A STUDY OF BACTERIOLOGICAL PROFILE AND ANTIMICROBIAL SPECTRUM OF DIABETIC FOOT ULCER

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ABSTRACT

BACKGROUND

There are various pathophysiological factors, which along with hyperglycaemic state is responsible for diabetic foot ulcer. Out of these, there are three important components, which play important role that is vascular changes, neuropathy and immune changes. Glycosylation of nerve proteins, endothelial dysfunction and increased lymphocyte apoptosis is the major pathology that leads to above dysfunction.

MATERIALS AND METHODS

A total of 60 cases were included in this study. For collection of sample, transport culture and sensitivity, we have followed standard operative procedure, samples collected were plated on blood agar, nutrient agar and MacConkey agar. Conventional method was followed for identification of organism isolated from agar plate like Gram staining, motility testing, oxidase testing and catalase testing.

RESULTS

In our study, out of 60 culture positive patient, we have found that Escherichia coli was 12 in number that is 20%. Klebsiella was found in 18 samples that is 30%. Pseudomonas was isolated in 12 specimen that is 20% and 10% of the wound having staphylococcus aureus infection. Proteus was found in nine specimens. Rest like CONSA, citrobacter and candida was present in one sample each.

CONCLUSION

The most common organism isolated out of 60 culture positive specimen was Klebsiella that is 30% of the isolate followed by Pseudomonas aeruginosa and Escherichia coli that is 20% each. We have come to conclusion that chloramphenicol, piperacillin-tazobactam, amikacin and imipenem adequately covered such infection.

KEYWORDS

Diabetic Foot Ulcer, Insulin, Phenytoin.

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BACKGROUND

There are various pathophysiological factors, which along with hyperglycaemic state is responsible for diabetic foot ulcer. Out of these, there are three important components, which play an important role.Those are vascular changes, neuropathy and immune changes. Glycosylation of nerve proteins, endothelial dysfunction and increased lymphocyte apoptosis are the major pathological factors that lead to above dysfunction.[1] All these pathological factors make diabetic foot ulcer a non-healing and chronic ulcer. Along with that, formation of a biofilm phenotype of ulcer is said to be the major cause of delay in healing.[2] These biofilms are mainly associated with diabetic foot ulcers and are due to two vareities of bacteria namely Pseudomonas aeruginosa and Staphylococcus aureus.[3]

Once a foot develop ulcer, the underlying subcutaneous tissue get colonized with bacteria. Initially it is a local process, but later if not controlled, infection typically spreads to deeper tissues and in the presence of neuropathy, vasculopathy and decreased immune response, poor granulation tissue and poor wound healing ensues along with bad odour. Wound infections in diabetic foot ulcers before admission to hospital is treated empirically, but if the appropriate information about wound becomes available treatment of infection is easy.

Various studies have been done on the bacteriology of diabetic foot ulcer and its anti-microbiological pattern with variying results and different drug sensitivity pattern. Present study has been attempted to evaluate the pattern of microbial agents present and the antimicrobial sensitivity pattern.

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MATERIALS AND METHODS

The present study was designed with a purpose to determine the bacteriology of diabetic foot ulcer and its anti-microbiological sensitivity pattern. Data was collated form the retrospective analysis of diabetic foot ulcer samples collected between August 2014 to September 2015. Before the start of the study, a written permission was obtained from institutional ethics committees.

A total of 60 cases were included in this study. For collection of sample, transport culture and sensitivity, we have followed a standard operative procedure, samples collected were plated on blood agar, nutrient agar and MacConkey agar. Conventional method was followed for identification of organism isolated from agar plate like Gram staining, motility testing, oxidase testing and catalase testing. The Kirby-Bauer disc diffusion method on Mueller-Hinton agar plates are used for susceptibility testing.[4]

RESULTS

In our study, mean of the patient was 54.68 years, out of 60 patients, 42 were males and 18 were females. 20.6% of the patient were having type-1 and 79.4% of the patients were having type-2 diabetes. Mean duration of diabetes in patients were 6.8 years and mean duration of ulcer was 28 days. Total 68% of the patient has taken treatment before joining in hospital and mean size of the wound was 6.8 cm.[2]

In our study, out of 60 culture-positive patients, we have found that Escherichia coli was 12 in number that is 20%, Klebsiella was found in 18 samples that is 30%, Pseudomonas was isolated in 12 specimens that is 20% and 10% of the wound had Staphylococcus aureus infection. Proteus was found in nine specimens. Rest like CONSA, citrobacter and candida were present in one sample each.

Diabetic Foot Ulcer under Various Stage of Healing

Parameters	Values
Age (mean)	54.68 years
Male	42 (70%)
Female	18 (30%)
Type 1 diabetes	20.6%
Type 2 diabetes	79.4%
Duration of diabetes in (year)(mean)	6.8
Mean duration of ulcer (days)	48
History of treatment before joining	62%
Mean size of wound (cm2)	6.8

Table 1. Characteristic of Study Population

Organism	Number Percentage
E. coli	12.20%
Pseudomonas	12.20%
Klebsiella	18.30%
Staph aureus	6.10%
Proteus	9.15%
CONSA	11.66%
Citrobacter	11.66%
Candid	11.66%

Table 2. Bacteria Isolated from Diabetic Foot Ulcer

CONSA (Coagulase-Negative Staph Aureus)

Antimicrobial Agent	E. coil	Pseudomonas	Klebsiella, sps	Staph aureus	CONSA	Proteus	Citrobacter
Co-trimoxazole	0	0	0	0	0	0	0
Ampicillin/sulbactam	10%	-	20%	50%	100%		
Amoxicillin sulbactam	-	-	-	-	-	-	-
Methicillin	-	-	-	-	-	-	
Ceftriaxone	-	-	-	-	-	-	-
Ceftazidime	10%	-	-	30%	-	-	-
Cefotaxime	20%	-	-	-	-	-	-
Cefixime	-	-	-	-	-	-	-
Ciprofloxacin	30%		-	-	-	-	-
Ofloxacin	40%	%	-	50%	-	30%	-
Levofloxacin	60%	-	-	-	-	30%	-
Chloramphenicol piperacillin	60%	60%	60%	-	-	40%	-
Tazobactam	60%	-	60%	60%	100%	60%	
Amikacin	60%	60%	100%	60%	100%	70%	100%
Imipenem	100%	60%	60%	-	-	100%	-
Linezolid	-	-	-	-	-	-	-
Meropenem	-	-	-	-	-	-	100%
Azithromycin	-	40%	-	50%	-	-	-
Clarithromycin							
Netilmicin	50%	-	-	-	-	-	-

Table 3. Antimicrobial Sensitivity Pattern of Various Organisms Isolated from Diabetic Foot Ulcer

As per Table 3, we have found that regarding E. coli, 10% of the isolate was sensitive to ampicillin/sulbactam and 20% were sensitive to ceftazidime. Sensitivity to ciprofloxacin, ofloxacin and levofloxacin was 30%, 40% and 60%, respectively, 60% of the E. coli isolated were sensitive to chloramphenicol, piperacillin/tazobactam and amikacin each. All the E. coli isolated was sensitive to imipenem and 50% of the E. coli isolated from wound was sensitivity to netilmicin.

Ten per cent of pseudomonas aeruginosa was sensitive to ciprofloxacin, 60% was sensitive to chloramphenicol and 60% was sensitive to amikacin, 60% of sensitive imipenem and 40% to azithromycin.

Klebsiella isolated from culture, 10% of it was sensitive to ampicillin/sulbactam, 60% was sensitive to chloramphenicol and piperacillin plus tazobactam. All organism were sensitive to amikacin, 60% was sensitive to imipenem.

Staph aureus was sensitive to ampicillin/sulbactam (50%), ceftazidime (30%), levofloxacin (50%), piperacillin-tazobactam (60%), amikacin (60%) and azithromycin (60%).

CONSA was sensitive to ampicillin + sulbactam, piperacillin-tazobactam and amikacin. Proteus was sensitive to ofloxacin (30%) levofloxacin + tazobactam (60%), amikacin (70%) and imipenem (100%). Citrobacter was sensitive to amikacin and meropenem.

DISCUSSION

Present study is a retrospective study conducted in the Department of General Surgery, Konaseema Institute of Medical Sciences, Amalapuram. In this study, we have found that various organism was isolated from that wound. The most common organism isolated out of 60 culture positive specimen was Klebsiella that is 30% of the isolate followed by Pseudomonas aeruginosa and Escherichia coli that is 20% each. As per Ramakant et al, most common pathogen was pseudomonas aeruginosa followed by Escherichia coli.[5] In the study of Nadeem et al, common organism was staphylococcus aureus, but Klebsiella was more common than E. coli.[6] But, as per Vaidehi et al, Klebsiella was second common isolate.[7] So, common organism isolated from wound was different in various studies. In our study, proteus was more common than staphylococcus, which is similar to the study of Gangania and Singh et al.[8]

In our study, we have found that Escherichia coli was less sensitive to cephalosporin and around 40% to 60% of the isolates were sensitive to quinolones, 60% of E. coli were sensitive to chloramphenicol, but they very much sensitive to imipenem. Pseudomonas was less sensitive to quinolones, but it was sensitive to aminoglycosides and imipenem, which is similar to the various study.[9] Klebsiella was sensitive to macrolides and aminoglycosides, staphylococcus aureus was sensitive to beta-lactam and macrolides. Proteus was sensitive to quinolones and aminoglycosides, which is similar to the study of Sekhar et al.[10]

CONCLUSION

Klebsiella, Pseudomonas aeruginosa, Escherichia coli, Proteus and Staphylococcus aureus are the common organism found in diabetic foot ulcer. In our study, we have come to conclusion that chloramphenicol, piperacillin-tazobactam, amikacin and imipenem adequately covered such infection.

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