Microbial profile and antibiotic susceptibility pattern of orthopedic infections in a tertiary care hospital: A study from South India

Vasundhara Devi P, Sreenivasulu Reddy P, Shabnum M

Department of Microbiology, Narayana Medical College, Nellore, Andhra Pradesh, India

Correspondence to: Shabnum M, E-mail: shabnummusaddiq@gmail.com

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ABSTRACT

Background: Orthopedic wound infections are one of the most important causes of morbidity and are difficult to treat. Changes in pathogenic microbial flora and the emergence of bacterial resistance are another problem in the management of orthopedic infections. **Objectives:** In this regard, an attempt was made to know the bacteriological profile and their antibiotic susceptibility pattern in our hospital. **Materials and Methods:** This study was conducted in the Department of Microbiology, Narayana Medical College & Hospital, Nellore, over a period of 1-year from June 2015 to May 2016. A total of 100 pus samples were collected and processed during the mentioned period. **Results:** Out of the samples processed, 68 (68%) of specimens showed culture positivity. *Pseudomonas aeruginosa* 18 (26.4%) was the predominant isolate followed by *Staphylococcus aureus* 17 (25%). All Gram-positive cocci were susceptible to vancomycin and linezolid. *Pseudomonas* isolates were susceptible to polymyxin B, piperacillin-tazobactam, and meropenem. **Conclusion:** Microbial analysis and their antibiogram of clinical samples are mandatory since it is deep seated infections with more pathogenic bacteria for optimal management of orthopedic infections.

KEY WORDS: Bacterial isolates; Antibiogram; Orthopedic infection; Wounds; Microbial flora

INTRODUCTION

Orthopedic infections are one of the most common which can occur in approximately 1% of all orthopedic operations.[1] The most common orthopedic infections are surgical site infections (SSI) and implant infections in open or closed wounds.[2,3] Wound is a breach in the skin leading to exposure of subcutaneous tissue caused by trauma, surgeries, burns, diabetic ulcers, etc. It provides a moist, warm and nutrient environment that is conductive to microbial colonization and proliferation that leads to serious bacterial infections and death. Wound infections are one of the most common hospital-acquired infections and are an important cause of morbidity and account for 70-80% mortality.[4]

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SSI as defined by US Centers for Diseases Control in 1992, is an infection occurring within 30-90 days after a surgical operation (or within 1 year if an implant is left in place after procedure) and affecting either incision or deep tissues at the operation site.[5] Orthopedic wound infections are one of the common causes of high morbidity and are difficult to treat. Due to the use of implants for open reduction and internal fixation, which are foreign bodies to the body, orthopedic wounds are at increased risk of microbiological contamination and infection.[6] Bone infection, at sites of relatively poor vascularity, can be difficult to treat, often requiring prolonged courses of antimicrobial therapy in association with surgical drainage or debridement. Delayed or ineffective treatment causes significant morbidity in terms of pain, loss of function and the need for further surgery and antibiotics.[7]

In addition to the irrational use of broad spectrum antibiotics, the changing pattern of microbial etiology and increasing antimicrobial resistance makes orthopedic infections a challenge for both the patient and clinician.

Keeping this in mind, the following study was aimed in finding out the various organisms causing orthopedic wound infections and to identify the antibiotic susceptibility pattern of the isolated organisms.

MATERIALS AND METHODS

This study was conducted in the Department of Microbiology, Narayana Medical College and Hospital, Nellore, from June 2015 to May 2016. Swabs were collected from infected wounds from orthopedic patients with aseptic precautions and immediately transported to the laboratory for culture and antibiotic sensitivity testing.

Swabs were inoculated on blood agar and MacConkey agar. Plates were incubated at 37°C for 24-48 h and examined for the presence of bacteria. All positive cultures were identified by colony morphology, Gram-staining and biochemical reactions.[8] Antimicrobial susceptibility testing was done on Muller-Hinton agar using antibiotic discs from Hi Media.

Table 1: Bacteriological profile of orthopedic infections

Bacterial isolates	*n* (%)
Staphylococcus aureus	17 (25)
CONS	15 (22)
Enterococci	1 (1.5)
Escherichia coli	5 (7.3)
Klebsiella sps.	4 (6)
Citrobacter sps.	5 (7.3)
Proteus sps.	2 (3)
Acinetobacter sps.	1 (1.5)
Pseudomonas sps.	18 (26.4)
Total	68 (100)

For Gram-positive organisms ampicillin, cefoxitin, cefixime, azithromycin, ofloxacin, amikacin, clindamycin, amoxicillin + clavulanic acid, vancomycin, and linezolid were used. For Gram-negative bacilli ampicillin, cefixime, ceftriaxone, cotrimoxazole, ciprofloxacin, ofloxacin, gentamicin, amikacin, amoxicillin-clavulanic acid, cefoperazone-sulbactam, piperacillin - tazobactam, and Imipenem were used.

For *Pseudomonas* spp. cefixime, ceftazidime, co-trimoxazole, ciprofloxacin, gentamicin, amikacin, cefoperazone + sulbactam, piperacillin + tazobactam, meropenem, polymyxin - B, and aztreonam were used. The test results were interpreted as sensitive, intermediate susceptible or resistant according to the Clinical and Laboratory Standards Institute guidelines.[9]

RESULTS

Out of 100 pus samples collected from orthopedic patients 68 (68%) samples yielded growth and 32 (32%) samples had no growth (Table 1).

Among the 68 culture positive, cases 33 (48%) were Gram-positive cocci and 35 (52%) were Gram-negative bacilli. Out of Gram-positive cocci *Staphylococcus aureus* 17 (25%) was the most common organism followed by CONS 15 (22%) and *Enterococci* 1 (1.5%) (Table 1).

Among Gram-negative bacilli *Pseudomonads*, 18 (26.4%) were the most common organisms followed by *Escherichia coli* 5 (7.3%), *Citrobacter* sps. 5 (7.3%), *Klebsiella* sps. 4 (6%), *Proteus* sps. 2 (3%), and *Acinetobacter* sps. 1 (1.5%) (Table 1).

This showed that Gram-positive cocci are the most common causes of orthopedic infections followed by *Pseudomonas*. Among the Gram-positive cocci, all were sensitive to vancomycin and linezolid followed by clindamycin and amikacin (Table 2).

Table 2: Antibiotic susceptibility patterns of Gram-positive cocci

Antibiotic	*Staphylococcus aureus* (17) (%)		CONS (15) (%)		*Enterococci* (1) (%)	
	Sensitive	Resistant	Sensitive	Resistant	Sensitive	Resistant
Ampicillin	5 (30)	12 (70)	10 (67)	5 (33)	1 (100)	0 (0)
Cefoxitin	12 (70)	5 (30)	15 (100)	0 (0)	1 (100)	0 (0)
Cefixime	4 (24)	13 (76)	7 (47)	8 (53)	0 (0)	1 (100)
Azithromycin	9 (53)	8 (47)	9 (60)	6 (40)	0 (0)	1 (100)
Ofloxacin	9 (53)	8 (47)	11 (73)	4 (27)	1 (100)	0 (0)
Amikacin	14 (82)	3 (18)	12 (80)	3 (20)	0 (0)	1 (100)
Clindamycin	15 (88)	2 (12)	10 (67)	5 (33)	0 (0)	1 (100)
Amoxicillin+clavulanic acid	8 (47)	9 (53)	13 (87)	2 (13)	1 (100)	0 (0)
Vancomycin	17 (100)	0 (0)	15 (100)	0 (0)	1 (100)	0 (0)
Linezolid	17 (100)	0 (0)	15 (100)	0 (0)	1 (100)	0 (0)

Among the Gram-negative bacilli, most of the isolates were sensitive to piperacillin + tazobactam followed by amikacin and imipenem. Among the *Pseudomonads*, most of the isolates were sensitive to polymyxin B, piperacillin + tazobactam and meropenem (Tables 3 and 4).

DISCUSSION

In our study, out of 100 samples, 68% samples yielded growth. Among them, predominant organisms were Gram-negative bacilli with *Pseudomonas* (18 isolates) being most common organism with the highest sensitivity to piperacillin + tazobactam, imipenem and amikacin. Among the Gram-positive organisms isolated, *S. aureus* (17 isolates) was the most common organism with maximum sensitivity to vancomycin and linezolid.

The culture positivity rates of 68% found in our study coincides with study conducted by Gomez et al.,[10] which showed 60% positivity. This is slightly higher than the findings of the study conducted by Lakshminarayana et al. who reported culture positivity of 45.31%.[11] The prevalence of Gram-negative bacteria is slightly higher 51.5% than Gram-positive cocci 48.5% which is in correlation with study done by Amatya et al.[12] and Sule et al.[13]

Table 3: Antibiotic susceptibility pattern of *Pseudomonads* (18)

Antibiotic	Sensitive %	Resistant %
Cefixime	1 (5)	17 (95)
Ceftazidime	4 (22)	14 (78)
Cotrimoxazole	5 (28)	13 (72)
Ciprofloxacin	12 (67)	6 (33)
Amikacin	7 (39)	11 (61)
Gentamicin	9 (50)	9 (50)
Cephaperazone+sulbactam	8 (45)	10 (55)
Piperacillin+tazobactam	13 (72)	5 (28)
Meropenem	14 (78)	4 (22)
Polymyxin B	16 (89)	2 (11)
Aztreonam	7 (39)	11 (61)

Pseudomonas aeruginosa is the predominant isolate (26.4%) in our study which is similar to Amatya et al.[12] who isolated *P. aeruginosa*. A study conducted by Benabdelsalem et al. also reported *Pseudomonas* as predominant Gram-negative bacilli with 17.6% isolates. *S. aureus* is the second isolate (25%) in our study which is in concordance with studies done by Sule et al.[13] and Benabdelsalem et al. (33.1%).[14]

In our study, members of Enterobacteriaceae family showed high sensitivity to imipenem followed by amikacin and piperacillin-tazobactam. This is similar to sensitivity reported by Mahamood.[15] Our study revealed polymyxin B, meropenem and piperacillin - tazobactam are most sensitive drugs against *Pseudomonads* which is in correlation with the study conducted by Shanmugam et al.[16] All the Gram-positive isolates were sensitive to vancomycin and linezolid in our study which was consonance with findings of Roel et al.[17] in their study.

From our results, ampicillin and cephalosporins cannot be recommended for use as an empirical therapy in orthopedic infections. Based on our antibiotic susceptibility data, we suggest that piperacillin-tazobactam and meropenem are the most effective against Gram-negative bacilli and clindamycin, vancomycin and linezolid are effective against Gram-positive organisms. This finding in our study might provide added advantage to clinicians in treating patients with better chances of reduction in morbidity and mortality. The limitation in our study was that anaerobic bacterial

Table 4: Antibiotic sensitivity pattern of Gram-negative bacilli

Antibiotic	*Escherichia coli* 5 (%)		*Klebsiella* sps. 4 (%)		*Citrobacter* sps. 5 (%)		*Proteus* sps. 2 (%)		*Acinetobacter* sps. 1 (%)	
	Sensitive	Resistant	Sensitive	Resistant	Sensitive	Resistant	Sensitive	Resistant	Sensitive	Resistant
Ampicillin	1 (20)	4 (80)			0 (0)	5 (100)	0 (0)	2 (100)	0 (0)	1 (100)
Cefixime	0 (0)	5 (100)	0 (0)	4 (100)	1 (20)	4 (80)	0 (0)	2 (100)	0 (0)	1 (100)
Ceftriaxone	1 (20)	4 (80)	1 (25)	3 (75)	1 (20)	4 (80)	2 (100)	0 (0)	0 (0)	1 (100)
Ofloxacin	2 (40)	3 (60)	2 (50)	2 (50)	2 (40)	3 (60)	1 (50)	1 (50)	0 (0)	1 (100)
Amikacin	4 (80)	1 (20)	3 (75)	1 (25)	1 (20)	4 (80)	0 (0)	2 (100)	1 (100)	0 (0)
Cotrimoxazole	1 (20)	4 (80)	1 (25)	3 (75)	2 (40)	3 (60)	0 (0)	2 (100)	0 (0)	1 (100)
Ciprofloxacin	2 (40)	3 (60)	2 (50)	2 (50)	2 (40)	3 (60)	2 100)	0 (0)	0 (0)	1 (100)
Gentamicin	3 (60)	2 (40)	2 (50)	2 (50)	2 (40)	3 (60)	0 (0)	2 (100)	1 (100)	0 (0)
Cefoperazone+sulbactam	3 (60)	2 (40)	3 (75)	1 (25)	1 (20)	4 (80)	1 (50)	1 (50)	1 (100)	0 (0)
Piperacillin+tazobactam	5 (100)	0 (0)	3 (75)	1 (25)	1 (20)	4 (80)	1 (50)	1 (50)	0 (0)	1 (100)
Amoxycillin+clavulanic acid	1 (20)	4 (80)	0 (0)	4 (100)	0 (0)	5 (100)	2 (100)	0 (0)		
Imipenem	4 (80)	1 (20)	4 (100)	0 (0)	4 (80)	1 (20)	1 (50)	1 (50)	1 (100)	0 (0)

profile and fungal cultures were not done. There is a need for further larger studies including these profiles.

CONCLUSION

As there is high antibiotic resistance observed in our study, it is necessary for routine microbial analysis of samples and their antibiogram. Multidisciplinary collaboration with orthopedic surgeons, infectious disease specialist and clinical microbiologist is needed to reduce the incidence of orthopedic infections. There is a need for formulation of antibiotic policy and formulary restriction.

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