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The Titbits of Multi-drug Resistant Organisms Reigning in the Diabetic Foot Ulcers: Regional Epidemiology From a Tertiary Care Hospital of Eastern India

Purba Mukherjee[a,*], Kajari Mandal[b], Atindra Kumar[a]

[a] *Department of Microbiology, Calcutta National Medical College and Hospital, Kolkata, The West Bengal University of Health Sciences, West Bengal, India*

[b] *Department of Pathology, Calcutta National Medical College and Hospital, Kolkata, The West Bengal University of Health Sciences, West Bengal, India*

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ABSTRACT

Background and aim: One of the worst complications of diabetes mellitus is diabetic foot infections (DFI). A varied presentation is reported for both the causative bacterial species and their drug resistance patterns. We intended to evaluate the prevalence of drug-resistant strains among aerobic bacterial profile of DFI -as there was no regional data available to implement a rational antibiotic therapy for better management.

Materials and methods: This cross-sectional observational study included 102 DFI cases attending this hospital with Wagner grade-1 or above ulcers. Wound swabs were taken from the base of the ulcers after a thorough cleaning. They were inoculated in blood agar, and MacConkey agar and drug sensitivity were performed Kirby Bauer disc diffusion method following the guidelines by the Clinical and Laboratory Standards Institute (CLSI) antimicrobial susceptibility testing standards.

Results: Altogether, 135 bacterial isolates were reported with an average of 1.32 bacteria per ulcer with Gram-negative bacilli in 63.7% and Gram-positive cocci in 36.3% cases. However, when individual isolates were considered, Staphylococcus aureus was the commonest species, followed by Klebsiella pneumoniae, Escherichia coli, Acinetobacter baumannii complex, and Pseudomonas aeruginosa. Drug resistance was rampant, with 69.1% multi-drug resistant organisms (MDRO) among them. Methicillin-resistant Staphylococcus aureus (MRSA) was 81.3%, MRCONS 66.7%, and extended-spectrum β-lactamase (ESBL)- producer Gram-negative Bacteria (GNB) 47.3%.

Conclusion: In this scenario, Vancomycin and linezolid were the only effective drugs against GPC. Piperacillin-tazobactam and imipenem were effective for GNB in general except ESBL or Metallo-beta-lactamase (MBL) producing Acinetobacter and Pseudomonas species, which showed a dangerous inclination for treatment failure.

1. Introduction

Diabetes Mellitus is one of the biggest health burdens of recent time. According to The In-ternational Diabetes Federation, the number of persons with diabetes will increase from 240 million in 2007 to 380 million in 2025.[1] Diabetic foot infection (DFI) is one of the com-monest long term complications of diabetes. Predisposing factors like impaired microvascu-lar circulation, anatomical alterations, neuropathy, and impaired immunity are collectively responsible for the development of diabetic foot ulcers.[2] The cumulative lifetime incidence rate of a diabetic foot ulcer is around 25%, with a rate of infection as high as 40-80%, rapidly spreading to cause vast tissue destruction and subsequent amputation.[3, 4] In fact, it is the most important cause of non-traumatic amputation of lower limbs contributing signifi-cantly to prolonged hospitalisation, disability, and a huge direct burden of medical cost per annum.[5, 6] Previous studies have shown vast variation in the bacteriological profile compris-ing of both aerobic and anaerobic bacteria in varied proportions often contradictory to each other.[6-8] According to some authors, the role of anaerobes was unclear or less important, particularly due to improper specimen collection and culture techniques.[7, 9-10] Commonly prescribed empirical antibiotics are often ineffective, requiring a specific antibiotic therapy for better outcome.[7] In our institution, we observed anaerobic bacteria being outnumbered by their aerobic counterparts in DFI cases having a predictable susceptibility of anaerobes to metronidazole.

In contrast, the aerobic bacteria demonstrated a significant level of drug resistance. We decided to evaluate the cases of established diabetic foot

* *Corresponding author. Purba Mukherjee*
E-mail address: purbamukherjee.nrs@gmail.com
Department of Microbiology, Calcutta National Medical College and Hospital, Kolkata, The West Bengal University of Health Sciences, West Bengal, India
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infections for their aerobic bacterial flora and antibiogram pattern, emphasizing multi-drug resistant organisms (MDRO) to up-grade the existing regional data. We also wanted to throw some light on effective and specif-ic antibiotic therapy guidelines applicable to MDRO isolates.

2. Materials and methods

This cross-sectional hospital-based observational study was expanded over one year in a tertiary care teaching hospital in West Bengal. One hundred two diabetic patients attending the hospital with infected diabetic foot ulcers of Wagner's Grade-1 or above were included in this study. After thoroughly cleaning the ulcers with sterile normal saline followed by debridement of the necrotic tissues, wound swabs were taken from the ulcers' base. The specimens were transported immediately to the Bacteriology lab and were processed and analysed to evaluate the aerobic bacterial profile. The specimens were inoculated in blood agar and MacConkey agar media and incubated for 18-24 hours under the aerobic condition at 37°C. Blood agar plates were incubated in the presence of 5-10% CO2. After overnight incubation, the bacterial growths were observed, and pure growths of organisms were obtained by individual subcultures from mixed bacterial growths. The species identification was done by standard phenotypic methods. The antibiogram of the isolated strains was done by Kirby-Bauer disc diffusion method, and sensitivity were interpreted following the latest CLSI guideline.[11]

The following antibiotic discs were employed: cefoxitin (30 µg/mL), erythromycin (15 µg/mL), clindamycin (10 µg/mL), co-trimoxazole (25 µg/mL), doxycycline (30 µg/mL), vancomycin (30 µg/mL), linezolid (30 µg/mL), amikacin (30 µg/mL), gentamicin (10 µg/mL), gentamicin (120 µg/mL for Enterococcus Spp.), ciprofloxacin (5 µg/mL), levofloxacin (5 µg/mL), amoxicillin –clavulanic acid (30 µg/mL), ceftriaxone (30 µg/mL), cefuroxime (30 µg/mL), cefotaxime (30 µg/mL), ceftazidime (30 µg/mL), azithromycin (15 µg/mL), ticarcillin-clavulanic acid (110 µg/mL) piperacillin- tazobactam (110 µg/mL), and imipenem (10 µg/mL).

3. Results

Among the 102 patients, 67 were males, and 35 were females (male: female ratio of 1.9: 1). The mean age was 48.8, with the range from 20 to 83 years. The bulk of patients was from the age group of 41-60 years. (Fig.1).

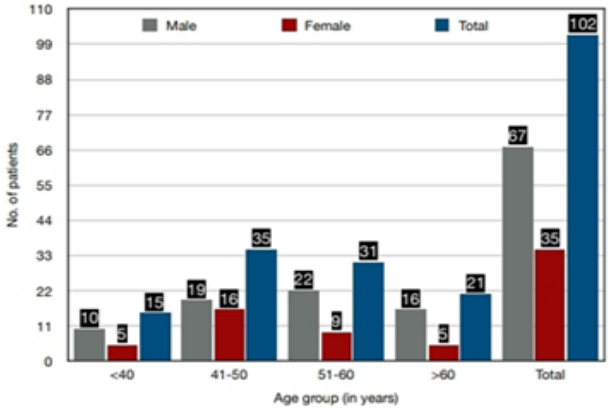

Fig 1. Age and gender wise distribution of the patients (n=102).

From 102 patients, 135 bacterial isolates were obtained. Monomicrobial bacteriological profiles were observed in 70 cases and polymicrobial in 32 cases. The bacteriological profile consisted of 86 isolates of Gram-negative bacilli and 49 isolates of Gram-positive cocci. The commonest species was Staphylococcus aureus (SA), with 32 isolates. The other bacterial species were Klebsiella pneumoniae (27), Escherichia coli (16), Pseudomonas aeruginosa (15), Acinetobacter baumannii complex (14), coagulase-negative Staphylococcus species/ CONS (12), Klebsiella oxytoca (6), Enterococcus species (5), Proteus mirabilis (5), Proteus vulgaris (2) and Citrobacter species (one case). (Fig.2).

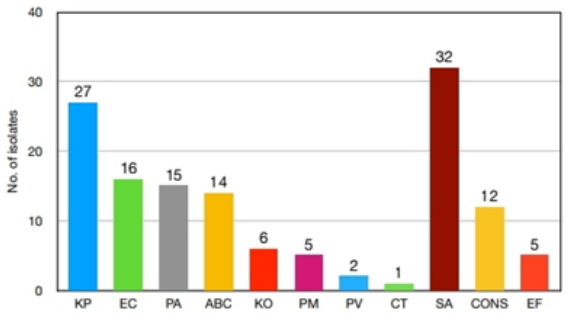

Fig. 2. Bacteriological profile of diabetic foot infection (n=135).

***Abbreviations for the name of bacterial species: KP-Klebsiella pneumoniae, EC-Escherichia coil, PA-Pseudomonas aeruginosa, ABC-Acinetobacter baumannii complex, KO-Klebsiella oxytoca, PM-Proteus mirabilis, PV-Proteus vulgaris, CT-Citrobacter species, SA-Staphylococcus aureus, CONS-Coagulase negative Staphylococcus species, EF-Enterococcus faecalis.**

Antibiotic resistance was significant. More than 90% of SA isolates were resistant to beta-lactam antibiotics. Methicillin resistance was shown by 26 (i.e., 81.3%) of Staphylococcus aureus and eight (i.e., 66.7%) of CONS isolates. 14 SA and five CONS isolates showed inducible clindamycin resistance. Nine out of 26 (34.6%) of the MRSA isolates were extended drug-resistant (XDR), showing simultaneous resistance to fluoroquinolone, cotrimoxazole, doxycycline, and gentamicin. Enterococcus species were intrinsically resistant to many common antibiotics and showed further resistance to doxycycline and high-level gentamicin (HLG) in 40% and 60% cases, respectively. However, all the gram-positive isolates showed uniform susceptibility to vancomycin and linezolid. (Table 1).

Table 1. Antibiotic resistance pattern of gram-positive isolates with percentage paradigm in paren-theses (n= 49).

Antibiotics	SA [32 isolates]	CONS [12 isolates]	*Enterococcus sp.* [5 isolates]
Cefoxitin screen positive	26 (81.3)	8 (66.7)	-----
Amoxyclav	31 (96.8)	8 (66.7)	5 (100)
Ceftriaxone	29 (90.6)	8 (66.7)	-----
Cefotaxime	26 (81.3)	8 (66.7)	-----
Cefuroxime	29(90.6)	8 (66.7)	-----
Gentamicin	15 (46.9)	6 (50)	3 (60) *
Doxycycline	17 (53.1)	6 (50)	2(40)

Erythromycin	18 (56.3)	7 (58.3)	3 (60)
Clindamycin	15 (46.9)	5 (41.7)	-----
Inducible Clindamycin resistance	14 (43.8)	5 (41.7)	-----
Levofloxacin	21 (65.6)	5 (41.7)	3 (60)
Ciprofloxacin	24 (75)	9 (75)	3 (60)
Vancomycin	0 (0)	0 (0)	0 (0)
Linezolid	0 (0)	0 (0)	0 (0)
Cotrimoxazole	21 (65.6)	6 (50)	-----

Abbreviations: SA- Staphylococcus aureus, CONS- coagulase-negative Staphylococcus species.
***- high-level gentamicin (120 mic) for Enterococcus species.**

All the Gram-negative Enterobacteriaceae showed beta-lactam-resistance, including cephoperazone-sulbactam and ticarcillin-clavulanic acid 66.7% to 100% cases. Piperacillin tazobactam was effective against Klebsiella oxytoca, Proteus vulgaris, and Citrobacter species but most of no help against the other ones. Among the 57 Enterobacteriaceae, 27 were extended-spectrum beta lactamase (ESBL) producers, 19 were XDR, and eight were pan-drug-resistant (PDR). Imipenem resistance was at least 25% or more, with Klebsiella pneu-moniae showing 51.8% imipenem resistant strains. (Table. 2).

Table 2. Antibiotic resistance pattern of gram-negative isolates with percentage paradigm in parentheses (n= 86).

Antibiotics	KP[27]	KO[6]	EC[16]	PM[5]	PV[2]	CT[1]	PA[15]	ABC[14]
AMC	27 (100)	6 (100)	15 (93.8)	5 (100)	2 (100)	1 (100)	15 (100)	14(100)
CTR	26 (96.3)	6 (100)	14 (87.5)	5 (100)	2 (100)	1 (100)	15 (100)	14(100)
CTX	26 (96.3)	6 (100)	14 (87.5)	5 (100)	2 (100)	1 (100)	15 (100)	14(100)
CAZ	26 (96.3)	6 (100)	14 (87.5)	5 (100)	2 (100)	1 (100)	10 (66.7)	12 (85.7)
CPM	26 (96.3)	6 (100)	14 (87.5)	5 (100)	2 (100)	1 (100)	8 (53.3)	-----
CFS	25 (92.5)	6 (100)	13 (81.3)	4 (80)	2 (100)	1 (100)	10 (66.7)	14(100)
TIC	21 (77.8)	4 (66.7)	11 (68.8)	4 (80)	2 (100)	0(0)	10 (66.7)	14(100)
PIT	19 (70.4)	0 (0)	9 (56.3)	5 (100)	0 (0)	0(0)	5 (33.3)	11 (78.6)

IMP	14 (51.8)	2 (33.3)	4 (25)	0 (0)	0 (0)	0(0)	11 (73.3)	10 (71.3)
AK	24 (88.9)	3 (50)	9 (56.3)	3 (60)	2 (100)	0(0)	9 (60)	12 (85.7)
GM	24 (88.9)	3 (50)	11 (68.8)	3 (60)	2 (100)	0(0)	9 (60)	12 (85.7)
CIP	23 (85.1)	4 (66.7)	14 (87.5)	3 (60)	2 (100)	0(0)	10 (66.7)	13 (92.9)
LE	22 (81.4)	2 (33.3)	9 (56.3)	3 (60)	2 (100)	0(0)	5 (33.3)	12 (85.7)
DO	20 (74.1)	2 (33.3)	10 (62.5)	3 (60)	0 (0)	1 (100)	12 (80)	12 (85.7)
AZM	19 (70.4)	6 (100)	11 (68.8)	5 (100)	2 (100)	1 (100)	10 (66.7)	13 (92.9)
COT	20 (74.1)	3 (50)	12 (75)	-----	-----	0(0)	-----	12 (85.7)

Abbreviations: AMC- amoxycillin-clavulanic acid, CTR- ceftriaxone, CTX- cefotaxime, CAZ- ceftazidime, CPM-cefepime, CFS- cefoperazone-sulbactam, TIC-ticarcillin- clavulanic acid, PIT-piperacillin tazobactam, IMP- imipenem, AK- amikacin, GM-gentamicin, CIP- ciprofloxacin, LE-levofloxacin, DO-doxycycline, AZM- azithromycin, COT- cotrimoxazole. KP- Klebsiella pneumoniae, KO- Klebsiella oxytoca, EC- Escherichia coli, PM- Proteus mirabilis, PV- Proteus vulgaris, CT- Citrobacter species, PA- Pseudomonas Aeruginosa, ABC- Acinetobacter baumannii complex. (-) - Not applicable.

Non-fermenters like Pseudomonas aeruginosa and Acinetobacter baumannii complex showed complete resistance against Amoxycillin-clavulanic acid and ceftriax-one/cefotaxime. Pseudomonas strains showed resistance to piperacillin-tazobactam and levofloxacin in 33.3% and ceftazidime cefoperazone-sulbactam and ticarcillin-clavulanic acid in 66.7% cases. MDR Pseudomonas were six in number with four XDR and two PDR strains. Acinetobacter species showed a minimum of 85% resistance against any of the available an-tibiotics except imipenem. Naturally, 78.6% (11 out of 14) of Acinetobacter were MDR, with six XDR among them. Due to carbapenemase production, 71.3% of Acinetobacter were imipenem resistant, rendering five of them as PDR. (Table. 2).

4. Discussion

This study reflected the clinico-bacteriological profile and sensitivity pattern of diabetic foot infections in this particular group of 102 patients. The majority of our patients were from the 41-60 years of age group with a male preponderance of 65.7%; the male: female ratio being 1.9:1 (Fig. 1). Some other studies also pointed out male sex as a significant risk factor for developing non-healing ulcers.[12, 13]

In 68.6% of cases, there were monomicrobial infections present in lower grade ulcers (Grade 1, 2, or 3). Whereas polymicrobial infections, associated with Wagner grade 3 to 5, were present in 31.4% of cases. This finding was in concordance with M Zubair et al., S Otta et al., and NS Raja,[12, 14, 15] but contrary to the majority, who found polymicrobial infections range of 59% to 83.3% of DFI cases.[6, 7, 10, 16] A range of one to eight aerobic bacteria per patient has been reportedly isolated from the infected Diabetic foot ulcers,[7, 16-18] while we found a lower value of 1.32 isolates per ulcer on average.

The current study observed an overall predominance of Gram-negative bacilli in 63.7% cases, contradicting the majority who reported a predominance of Gram-positive cocci;[6, 19, 20] another group of researchers strongly supported.[21-23] The rate of isolation of Staphylococcus aureus (23.7%) was in concordance with that of other studies with a prevalence rate between 24.1 to 42%;[6, 7, 10] contrary to CN Dang.[24] While some study reported Escherichia coli or Pseudomonas aeruginosa as the commonest bacteria,[5,19, 25] we found Klebsiella pneumoniae (20%) as the commonest GNB supporting Jain and Patel (22.29%).[26]

Antibiotic resistance among the isolates was a matter of grave concern. We observed an overall rising trend of resistance patterns. The reported prevalence of MRSA was in the range of 10.6% to 77.8% in various studies.[6, 10, 14, 16, 23] In 2005, MRSA recovery rate was 10.3% in South India.[25] The rate of isolation of MRSA from DFI cases was progressively increasing and over a three-year time-span almost doubled to reach the figure of 30.2% in 2003.[24] We found 81.3% of all S. aureus isolates as MRSA - a frequency alarmingly higher than all the aforementioned studies. The prevalence of MRCONS also increased from around 45% in 2002 to 66.7% in this study.[10] The incidence of inducible clindamycin resistance was consistent with 43.8% and 41.7% among S.aureus and CONS, respectively.[10] The MRSA and MRCONS isolates were already multi-drug resistant (MDR) by virtue of being methicillin-resistant, and 34.6% of all MRSA were extended drug-resistant (XDR), being additionally resistant to fluoroquinolones, aminoglycosides, eryth-romycin, clindamycin, and cotrimoxazole.[11] Enterococcus species, intrinsically resistant to many antibiotics, though showed acquired resistance to levofloxacin and high-level gen-tamicin in 60% cases, had no MDR strains among them. All GPC were uniformly sensitive to vancomycin and linezolid-similar to the findings of Citron et al.[7] According to some authors, gram-positive organisms were associated with mild to moderate forms of the dis-ease. At the same time, there was a significant increase in the GNB population in severe ul-cer forms.[19]

Gram-negative bacilli did not reflect a better picture either. Imipenem, meropenem, and cefepime were so far reported to be most effective against GNB.[19] However, we found a decreased susceptibility to all the drugs, though imipenem still retained its efficacy to some extent against Enterobacteriaceae. The most predominant species producing ESBL were Acinetobacter, Klebsiella, Pseudomonas, and E. coli, similar to Shobha et al.[27] The frequency of ESBL producing Enterobacteriaceae were 47.4%- higher than Akhi et al. (31%), S. Otta et al. (42.1%) and Gadepalli et al. (44.7%).[6, 14, 21] Approximately 50% Enterobacteriaceae were MDR with 33.3% XDR and 14% PDR strains among them. Among the non-fermenters, 51.7% were ESBL producers similar to Akhi et al.[6] Pseudomonas species showed relatively higher sensitivity to pip-Tazo and levofloxacin.[21, 22] MDR strains among Pseudomonas aeruginosa were 40%- quite similar to the finding of Shankar et al.,[25] with four (26.7%) XDR and two (13.3%) PDR strains among them. The number of car-bapenemase producers was highest among Acinetobacter species rendering 71.3% of them resistant to imipenem. Out of 14 isolates, 78.6% were MDR with six (42.9%) XDR and five (35.7%) PDR strains. Our study reinforced the finding that MDR infection in hospitalised patients with diabetic foot ulcers was quite common.[28] Some authors opined that the presence of MDR organisms in the infected ulcer was the only significant independent predictor of glycemic control.[21] In our study population, 59.3% of cases were infected with one or more MDR strains, significantly higher than the previous study.[28]

5. Conclusion

This high rate of presence of MDR organisms in our study reflected that a high degree of usage of broad spectrum antibiotics had benefitted the MDRO with a selective survival advantage. Increased prevalence of MDRO was quite a trouble to select proper antibiotics. As of now, vancomycin and linezolid were of predictable efficacy in gram-positive cocci, and imipenem still retained its efficacy against most of the GNB. Imipenem and linezol-id/vancomycin combination may be started as empirical therapy. However, there should always be an effort to spare the newer or last resort antibiotics like ceftazidime/vaborbactam or colistin for specific indications. There should be further focus to initiate step-down therapy as early as possible. Guided therapy following in vitro drug sensitivity testing report should be made mandatory. Along with this, tight glycemic control, vigorous hand hygiene, and wound care as prophylactic measures should be adopted to prevent the occurrence of wound infection which is not at all an easy task.

Conflict of Interest

The authors declared that there is no conflict of interest.

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