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Original Research Article

TUBOTYMPANIC TYPE OF CHRONIC OTITIS MEDIA (SAFE TYPE): BACTERIOLOGICAL PROFILE AND ANTIBIOTIC SENSITIVITY PATTERN IN A TERTIARY CARE HOSPITAL

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Abstract

AIMS: The aim of this study is to evaluate the bacteriological profile of active tubotympanic chronic otitis media (safe type) and the sensitivity pattern to available antibiotics.

METHODOLOGY: Here we have conducted a prospective study in a tertiary care hospital , Bengaluru. Patients presenting with active tubotympanic COM who did not receive antibiotic therapy in the last 20 days were included in the study. Discharge from the middle ear was collected under strict aseptic precautions with the ear swabs. The isolates were grown on blood agar and identified according to standard microbiological and biochemical methods. The antibiotic sensitivity profile of the isolates was determined by Kirby–Bauer disc diffusion method on Mueller Hinton agar.

RESULTS: Out of total 160 (100%) samples the commonest micro-organism isolated was Staphylococcus aureus 60 (37.5%) followed by Pseudomonas aeruginosa 30 (18.75%). Staphylococcus aureus was highly sensitive to linezolid and vancomycin followed by ciprofloxacin. Pseudomonas aeruginosa was highly sensitive to polymyxin B followed by meropenem, cefoperazone plus sulbactam, and ciprofloxacin.

CONCLUSION: The present study indicates that due to widespread use of antibiotics there can be a variation in the bacterial aetiologies of COM and their sensitivity pattern. So we have to be careful while conducting periodic evaluation of microbiological pattern and antibiotic sensitivity of COM.

Keywords: COM-Chronic otitis media; Tubotympanic ;Staphylococcus aureus ;Antibiotic

Introduction

It is important to know the major bacterial aetiologies of COM and their antibiotic sensitivity patterns, both for selection of the most appropriate treatment and prevention of the emergence of resistant strains. [1]

It can cause severe complications if timely interventions are not taken. Many of these complications have been reduced to a greater extent with the invention of antimicrobial agents. But the indiscriminate, haphazard, and half-hearted use of antibiotics have resulted in persistence of low grade infections and antibiotic resistance.[2]

Chronic otitis media (COM) is chronic inflammation of the middle ear and mastoid cavity, characterised by tympanic membrane perforation with recurrent or persistent ear discharge. COM is classified into two types, tubotympanic and atticoantral depending on whether the disease process affects the pars tensa or pars flaccida of tympanic membrane. The principal

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treatment for active tubotympanic COM is meticulous aural toilet and instillation of a topical antimicrobial agent[3]

The aim of the study is to evaluate the current bacteriological profile of active tubotympanic COM and the sensitivity pattern to most of the currently available antibiotics.

MATERIALS AND METHODS

This is a prospective study conducted from November 2020 to August 2021 in a tertiary care Hospital ,Bengaluru over a period one year. Informed consent from patients was taken. Patients presenting with chronic or recurrent ear discharge and on clinical examination found to have ear discharge with central perforation of the tympanic membrane who did not receive antimicrobial therapy for the last 20 days were included in the study.

The exclusion criteria was patients with atticoantral type of COM and patients who had used antibiotic within 20 days of clinical presentation. Under strict aseptic precautions middle ear swab was collected using sterile swabs after dry mopping external auditory canal. The swab samples were immediately sent to the microbiology laboratory in sterile test tubes. The swab samples were inoculated on blood agar, and incubated aerobically at 37 _C for 24–48 h. The isolates were identified according to standard microbiological and biochemical methods. The antibiotic sensitivity profile of the isolates was determined by Kirby–Bauer disc diffusion method on Mueller Hinton agar, and the results were interpreted according to Clinical and Laboratory Standards Institute guidelines. The antibiotic discs used included: cotrimoxazole, amoxicillin plus clavulanic acid, cefoperazone plus sulbactam, cefotaxime, ciprofloxacin, azithromycin, gentamicin, meropenem, vancomycin, linezolid, and polymixin B. For quality controls, the various standard strains were used based on Clinical and Laboratory Standards Institute recommendations.

RESULTS

Total 160 patients with the history of unilateral COM were included in the present study. Total number of samples studied was 160. There were 64 male and 96 female patients.Maximum number of patients were in the 3rd decade of life (Table-1). Out of 160 ear swabs processed, microbial growth was found in 150 samples, while 10 samples showed no growth.

The commonest micro-organism isolated was Staphylococcus aureus (37.5%) followed by Pseudomonas aeruginosa (18.75%). Other micro-organisms isolated were Klebsiella pneumoniae (12.5%), Escherechia coli (7.5%), Acinetobacter baumanii (5%), Proteus sp. (4.3%), Coagulase negative Staphylococcus (2.5%), Streptococcus pneumoniae (1.8%), Morganella morganii (1.8%), Diphtheroids (1.25%), and Candida sp. (1.25%) (Table 1). Gram positive cocci (Staphylococcusaureus, Coagulase negative Staphylococcus, Streptococcus pneumoniae) were highly sensitive to linezolid and vancomycin followed by ciprofloxacin. Gram negative bacilli (Pseudomonas aeruginosa, Proteus sp., Escherechia coli, Klebsiella pneumoniae, Acinetobacter baumanii, Morganella morganii) were highly sensitive to polymyxin B followed by meropenem, cefoperazone plus sulbactam, and ciprofloxacin (Table 2).

Table 1:

SL	Age group(Years)	Number of patients (%)
1	Less than or equal to 10	26(17.3%)
2	11-20	36(24%)

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3	**21-30**	**46(30.66%)**
4	31-40	23(15.33%)
5	41-50	10(6.66%)
6	51-60	6(4%)
7	More than 60	3(2%)
	Total	150(100%)

Table 2:

Samples distribution according to micro-organism profile		
SL	Micro-organism name	Number (%)
1	Staphylococcus aureus	60(37.5%)
2	Pseudomonas aeruginosa	30(18.75%)
3	Klebsiella	20(12.5%)
4	Escherechia coli	12(7.5%)
5	Acinetobacter baumanii	8(5%)
6	Proteus sp.	7(4.3%)
7	Coagulase negative Staphylococcus	4(2.5%)
8	Streptococcus pneumoniae 4 2.02	3(1.8%)
9	Morganella morganii	3(1.8%)
10	Diphtheroids	2(1.25%)
11	Candida sp.	2(1.25%)
12	No growth	9(5.6%)
	Total	160(100%)

Table 3:

Samples distribution according to antibiotic sensitivity of the causative bacteria											
Bacteria	Antibiotic sensitivity (%)										
	COT	**AMO**	**CEFP SUL**	**CEFT**	**CIP**	**AZI**	**GEN**	**MER**	**VAN**	**LIN**	**POL**
Staphylococcus aureus	71	50	NT	60	77	72	65	NT	84	95	NT
Coagulase negative Staphylococcus	83	78	NT	82	90	83	85	NT	98	95	NT
Streptococcus pneumoniae	60	53	NT	72	80	74	70	NT	90	97	NT
Pseudomonas aeruginosa	NT	22	74	42	54	NT	20	80	NT	NT	94
Proteus sp.	NT	41	83	NT	63	NT	53	90	NT	NT	98
Escherechia coli	70	58	89	74	76	NT	66	90	NT	NT	100
Klebsiella	62	44	82	62	70		58	88	NT	NT	99
Acinetobacter baumanii	22	42	80	46	70	NT	52	84	NT	NT	98
Morganella morganii	44	50	78	NT	66	NT	52	90	NT	NT	97

COT Cotrimoxazole, AMO Amoxicillin plus clavulanic acid, CEFP-SUL Cefoperazone plus Sulbactum, CEFT Cefotaxime, CIP Ciprofloxacin, AZI Azithromycin, GEN Gentamicin, MER Meropenem, VAN Vancomycin, LIN Linezolid, POL Polymixin B, NT Not tested

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Comparison of micro-organism profile of CSOM between different studies

Table 4: Comparison of antibiotic sensitivity profile of *Staphylococcus aureus* between different studies

	Present study 2019	C Shilpa et al. [4] 2018	M R Mofatteh et al. [9] 2018	Samanth T U et al [2] 2017	M J Kazeem et al. [12] 2016	G J Lakshmi et al. [10] 2014	P N S Moorthy et al. [13] 2013	S Ahmad et al. [11] 2013	A H Singh et al. [3] 2012
Staphylococcus aureus	37.5	18	29.2	35	23.2	28.2	11.3	56.7	36
Coagulase negative Staphylococcus	2.5	8	35.7	ND	ND	2.5	8	5.5	20
Streptococcus pneumoniae	1.8	ND	ND	ND	0.5	3.8	1.6	ND	2
Pseudomonas aeruginosa	18.75	49	10.3	31	31.5	41	54	19.5	24
Proteus sp	4.3	ND	9.2	1	21.9	7.6	14.51	3.7	32
Escherechia coli	7.5	ND	ND	7	13.7	5.1	3.25	2.4	4
Klebsiella	12.5	5	12.9	17	9.2	3.8	8.06	ND	8
Acinetobacterbaumanii	5	ND	ND	ND	ND	ND	ND	ND	ND
Morganellamorganii	1.8	ND	ND	ND	ND	ND	ND	ND	ND
Diptheroids	1.25	ND	ND	ND	ND	ND	ND	ND	ND
Candida	1.25	ND	ND	ND	ND	1.3	ND	ND	ND
ND Not Done									

Table 5:

Antibiotic	Sensitivity (in percentage)								
	Present study	C Shilpa et al. [4] 2018	M R Mofatteh et al. [9] 2018	Samanth T U et al. [2] 2017	M J Kazeem et al. [12] 2016	G J Lakshmi et al. [10] 2014	P N S Moorthy et al. [13] 2013	S Ahmad et al. [11] 2013	A H Singh et al. [3] 2012
COT	71	NT	15	100	48.8	12.5	15	31	74
AMO	50	NT	NT	0	68.6	NT	NT	100	22
CEF ? SUL	NT	NT	NT	NT	NT	NT	NT	NT	NT
CEF	60	NT	NT	95	NT	71.4	28	NT	NT
CIP	77	0	13.3	90	NT	NT	85	36.8	88
AZI	72	NT	NT	52	NT	NT	NT	NT	NT
GEN	65	81	NT	100	88.4	98	72	15.8	84
MER	NT	NT	NT	NT	NT	NT	NT	NT	NT
VAN	84	90	NT	100	NT	28	NT	NT	NT
LIN	95	NT	NT	90	NT	NT	57	NT	NT
POL	NT	NT	NT	NT	NT	NT	NT	NT	NT

COT Cotrimoxazole, *AMO* Amoxicillin plus clavulanic acid, *CEFP ? SUL* Cefoperazone plus Sulbactum, *CEFT* Cefotaxime, *CIP* Cipro- floxacin, *AZI* Azithromycin, *GEN* Gentamicin, *MER* Meropenem, *VAN* Vancomycin, *LIN* Linezolid, *POL* Polymixin B, *NT* Not tested

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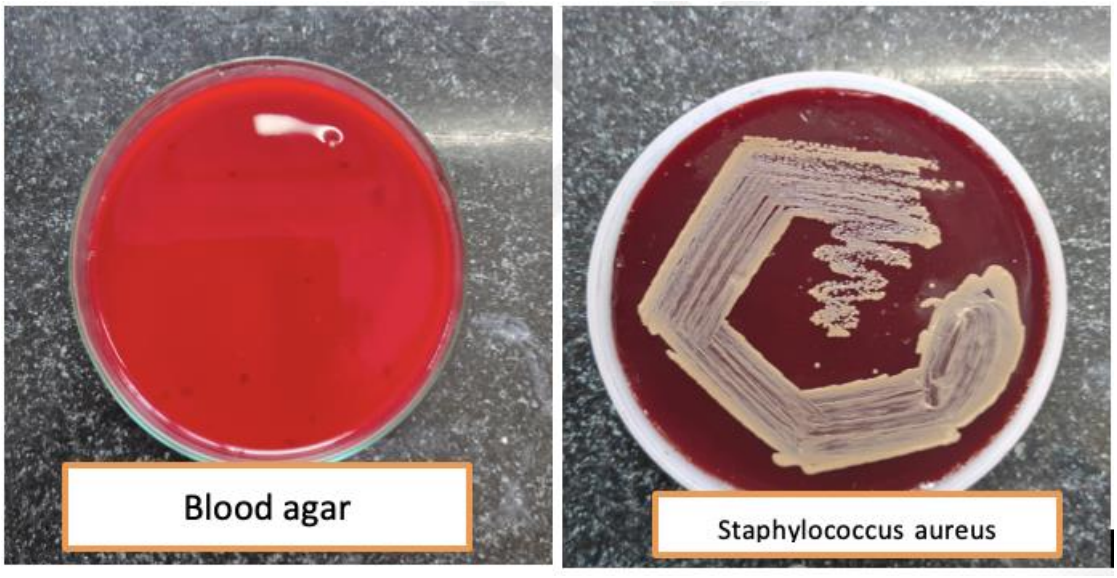
Comparison of antibiotic sensitivity profile of *Pseudomonas aeruginosa* between different studies

Table 6:

Antibiotic	Sensitivity (in percentage)								
	Present study	C Shilpa et al. [4] 2018	M R Mofatteh et al. [9] 2018	Samanth T U et al. [2] 2017	M J Kazeem et al. [12] 2016	G J Lakshmi et al. [10] 2014	P N S Moorthy et al. [13] 2013	S Ahmad et al. [11] 2013	A H Singh et al. [1] 2012
COT	NT	NT	100	32	23.1	18	NT	NT	NT
AMO	22	NT	NT	5	24.8	NT	NT	NT	NT
CEF? SUL	74	96	NT	NT	NT	NT	NT	NT	NT
CEF	42	NT	NT	47	NT	71.8	40	NT	NT
CIP	54	57	6.3	42	NT	NT	85	15.6	82
AZI	NT	NT	NT	NT	NT	NT	NT	NT	NT
GEN	20	76	33.3	48	76.9	69	48	9.4	66
MER	80	NT	NT	100	NT	NT	NT	NT	NT
VAN	NT	NT	NT	NT	NT	NT	NT	NT	NT
LIN	NT	NT	NT	NT	NT	NT	NT	NT	NT
POL	94	NT	NT	NT	NT	NT	NT	71.9	NT

COT Cotrimoxazole, *AMO* Amoxicillin plus clavulanic acid, *CEFP ? SUL* Cefoperazone plus Sulbactum, *CEFT* Cefotaxime, *CIP* Cipro- floxacin, *AZI* Azithromycin, *GEN* Gentamicin, *MER* Meropenem, *VAN* Vancomycin, *LIN* Linezolid, *POL* Polymixin B, *NT* Not tested



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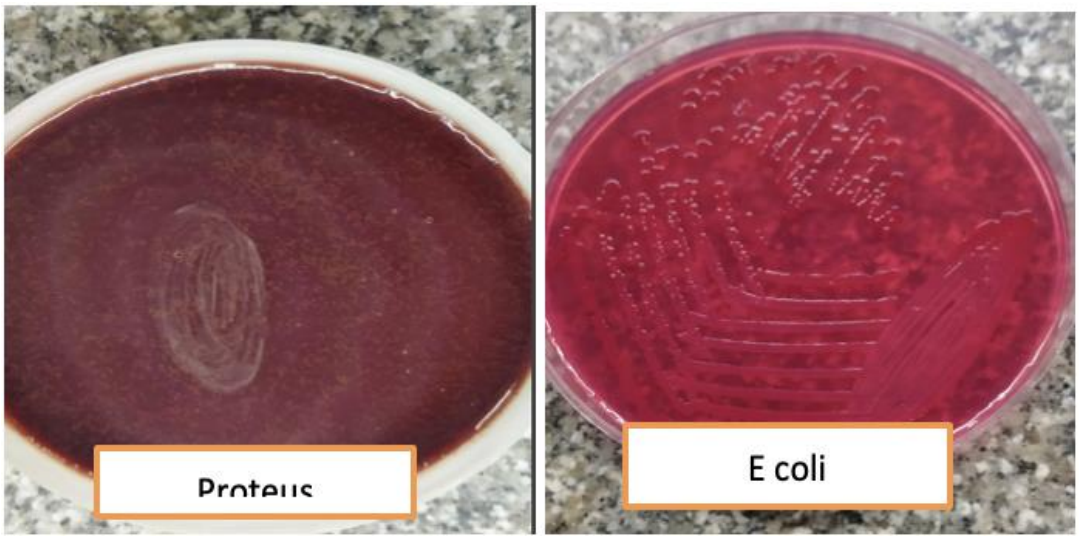

Discussion

In the developing countries COM is a major health problem. CSOM is an important cause of preventable hearing loss particularly in the developing countries [5]. India is one of the countries with a high prevalencerate [4]. Knowledge of the local bacteriological pattern causing CSOM and their antibiotic sensitivity is therefore essential to start an effective treatment [1]. In the present study, microbial growth was seen in 93.72% of samples, while 6.25% showed no growth. The results of the current study are in line with the results of other researches [6]. There was no mixed growth in the present study. This may be attributed to the fact that due to non-availability of anaerobic cultures we could not perform it.This is a drawback of the present study. Though the chance of finding anaerobic bacteria is low as we excluded patients of atticoantral COM from the present study. In case of atticoantral COM we do not wait for the discharge to subside as complications can occur even during seemingly discharge free interval or the discharge may never subside. For this reason we have excluded patients with atticoantral type of COM from the present study.

The highest numbers of COM patients in the present study were between 21 and 30 years of age. Loy et al. showed an increased prevalence of COM in the fourth decade of life [1]. In another study, the highest numbers of COM patients were seen in the 11–20 year age group [7]. In contrast, numerous studies have found that the majority of COM patients were aged less than 20 years [8]. In the present study, there was predominance of female patients compared to male patients, which is consistent with some other studies [1, 8]. Staphylococcus aureus was the most common bacteria isolated, followed by Pseudomonas aeruginosa in the present study, which is in line with reports of some other studies in different parts of the world (Table 3) [3, 9, 11]. However, other researchers have reported that Pseudomonas aeruginosa is the most common isolated pathogenic bacteria in COM patients [2, 4, 10, 12, 13]. Also, in cases of long standing perforation who are attending the hospital frequently, it may be seen there is contamination with nosocomial flora (Acinetobacter sp., Proteus sp., Morganella sp.). Overall, the present study showed significant difference in antibacterial sensitivity patterns in COM patients compared to previous studies conducted (Table 4,5).[3, 2, 4, 9–13] Staphylococcus aureus and other gram positive cocci were highly sensitive to linezolid and vancomycin followed by ciprofloxacin in the present study. Staphylococcus aureus was very less sensitive to amoxicillin plus clavulanic acid, cefotaxime and gentamicin.

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Pseudomonas aeruginosa and other gram negative bacilli were highly sensitive to polymixin B followed by meropenem, cefoperazone plus sulbactam, and ciprofloxacin in the present study. They were very less sensitive to amoxicillin plus clavulanic acid, gentamicin and cefotaxime. The rising prevalence of antibiotic resistance especially in developing countries can be attributed to the overuse and incorrect use of antibiotics. For the antibiotics commonly available as topical ear drops, ciprofloxacin was shown to be most effective with sensitivities for the most commonly isolated bacterias in the present study.

Conclusion

This study shows that due to widespread use of antibiotics there can be a variation in the bacterial aetiologies of chronic otitis media. In the cases of long standing perforation who are regularly attending the hospital, it may be seen there is contamination with nosocomial flora. Periodic evaluation of microbiological pattern and antibiotic sensitivity of COM is required to decrease risk of complications by early institution of appropriate treatment. The patients should also be advised to take the drugs for the complete prescribed duration. This will not only help in minimizing the complications but also help in preventing the emergence of resistant strains.

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