomycin (100%) and Linezolid (100%). *Pseudomonas aeruginosa* isolates were 100% sensitive to Amikacin and Tobramicin, Piperacillin-Tazobactm and Ciprofloxacin. Klebsiella pneumoniae showed high resistance to Cefepime (87.5%) and Piperacillin-Tazobactm (75%). *Escherichea coli* isolate showed 100% sensitivity towards Gentamicin. Acinetobacter baumanni showed 100% sensitivity for Imipenem and Meropenem.

Keywords: Diabetic Foot Infection, Pseudomonas aeruginosa, MRSA, ESBLs.

INTRODUCTION

Diabetes mellitus (DM) is one of the major public health problems and is an important cause of morbidity and mortality worldwide. One of the serious complications of diabetes is the development of foot ulcers. Diabetic foot ulcers (DFUs) are the most common cause of diabetes-related hospital admissions [1]. DFU can lead to infections, gangrene, amputation, and even death if necessary care is not provided [2]. A diabetic foot infection is defined as the presence of an inflammatory response and tissue injury due to interaction between the host and multiplying bacteria [3]. The clinical spectrum of the disease varies from simple, superficial cellulitis to chronic osteomyelitis [4].

The most common pathogens in DFUs with acute infections, which have been untreated, are gram-positive bacteria, particularly, *Staphylococcus aureus* and *Streptococci* (Group A, B and others) [6]. Infections in patients who have recently received antibiotics or who have deep limb threatening infection or chronic wounds are polymicrobial in nature involving gram-negative and obligate anaerobic organisms [2, 5].

However, the spectrum of microorganisms depends on various factors like microbial flora of the lower limb, metabolic factors, foot hygiene and the use of antibiotics [6]. The proper management of these infections requires an appropriate antibiotic selection, based on the culture and the antimicrobial susceptibility results [7].

Hence, the present study was carried out to have a better understanding towards bacteriological profile of pathogenic bacteria in DFI and to study the antibiotic susceptibility pattern of the isolates for improving the practices for judicious use of antibiotics.

MATERIAL AND METHODS

The present study was carried out in a tertiary care hospital in Navi Mumbai over a period of one year (October 2017-September 2018).

A total number of 123 patients with clinically diagnosed DFIs were included in the study. The clinical specimens included were purulent draining pus, deep soft tissue or bone. Deep tissue samples were preferred over superficial swabs. All the specimens were collected at the time of admission, before starting the antibiotic therapy.

The samples were processed as per the standard protocol for isolation and identification of aerobic bacteria. The antibiotic susceptibility testing was carried out for Ampicillin (10 µg), Piperacillin-Tazobactam (100/10µg), Ceftriaxone (30µg), Ceftazidime (30µg), Cefotaxime (30µg), Cefepime (30µg), Imipenem (10µg), Amikacin (30µg), Gentamicin (10µg), Ciprofloxacin (5µg), Trimethoprim-Sulfamethoxazole (1.25/23.75µg), Aztreonam (30µg), Tobramycin (10µg), Linezolid (30µg), Vancomycin (30µg), Erythromycin (15µg), Penicillin (10 U), Cefoxitin by Kirby-Bauer disc diffusion technique [8].

RESULTS

A total of 123 patients were included in the study. Out of which, 74 were males and 49 were females (1.5:1). Most of the patients (34%) belong to the age group of 51-60 years (Fig 1).

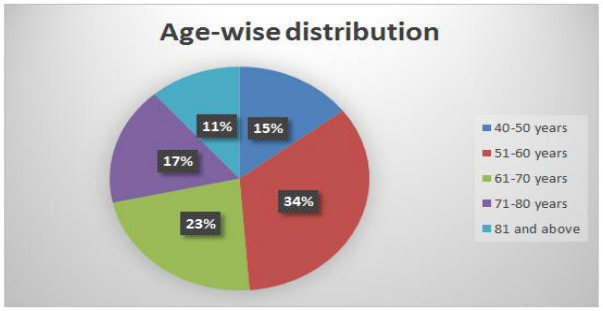

Fig-1: Age-wise distribution of patients with DFI

Out of 123 samples, a total of 52 pus swabs and 71 deep tissue/bone specimens were processed. A total of 132 isolates were obtained from 112 (91.05%) specimens while 11 (8.94%) specimens did not show any growth in culture.

In this study, there were 92 (74.8%) monomicrobial cases while 20 (16.2%) cases were polymicrobial. Among the isolates, gram-negative bacilli were 94 (71.21%) while 38 (28.78%) were gram-positive cocci. *Pseudomonas aeruginosa* (29.5%) was the most predominant isolate followed by *Staphylococcus aureus* (16.6%) and *Escherichia coli* (12.8%) as shown in Table 1.

Table-1: Spectrum of isolates

Organism	**n (%)**
Pseudomonas aeruginosa	39 (29.5)
Escherichia coli	17(12.8)
Klebsiella pneumoniae	16 (12.12)
Proteus spp.	10 (7.5)
Acinetobacter baumanni	10 (7.5)
Citrobacter spp.	2 (1.5)
Staphylococcus aureus	22 (16.6)
Enterococcus faecalis	12 (9.09)
Coagulase negative Staphylococcus	4 (3.03)

Out of 22 isolates *of Staphylococcus aureus*, 6 (27.27%) were resistant to Methicillin (MRSA). All the gram positive organisms, *Staphylococcus aureus, Enterococcus faecalis* and *Coagulase negative Staphylococcus* were sensitive to vancomycin (100%) and Linezolid (100%) (Table 2).

Table-2: Antibiotic susceptibility Pattern of Gram Positive isolates

Antibiotic	***Staphylococcus aureus* n=22**		**Coagulase Negative Staphylococci n=4**		**Enterococcus Faecalis n=12**	
	No.	**%**	**No.**	**%**	**No.**	**%**
Penicillin	0	0	0	0	0	0
Gentamicin	12	54.54	1	25	0	0
Cefoxitin	16	72.7	0	0	-	-
Vancomycin	22	100	4	100	12	100
Linezolid	22	100	4	100	12	100
Cotrimoxazole	19	86.36	2	50	0	0
Erythromycin	4	18.18	0	0	0	0
Ciprofloxacin	19	86.36	2	50	5	41.66

Pseudomonas aeruginosa isolates were 100% sensitive to Amikacin and Tobramicin, Piperacillin-Tazobactm and Ciprofloxacin while 33% were resistant to Imipenem and Meropenem. Only 33% of the *Pseudomonas aeruginosa* isolates were sensitive to Cefepime and Ceftazidime while they were 100% resistant to Aztreonam.

Among the *Enterobacteriaceaee*, all the strains of *Proteus spp.* and *Citrobacter spp.* were sensitive to Imipenem (100%), Meropenem (100%) and Piperacillin-Tazobactm (100%). We found 90% of the *Proteus* strains to be sensitive for Amikacin and Gentamicin whereas both the strains of *Citrobacter spp.* were sensitive to these two antibiotics.

Out of 16 isolates of *Klebsiella pneumonia*e, 50 % were sensitive to Imipenem, Meropenem, Amikacin and Gentamicin. It showed high resistance to Cefepime (87.5%) and Piperacillin-Tazobactm (75%).

Most of the *Escherichea coli* isolate showed sensitivity towards Gentamicin (100%) while sensitivity was low for Imipenem (47%) and Meropenem (47%), Ciprofloxacin (35.2%) and Cefepime (23.5%).

All the *Enterobacteriaceaee* isolates were extended-spectrum beta-lactamase (ESBL) producers. Acinetobacter baumanni showed 100% sensitivity for Imipenem and Meropenem. Out of 10 isolates, 40% were sensitive to Ciprofloxacin while all the isolates were resistant to Amikacin, Gentamicin, Piperacillin-Tazobactm and Cefotaxime (Table 3).

Table-3: Antibiotic susceptibility Pattern of Gram Negative isolates

Antibiotic	*Pseudomonas aeruginosa* n=39		Escherichia coli n=17		Klebsiella pneumoniae n=16		Proteus spp. n=10		Citrobacter spp. n=2		Acinetobacter baumanni n=10	
	No.	%	No.	%	No.	%	No.	%	No.	%	No.	%
Ampicillin	-	-	0	0	0	0	0	0	0	0	0	0
Amikacin	39	100	0	0	8	50	9	90	2	100	0	0
Gentamicin	-	-	17	100	8	50	9	90	2	100	0	0
Tobramicin	39	100	-	-	-	-	-	-	-	-	-	-
Imipenem	26	67	8	47	8	50	10	100	2	100	10	100
Meropenem	26	67	8	47	8	50	10	100	2	100	10	100
Ceftazidime	12	33	-	-	-	-	-	-	-	-	-	-
Cefotaxime	-	-	0	0	0	0	0		0	0	0	0
Ceftriaxone	-	-	0	0	0	0	0		0	0	0	0
Cefipime	12	33	4	23.5	2	12.5	1	10	0	0	0	0
Ciprofloxacin	39	100	6	35.2	11	75	8	80	1	50	4	40
Aztreonam	0	0	-	-	-	-	-	-	-	-	-	-
Piperacilln-Tazobactam	39	100	10	58.8	4	25	10	100	2	100	0	0

DISCUSSION

Foot infection is the most common and feared consequence of diabetes. It accelerates with devastating consequences if appropriate treatment is not given timely.

Several studies have reported a high prevalence rate of polymicrobial infections (55.7% 66%, 75%) than monomicrobial infections [11-13].

In this study, we reported 74.8% monomicrobial and 16.2% polymicrobial cases. Bansal *et al*. (65%) and Jain and Burman (64%) also reported a preponderance of monomicrobial infections in their study [6, 7]. Similarly, Otta *et al.* and Konar and Das found 62.2% and 87% monomicrobial infections, respectively in their study [9, 10].

The reason for high prevalence of monomicrobial cultures could be attributed to the use of aerobic culture media in our study. This must be the reason for failure to isolate anaerobic and fungal pathogens.

We observed a predominance of Gram-negative organisms (71.21%) as compared to Gram-positive organisms (38.78%). This is in accordance with the various studies conducted world-wide.

In a study by Konar and Das, 72.36% of the isolates were gram-negative. [10] Amaefule *et al*. reported 60% of the isolates to be gram-negative in their study. [14] Similarly, gram-negative organisms were predominant in studies by Shanmugam *et al.* (65.1%), Jain and Burban (59%), Sasidharan *et al*. (58.5 %) and Bansal *et al*. (76%) [15, 7, 11, 6] However, some studies reported a high prevalence of Gram-positive organisms.

Tae Son *et al*. reported 57.5% of the isolates to be gram-positives in their study [16]. Similarly, Arias *et al*. And Citron *et al*. showed 63% and 80.3% gram-positive isolates in their study, respectively [17, 18].

In our study, *Pseudomonas aeruginosa* (29.5%) was the most commonly isolated organism followed by *Staphylococcus aureus* (16.6%), *Escherichia coli* (12.8%), and *Klebsiella pneumoniae* (12.12%).

Bansal *et al*. also reported the similar findings in their study. They observed *Pseudomonas aeruginosa* (21.67%) to be predominant followed by *Staphylococcus aureus* (18.88%), *Escherichia coli* (18.18%) and *Klebsiella pneumoniae* (16.78%). [6] However, Otta *et al*. and Saltoglu *et al*. reported *Staphylococcus aureus* (30%, 20%) to be the predominant isolate followed by *Pseudomonas aeruginosa* (11.7%, 19%) and *Escherichia coli* (10%, 12%) [9, 19]

In contrast, Konar and Das reported *Pseudomonas aeruginosa* (31.34%) as the most commonly isolated organism followed by *Escherichia coli* (23.8%) and *Staphylococcus aureus* (22.4%) [10]. This is similar to the findings by Shanmugam *et al*. who reported *Pseudomonas spp* (16%) followed by *Escherichia coli* (14.6%) [15]. we reported 27.27% MRSA isolates in our study. However, a vast variation is observed by various other studies as compared to our findings.

In accordance to our study, Konar & Das, Saseedharan *et al*. and Saltoglu *et al*. reported 36.84%, 23.7% & 31% MRSA isolates, respectively [10, 11, 19]. However, Bansal *et al.* and Otta *et al*. observed 55.56% and 77.8 %MRSA isolates in their study which is high in comparison to our study [6, 9].

Among *Enterobacteriaceaee*, we found 100% ESBL producing strains which is in contrast with other studies. Otta *et al*. Konar & Das, Shanmugam *et al*. and Saltoglu *et al*. isolated 42.1%, 46%, 37.5%, 38% ESBL producers, respectively [9, 10, 15, 19].

CONCLUSION

Early diagnosis and appropriate treatment are the keys to check DFI. In most of the cases, the severity of wound and local antimicrobial susceptibility pattern are considered to be the basis of empiric treatment. There is an alarming rise in multidrug resistant organisms associated with these ulcers which hinders the prognosis. Hence, we suggest the implementation of proper institutional antimicrobial guidelines to reduce the inappropriate and misuse of antibiotics. Additionally, it is also important to study the prevalence of anaerobes in DFI cases. Proper care must be provided and knowledge of antimicrobial susceptibility pattern is essential for institution of appropriate antibiotic therapy.

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