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

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Abstract

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 antibiotic. 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 enterobacteriaceae. 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 pneunoniae 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).

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).

| Antibiotic   | Staphylococcus aureus n=22 | Coagulase Negative Staphylococci n=4 | Enterococcus Faecalis n=12 |
|--------------|----------------------------|--------------------------------------|---------------------------|
| Penicillin   | 0                          | 0                                    | 0                         |
| Gentamicin   | 12                         | 54.54                                | 0                         |
| Cefoxitin    | 16                         | 72.7                                 | 0                         |
| Vancomycin   | 22                         | 100                                  | 0                         |
| Linezolid    | 22                         | 100                                  | 0                         |
| Cotrimoxazole| 19                         | 86.36                                | 2                         |
| Erythromycin | 4                          | 18.18                                | 0                         |
| Ciprofloxacin| 19                         | 86.36                                | 2                         |

*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 *Enterobacteriaceae*, all the strains of *Proteus* spp. and *Citrobacter* spp. were sensitive to Imipenem (100%), Meropenem (100%) and Piperacillin-Tazobactam (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 pneumoniae*, 50% were sensitive to Imipenem, Meropenem, Aztreonam and Gentamicin. It showed high resistance to Cefepime (87.5%) and Piperacillin-Tazobactam (75%).

Most of the *Escherichia 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 *Enterobacteriaceae* isolates were extended-spectrum beta-lactamase (ESBL) producers. Acinetobacter baumannii 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-Tazobactam and Ceftaxime (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 baumannii n=10* |
|-----------------------|-------------------------------|------------------------|-----------------------------|---------------------|------------------------|-------------------------------|
| No. %                 | No. %                         | No. %                  | No. %                       | No. %               | No. %                  | No. %                         |
| Amoxicillin           | - -                           | 0 0 0                  | 0 0                         | 0 0                 | 0 0                    | 0 0                           |
| Amikacin              | 39 100                        | 0 0 8                  | 50 9                       | 90 2 100            | 0 0 0                  | 10 100                        |
| Gentamicin            | - - 17 100                    | 8 50                   | 90 2 100                    | 0 0 0               | 0 0 0                  | 0 100                         |
| Tobramycin            | 39 100                        | - - -                  | - -                        | - -                 | - -                    | - -                           |
| Imipenem              | 26 67 8 47                    | 8 50                   | 10 100                     | 2 100 100           | 10 100                 | 10 100                        |
| Meropenem             | 26 67 8 47                    | 8 50                   | 10 100 2 100               | 10 100              | 10 100                 | - -                           |
| Ceftazidime           | 12 33 -                       | - - -                  | - -                        | - -                 | - -                    | - -                           |
| Cefotaxime            | - - 0 0 0                     | 0 0 0                  | 0 0                        | 0 0 0               | 0 0 0                  | 0 0                            |
| Ceftriaxone           | - -                           | 0 0 0                  | 0 0                        | 0 0 0               | 0 0 0                  | 0 0                            |
| Cefepine              | 12 33 4                       | 23.5 12.5              | 1 10                       | 0 0 0               | 0 0 0                  | 0 0                            |
| Ciprofloxacin         | 39 100 6                      | 35.2 11 75             | 8 80                       | 1 50 4              | 0 0 0                  | 0 0                            |
| Aztreonam             | 0 0                           | - - -                  | - -                        | - -                 | - -                    | - -                           |
| Piperacillin-Tazobactam | 39 100 10 58.8              | 4 25 10 100            | 2 100                      | 0 0 0               | 0 0 0                  | 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 Burman (59%), Sasidharan *et al.* (58.5%) and Bansal *et al.* (76%) [15, 7, 11, 6] However, some studies reported a high prevalence of Gram-positiveorganisms.

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* (12.1%).
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 Shannugam 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 *Enterobacteriaceae*, we found 100% ESBL producing strains which is in contrast to other studies. Otta et al., Konar & Das, Shannugam 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.

**REFERENCES**

1. Jneid J, Lavigne JP, La Scola B, Cassir N. The diabetic foot microbiota: a review. Human Microbiome Journal. 2017 Dec 1;5:1-6.
2. Swati V. Patil and Roshan R. Mane. Bacterial and clinical profile of diabetic foot ulcer using optimal culture techniques. Int J Res Med Sci. 2017; 5(2): 496-502.
3. Williams DT, Hilton JR, Harding KG. Diagnosing foot infection in diabetes. Clinical Infectious Diseases. 2004 Aug 1;39(Supplement_2):S83-6.
4. Ashok Damir. Diabetic foot Infections. JIMSA. Oct-Dec. 2011; 24(4): 207-212.
5. Mazen S. Bader. Diabetic foot Infection. Am FAM Physician. 2008; 78(1): 71-79.
6. Ekta Bansal, Ashish Garg, Sanjeev Bhatia, A. K. Attri, Jagdish Chander. Spectrum of microbial flora in diabetic foot ulcers. Indian J Pathol Micr. 2008; 51(2):204-208.
7. Sudhir K. Jain, Rashmisnala Barman, Bacteriological profile of diabetic foot ulcer with special reference to drug-resistant strains in a tertiary care centre in North-East India. Indian J Endocrin Metab. 2017; (5): 688-694.
8. Wayne PA. Clinical and Laboratory Standards Institute (CLSI). Performance standards for antimicrobial susceptibility testing. 27th edition. CLSI supplement M100. Clinical and Laboratory Standards Institute; 2017.
9. Sarita Otta, Nagen Kumar Debata, Bichitrananda Swain. Bacteriological profile of Diabetic foot ulcers. CHRISMED J Health Res2019; 6(1): 7-11.
10. Jayashree Konar, Sanjeev Das. Bacteriological profile of Diabetic foot ulcers, with a special reference to antibiotic in a tertiary care hospital in eastern India. J Evol Med Dent Sci. 2013; 2(48): 9323-9328.
11. Sanjith Sasedharan, Manisha Sahu, Roonam Chaddha, Edwin Pathrose, Arun Bal, Pallavi Bhalekar, Pradharshi Sekar, Padma Krishnan. Epidemiology of diabetic foot infections in India. Braz J Microbiol. 2018; 49: 401-406.
12. Ramakant P, Verma AK, Mishra R, Prasad KN, Chand G, Mishra A, Agarwal A, Mishra SK. Changing microbiological profile of pathogenic bacteria in diabetic foot infections: time to rethink on which empirical therapy to choose? Diabetologia. 2011; 54:58-64.
13. Khalifa Al Benwan, Ahmed Al Mulla, Vincent O. Rotimi. A study of the microbiology of diabetic foot infections in a teaching hospital in Kuwait. J Infect Public Heal. 2012; 5: 1-8.
14. Kenneth Ezenwa Amaefule, Ismail Lawal Dahiru, Innocent Onoja Okpe, S. Aliyu, A. A. Aruna. Sahel Med. J. 2019; 22(1): 28-32.
15. Priyadarshini Shannugam, Jeya M, Linda Susan S. The bacteriology of diabetic foot ulcers, with a special reference to multidrug resistant strains. J Clin Diagn Res. 2013; 7(3):441-445.
16. Seung Tae Son, Seung-Kyu Han, Tae Yul Lee, Sik Namgoong, Eun-Sang Dhong. The microbiology of diabetic foot infections in Korea. J Wound Management Res. 2017; 13(1): 8-12.
17. Mauclo Arias, Sittiga Hassan-Reshat, William Newsholme. Retrospective analysis of diabetic foot osteomyelitis management and outcome at a tertiary care hospital in the UK. PLoS One. 2019; 14(5): 1-16.
18. Diane M. Citron, Ellie JC. Goldstein, Vreni Merriam C, Benjamin A. Lipsky, Murray A. Abramson. Bacteriology of Moderate-to-Severe Diabetic Foot Infections and In Vitro Activity of Antimicrobial Agents. J. Clin. Microbiol. 2007; 46(9): 2819-2828.

19. Nese Saltoglua, Onder Ergonul, Necla Tulek, Mucahit Yemisen, Ayten Kadanali, Gul Karagoz, Ayse Batirel, Oznur Ak, Cagla Sonmezer, Haluk Eraksoy, Atahan Cagatay, Serkan Surme, Salih A. Nemli, Tuna Demirdal, Omer Coskun, Derya Ozturk, Nurgul Ceron, Filiz Pehlivanoglu, Gonul Sengoz, Turan Aslan, Yasemin Akkoynunlu, Oral Oncul, Hakan Ay, Lutfiye Mulazmoglu, Buket Erturk, Fatma Yilmaz, Gulsen Yoruk, Nuray Uzun, Funda Simsek, Taner Yildirmak, Kadriye Kart Yasar, Meral Sonmezoglu, Yasar Kucukardali, Nazan Tuna, Oguz Karabay, Nail Oztunec, Fatma Sargun. Influence of multidrug resistant organisms on the outcome of diabetic foot infection. J. Infect. Dis. 2018; 70: 10-14.