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Original Research Article

Evaluation of microbial infections of ear and their susceptibility pattern in a tertiary care hospital

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ABSTRACT

Background: Nearly 0.065-0.33 billion people suffer from ear infections leading to loss of hearing in 60% of them. As the middle ear is in close proximity to the brain, infections can lead to intracranial complications. Inappropriate use of antibiotics in these situations can lead to multi drug resistant bacterial strains. Hence, the knowledge of commonest bacteria causing these infections along with its susceptibility pattern remains a key to unravel the void left in otological microbiome.

Materials and Methods: Aretrospective analysis of samples obtained from middle ear infections were analyzed for a period of 4 months (2019) at the Department of Microbiology, SRIHER using Hospital information system. The results of microbiological profile and their susceptibility pattern were tabulated and statistically analyzed.

Results: Out of 325 samples enrolled, 302 samples grew pathogens(GPC:122,GNB:186, Fungi:17 & 23 of them grew more than 1 pathogen). The microbiological profile of 325 pathogens were: Pseudomonas aeruginosa 41.8%, Staphylococcus aureus 27.6%, CONS 7.6%, Klebsiella pneumoniae 4.6%, Proteus species 4.6%,Candida species 3.3%, Streptococcus species 2.2%,Escherichia coli 1.8%, Aspergillus species 1.8%, Acinetobacter species 1.2%, Enterobacter species 1.2%, Citrobacter species 0.9%, Morganella species 0.6%, Providencia species 0.3%. Multi-drug-resistant strains were seen in 17 of GNB 9.1%(n=186), predominantly in Pseudomonas species 8.8%(n=136). Methicillin resistance among the Staphylococcus species was 22%(n=115), predominantly in CONS 64%(n=25). Pan-drug resistance was not reported.

Conclusion: Based on our study, a total of 43(13.2%) isolates were MDR strains, hence it is imperative to do a culture and sensitivity pattern of ear infections for efficacious management, thereby reducing further complications.

1. Background

Ear infections are common worldwide. Nearly 0.065 to 0.33 billion people suffer from ear infections leading to loss of hearing in about 60% of them.[1] Because of its close proximity of the middle ear to the brain, infections of them if not treated appropriately and promptly can lead to intracranial infections and complications with high morbidity and mortality.[2] The majority of these infections are bacterial in origin with increasing pyogenicity.[3] The imperceptive, inaccurate, inappropriate use of antibiotics has caused the advent of multiple resistant strains of bacteria which is now a worldwide public health threat.[4,5] Some factors such as low socio-economic status, lack of hygiene, insufficient health care, overcrowding and recurrent upper respiratory tract infections plays a major role for ear infections in low and middle-income countries.[6,7] Hence, the importance of knowledge of the local pattern of infective

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organisms, their susceptibility pattern and their extent of antibiotic resistance is essential in the developing countries for proper management of patients with ear infections.[8] However, antibiotic resistance is a concerning global issue listed among the major threats to public health by the World Health Organization.[9]

Keeping in view the widespread use of antibiotics in the community and the high rate of antibiotic resistance, this study was undertaken to unravel the void left in otological microbiome.

2. Aims and Objectives

1. To study the microbiological profile of ear infections
2. To study the antibiotic susceptibility pattern of the bacterial isolates.

3. Materials and Methods

A retrospective analysis of culture and antibiotic susceptibility reports of ear samples representing middle ear infections sent from the Otorhinolaryngology department during the period 1^{st} June to 30^{th} September 2019 were retrieved using HIS (Hospital information software) at a tertiary care center in South India.

3.1. Isolation and identification of bacteria

The samples that were received at the Clinical Microbiology laboratory were subjected to Gram stain and then processed for the isolation of pathogens by inoculating into Blood agar, Chocolate agar and Mac-Conkey agar. The culture plates were incubated at 37°C and observed for the presence of growth at the end of 24 and 48hrs. Plates showing no growth at the end of 48 hours were reported as NO Growth. Those plates which showed growth were further processed for the identification of pathogens conventionally using appropriate biochemical reactions. Antibiotic susceptibility testing of the isolates were performed as per CLSI guidelines (2016 guidelines). The culture plates which grew mould and yeast were further subcultured into Sabouraud's Dextrose Agar and identified at species level using appropriate techniques.

The test results archived from the HIS were tabulated to look for the microbiological profile and the susceptibility pattern of the pathogens.

4. Results

A total of 325 middle ear samples were analyzed during the study period out of which 23 of them showed no growth. Amongst the 302 samples, 325 pathogens were isolated in which 23 of them grew 2 pathogens. Out of the 325 pathogens that were analyzed, it was almost equally distributed between both genders. 50.63 % in men and 49.38% in women. (n=325) The predominant age group affected was the 30-45 years which was about 32.3% (n-325). The majority of the isolates were Gram negative bacilli 57 % (n-186), followed by Gram positive cocci 38 % (n- 122) and the remaining 5 % were fungi (n-17). (Figure 1) shows the breakdown of organisms isolated from various specimens in this study.

The Antibiotic susceptibility pattern of Gram-negative bacilli in this study is shown in (Table 1). Multidrug resistance among GNB were seen in 17 isolates (9.1%), with the most common organism being Pseudomonas aeruginosa 12(6.4%), followed by Klebsiella pneumoniae 2 (1.07%), Proteus spp, 2(1.07%), Acinetobacter spp 1(0.5%).

The Antibiotic susceptibility pattern of Gram-positive cocci in this study is shown in (Table 2). Methicillin resistance among Staphylococcal isolates was 22.6%(n=122) of which 10 were Staph aureus (11.12%; n=90) and the rest 16 were CONS (64%; n=25). Overall susceptibility percentage of the antibiotics towards the clinical isolates is shown in (Table 3).

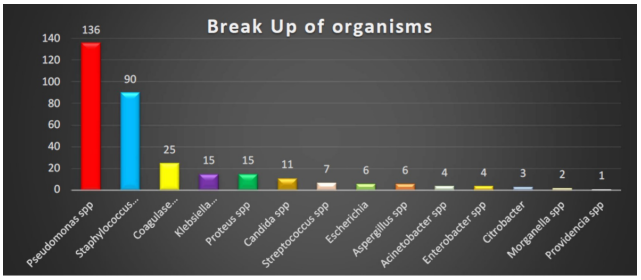

Fig. 1:

5. Discussion

In this study the prevalence of bacteria was 94.76 %. Gram-negative bacteria (GNB) were predominantly isolated from the discharging ears (57%) compared to Gram- positive bacteria (38%). This study revealed that gender does not have an influence on the chances of getting an infected middle ear. Similarly, most studies have reported that there isn't any clear gender-based differences in the risk of acquiring ear infections.[10,11] The infections of the ear are common among all age groups[12] so identifying the microbial etiology and antibiotic susceptibility appropriately will help in the management and prevention of antibiotic resistance. In our study the most common age group affected was 30-60 years of age which corresponds with other Indian studies as well.[13] Whereas in some studies it shows a predilection to young children and adolescents.[14,15]

The most commonly isolated pathogen in our study was Pseudomonas aeruginosa. It is highly virulent; even though it may be regarded as an opportunistic pathogen, it can infect immunocompetent persons affecting any type of tissue.[16] Our finding is consistent with studies done

Table 1: shows the Antibiotic susceptibility pattern of Gram negative bacilli in this study

Antibiotics	Escherichia (n=6)%	Klebsiella pneumoniae (n=15)%	Acinetobacte (pp (n=4)%	Enterobacter spp (n=4)%	Proteus spp (n=15)%	Morganella spp (n=2)%	Providencia spp (n=1)%	Citrobacter spp(n=3) %	Pseudomonas spp (n=136)%
Ampicillin	3 (50%)	Not reported	Not reported						
Cephalexin	3 (50%)	6 (40%)							
Cefotaxime	4 (66.6%)	11 (73.3%)	3 (75%)	4 (100%)	11 (73.3%)	2 (100%)	1 (100%)	2 (66.6%)	Not reported
Cefatazidime	4 (66.6%)	11 (73.3%)	3 (75%)	4 (100%)	11 (73.3%)	2 (100%)	1 (100%)	2 (66.6%)	111 (81.6%)
Cefaperazone sulbactum	6 (100%)	15 (100%)	3 (75%)	4 (100%)	15 (100%)	2 (100%)	1 (100%)	3 (100%)	125 (91.9%)
Piperacillin tazobactum	6 (100%)	15 (100%)	3 (75%)	4 (100%)	15 (100%)	2 (100%)	1 (100%)	3 (100%)	125 (91.9%)
Ciprofloxacin	2 (33.3%)	11 (73.3%)	3 (75%)	4 (100%)	13 (86.6%)	1 (50%)	1 (100%)	2 (66.6%)	104 (76.4%)
Levofloxacin	4 (66.6%)	13 (86.6%)	4 (100%)	4 (100%)	14 (93.3%)	1 (50%)	1 (100%)	3 (100%)	112 (82.3%)
Amikacin	6 (100%)	15 (100%)	4 (100%)	4 (100%)	13 (86.6%)	2 (100%)	1 (100%)	3 (100%)	114 (83.8%)
Tobramycin	6 (100%)	15 (100%)	4 (100%)	4 (100%)	13 (86.6%)	2 (100%)	1 (100%)	3 (100%)	115 (84.5%)
Cefipime	6 (100%)	13 (86.6%)	3 (75%)	4 (100%)	14 (93.3%)	2 (100%)	1 (100%)	3 (100%)	125 (91.9%)
Imipenam	6 (100%)	15 (100%)	3 (75%)	4 (100%)	15 (100%)	2 (100%)	1 (100%)	3 (100%)	136 (100%)
Meropenam	6 (100%)	15 (100%)	3 (75%)	4 (100%)	15 (100%)	2 (100%)	1 (100%)	3 (100%)	136 (100%)
Polymyxin B	6 (100%)	15 (100%)	4 (100%)	4 (100%)		Not reported		3 (100%)	136 (100%)

Table 2: shows the Antibiotic susceptibility pattern of Gram positivecocci in this study

Antibiotics	Staphylococcus aureus (n=90)%	Coagulase Negative Staphylococcus (n=25)%	Streptococcus spp(n=7)%
Ampicillin	50 (55.5%)	9 (36%)	5 (71.4%)
Cephalexin	82(91.1%)	18 (72%)	5 (71.4%)
Cefotaxime	80 (88.8%)	19 (76%)	5 (71.4%)
Gentamycin	74 (82.2%)	22 (88%)	Not reported
Ciprofloxacin	53 (58.8%)	12 (48%)	7 (100%)
Erythromycin	53 (58.8%)	9 (36%)	7 (100%)
Clindamycin	79 (87.7%)	20 (80%)	7 (100%)
Vancomycin	90 (100%)	25(100%)	6 (85.7%)
Linezolid	90 (100%)	25 (100%)	6 (85.7%)

in Riyadh,[17] UAE,[18] Pakistan[19] and Saudi Arabia.[20] Following Pseudomonas aeruginosa, the second most common organism isolated was Staphylococcus aureus. It is observed that both Gram-positive and Gram-negative organisms are responsible for middle ear infections. The results of this present work showed that P. aeruginosa was the most commonly isolated pathogen (41.8%) followed by S. aureus, Klebsiella pneumoniae, Proteus spp., respectively. Similar findings have been observed in Ireland,[21] Pakistan,[22] Greece[23] and other parts of the world which reported that P. aeruginosa and S. aureus are the most common organisms isolated from the cases of otitis media.

This study also showed that 17 swabs (5%) showed the presence of fungus (yeast/mould). The probable reasons for fungal ear infection include perennial warm, humid temperature and environmental pollution.[24–26] The magnitude of fungal infections is lesser when compared to bacterial ear infections. There is a similar pattern of organisms isolated in the tropical countries such as Africa, Singapore, Nigeria, and Pakistan when compared to the studies in India. There would be variations in the microbial profile of the organisms isolated in different parts of the world. Still, Pseudomonas and Staphylococci cause the majority (65.91%) of middle ear infections in tropical

Table 3: shows the overall susceptibility percentage of the antibiotics towards the clinical isolates

Drugs	GPC%	GNB%	Combined%
Ampicillin	52.45% (n=122)	50% (n=6)	52.34%(n=128)
Cephalexin	86.06%(n=122)	42.85%(n=21)	79.72%(n=143)
Cefotaxim	85.24%(n=122)	78%(n=50)	83.13%(n=172)
Ceftazidime		81.18%(n=186)	81.18%(n=186)
Cefaperazone sulbactum		93.54%(n=186)	93.54%(n=186)
Piperacillin tazobactum		93.54%(n=186)	93.54%(n=186)
Cefipime		91.93%(n=186)	91.93%(n=186)
Amikacin	Not reported	87.09%(n=186)	87.09%(n=186)
Tobaramycin		87.63%(n=186)	87.63%(n=186)
Imipenem		99.46%(n=186)	99.46%(n=186)
Meropenem		99.46%(n=186)	99.46%(n=186)
Polymyxin B		100%(n=186)	100%(n=186)
Vancomycin	100%(n=122)		100%(n=122)
Linezolid	100%(n=122)		100%(n=122)
Gentamycin	83.47%(n=115)	Not reported	83.47%(n=115)
Erythromycin	56.55%(n=122)		56.55%(n=122)
Clindamycin	86.08%(n=115)		86.08%(n=115)

Table 4: shows the guidelines for the efficacious management of ear infections followed in our institution

Organisms	1^{st} Line	2^{nd} Line	Topical	Remarks if any
Gram positive organisms				
Staphylococcus aureus & CONS	**1^{st} Preferences** Amoxicillin/ Ampicillin+ cloxacillin Cephalexin Erythromycin Ciprofloxacin **2^{nd} Preferences** Amoxy-clauvulinic acid	**1^{st} Preferences** Cefotaxime Gentamycin **2^{nd} Preferences** Vancomycin Linezolid Clindamycin	Ciprofloxacin Ofloxacin Gentamycin Mupirocin	If allergic to penicillin group other group of antibiotics like macrolides or Quinolones to be considered for the treatment
Streptococcus spp	**1^{st} Preferences** Ampicillin Cephalexin Erythromycin Ciprofloxacin Azithromycin	**1^{st} Preferences** Cefotaxime **2^{nd} Preferences** Vancomycin Linezolid	Ciprofloxacin Mupirocin	If allergic to penicillin group other group of antibiotics macrolides or Quinolones to be considered for the treatment
Gram Negative organism				
Pseudomonas spp Klebsiella pneumoniae Proteus spp Acinetobacter spp Escherichia coli Enterobacter spp Morganella spp Providencia spp	Amoxy-clauvulinic acid (not for Non-fermenters) Ciprofloxacin/ Ofloxacin	**1^{st} Preferences** Cefotaxime Ceftazidime Cefaperazone-sulbactum Piperacillin-tazobactum Amikacin **2^{nd} Preferences** Levofloxacin Cefipime Imipenam Meropenam Polymyxin B	Amikacin Tobaramycin Ciprofloxacin Oflaxacin	-Pseudomonas spp intrinsically resistant to Cefotaxime, - Proteus spp, Morganella spp & Providencia spp are intrinsically resistant to Polymyxin B

countries.[27]

Pseudomonas aeruginosa showed 76.4% sensitivity with ciprofloxacin, 81.6% with ceftazidime, 83.8% with amikacin, 91.9% sensitivity with piperacillin/tazobactam, and 100% sensitivity with Imipenem, Meropenem, Colistin, and Polymyxin B in our study. MDR strains accounted to 9.1% and is slowly on the rise. The higher rate of multidrug resistance may be due to the miss use of antibiotics.[28] These results were found to be in concordance with other Indian and world studies as well.[14,15,28–34]

Staphylococcus species were susceptible with ampicillin in 55.5% cases in our study. In study by Aslam et al[33] resistance with ampicillin and amoxycillin was found to be 77.2%. Sensitivity with ciprofloxacin was 58.8% in our study. In some other studies[29,30,34] the Staphylococcus species sensitivity with ciprofloxacin was higher (83.0%-95.0%). Vancomycin, linezolid, and teicoplanin were 100% sensitive and also against MRSA (22.6%), thus making these agents as the drug of choice for same.[32] No pan-drug resistant isolates were encountered in our study and a total of 43 isolates have shown multi drug resistance in our study (13.2%) which is significant in number.

Hence it is imperative to do a culture and sensitivity pattern of ear infections for effective management; thereby reducing further complications and improving clinical outcomes.

Based upon our study, the following guidelines are used for the efficacious management of ear infections is shown in (Table 4).

6. Conclusion

In accordance with many other studies, this study displays that there can be differences in the organisms affecting the middle ear and their susceptibility patterns. Pseudomonas aeruginosa and Staphylococcus spp., were found to be the most common organisms in our study. Pseudomonas aeruginosa was showing resistance against commonly used antimicrobials like Fluoroquinolones, cephalosporins and reduced sensitivity to aminoglycosides and macrolides. Staphylococcus species were highly resistant to ampicillin and beta-lactam antibiotics and ciprofloxacin. Therefore, evaluation of microbiological pattern and highlighting the need for routine culture and antimicrobial susceptibility testing in local area becomes useful in prescribing empirical antibiotics for efficacious treatment of otitis media, thereby minimalizing its complications and emergence of resistant strains.[32]

7. Conflicts of Interest

The authors declare no potential conflict of interest with respect to research, authorship, and/or publication of this article.

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