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Original Research Article

Bacteriological profile and antibiotic resistance in cases of chronic otitis media and its clinical implications

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ABSTRACT

Background: Chronic otitis media (COM) is the commonest otologic conditions worldwide with great risk of irreversible complications. Early bacteriological diagnosis is essential for appropriate effective therapy to reduce the disease burden. However in our clinical practice, it was noticed that the morbidity of the disease was mostly non responsive to standard antibiotic medical care. The poor response to routine treatment gave rise to suspicion of antibiotic resistance. This prompted us to undertake this study with the objective to isolate and identify the causative organisms in COM in our clientele and study their antimicrobial susceptibility pattern for a better analysis and institution of accurate therapy.

Methods: A prospective cross sectional analysis was performed using culture and antibiotic susceptibility test results of 500 patients who visited the ENT OPD at a tertiary care centre between July 2016 to June 2017.

Results: A positive culture was obtained in 466/500 (93.2%) of the samples. No growth was seen in 34 patients (6.8%). 454 samples showed single bacterium while 12 samples had mixed growth. *Pseudomonas aeruginosa* was the *predominant organism* (54%) followed by *Staphylococcus aureus*. On antibiotic sensitivity, high resistance patterns to most common first line antibiotics used in COM was observed.

Conclusions: Irrational use of antibiotics for management of COM has led to the emergence of multidrug-resistant bacterial strains. Evaluation of micro bacterial growth and their antibiotic sensitivity pattern in local area helps in prescribing empirical antibiotics for successful treatment of COM.

Keywords: Antibiotic sensitivity, Chronic otitis media, Ear discharge

INTRODUCTION

Chronic otitis media (COM) is defined as chronic inflammation of middle ear and mastoid cavity that may present with recurrent ear discharges or otorrhoea through a tympanic perforation.[1] COM is prevalent worldwide maximally affecting the developing or underdeveloped countries especially in areas of poor socio-economic standards owing to factors such as malnutrition, overcrowding and poor hygiene.[2] Due to its recurrent nature and the development of resistant pathogenic organisms, control of infection in COM now poses a greatest therapeutic challenge. Often, the primary care physicians, who first see these patients rely on empirical antibiotic therapy. Irrational and unethical use of antibiotics has led to high resistance patterns and increase in burden of the disease and its complications. This has been confirmed by various studies which have brought out the changes in bacterial flora and their resistance patterns in COM in the last decade.[3,4]

The objective of this cross sectional prospective study on COM was to study the etiological bacterial diversity and their antibiotic resistance pattern with the aim of developing effective treatment protocols to reduce the morbidity from the disease. The study was conducted as a cohort study at a tertiary care centre in the National capital region of India. To the best of our knowledge no such study data is available from this region.

METHODS

Place of study: ENT Department in a tertiary care referral centre in New Delhi

Period of study: July 16 to June 17

Type of study: Prospective cross sectional observational study

Inclusion criteria

All cases of COM both mucosal and squamous, who reported to the ENT OPD of a tertiary care defence hospital between Jul 16 to Jun 17, with history of ear discharge of more than 3 months, were included in the study. Only samples growing aerobic bacterial organisms were included in the study.

Exclusion criteria

Cases exhibited antibiotic either systemic or topical in the ear in last 2 weeks or patients who had clinical evidence of otomycosis, otitis externa, and or acute otitis media.

Sample collection

Cotton tipped swab was taken from each patient and sent for bacteriological culture and antibiotic sensitivity pattern. All care was taken to avoid surface contamination and the swabs were taken to the microbiology laboratory for further bacteriological processing. Non bacterial flora such as fungi and anaerobic organisms were not included in the present study.

Statistical analysis

The frequency and prevalence of organisms was determined and expressed in percentage. Mean and ratio proportion was calculated for analysis using Statistical Package for Social Sciences (SPSS) version 20.

RESULTS

A total of 500 samples were collected during the period of study from cases of COM both mucosal type (74.2%) and squamous type (25.8%). In our study, age group of patients ranged from 0 to 80 years (mean age - 31.26 years). Maximum incidence of COM was observed in patients of 16–35 years age group (171/500). The sex ratio obtained was female to male ratio preponderance was 1.4:1 (Table 1).

Table 1: Age and sex pattern in cases of COM.

	Total no of cases
Age group (in yrs)	
<5	12
5-15 yrs	92
16-35 yrs	171
36-50	117
>50	108
	500
Gender	
Male	206
Female	294

Table 2: Bacteria isolated from cases of COM with positive culture growth.

Bacteria isolated	Total no.	Percentage (%)
Pseudomonas	261	56.01
Staphylococcus gp	112	24.03
Proteus	19	4.08
E.Coli	28	6.01
K.Pneumoniae	28	6.01
Acinetobacter	08	1.72
Strepto viridans	10	2.14
Total	466	100

A positive bacterial growth on culture was obtained in 466/500 (93.2%) of the samples. Out of these, 454 showed growth of a single bacterium only. In remaining 12 samples, mixed growth was obtained. No growth was seen in 34 patients (6.8%). *Pseudomonas aeruginosa* was the predominant organism 261/466 (56%) followed by *Staphylococcus aureus* (Table 2).

Other bacteria isolated were Proteus spp. (4.08%), *Klebsiella pneumoniae* (6%), *Escherichia coli* (6%), *Acinetobacter* (1.72%) and *Streptococcus viridans* (2.14%). Among the *Staphylococci* species, *Staph aureus* was detected in 110 cases, and Coagulase negative Staph (CoNS) in 2 cases.

The sensitivity patterns of organisms isolated are shown in Table 3. Pseudomonas showed 100% resistance to Ampicillin and Amoxycillin-Clauvilinic acid combination, both considered 1st line antibiotics in COM. Moderate degree of resistance was seen in other Aminoglycosides (162/261 for Gentamycin and 171/261 to Amikacin). 3rd and 4th generation Cephaloporins also showed certain degree of resistance pattern (Ceftriazone 41/261 and Cefepime 27/261 resistance). However there was 100% sensitive to Colistin.

Staph.aureus showed high degree of resistance to Benzylpenicillin and Triamethoprim/Sulphamethoxazol combination, with moderate resistance to Ciprofloxacin and Levofloxacin. However there was 100% sensitivity to Linezolid and Vancomycin (Table 4).

Table 3: Details of bacteriology and sensitivity pattern in cases of COM

Antimicrobial	Pseudomonas – S	Pseudomonas - R	Klebsiella- S	KlebSiella - R	Proteus -S	Proteus -R	E. Coli -S	E. Coli -- R	AcinetoBacter- S	AcinetoBacter - R	Streptoviridans -S	Streptoviridans -R
Ampicillin	0	261	0	28	0	19	0	28	0	18	10	0
Amoxy-clav	0	261	7	21	0	19	0	28	0	18	5	5
Piperacillin/ Tazobactam	234	27	26	2	19	0	28	0	18	0	10	0
Cefuroxime	199	62	26	2	19	0	28	0	0	0	10	0
Ceftriazone	220	41	26	2	19	0	28	0	0	0	10	0
Cefoperazone /Sulbactam	198	63	26	2	19	0	19	9	9	9	10	0
Cefepime	234	27	26	2	19	0	26	2	9	9	9	1
Ertapenam	224	37	26	2	19	0	28	0	0	0	10	0
Imipenam	234	27	26	2	19	0	28	0	18	0	10	0
Meropenam	225	36	26	2	19	0	19	9	18	0	10	0
Amikacin	90	171	26	2	19	0	15	13	9	9	7	3
Gentamycin	99	162	26	2	6	13	6	22	9	9	6	4
Nalidixic acid	9	252	26	2	4	15	1	27	0	18	3	7
Ciprofloxacin	72	189	26	2	5	14	1	27	0	18	5	5
Tigecycline	252	9	26	2	19	0	19	9	0	18	8	2
Nitrofurantoin	30	231	0	28	1	18	19	9	0	18	3	7
Colistin	261	0	28	0	19	0	28	0	18	0	10	0
Triamethoprim /Sulphameth oxazole	0	261	28	0	1	18	1	27	0	18	3	7

S- Sensitive, R- Resistant.

Table 3: Sensitivity pattern of *Staphylococcus* species.

Antimicrobial	Staph aureus -S	Staph aureus- R	CONS -S	CONS-R
Cefoxetin screen	80	30	2	0
Benzylpenicillin	0	110	1	1
Oxacillin	33	77	2	0
Ciprofloxacillin	7	103	2	0
Levofloxacillin	7	103	2	0
Gentamycin	68	42	2	0
Erytheromycin	23	87	2	0
Clindamycin	100	10	2	0
Linezolid	110	0	2	0
Daptomycin	110	0	2	0
Teicoplanin	108	2	2	0
Vancomycin	110	0	2	0
Tetracycline	15	95	2	0
Tigecycline	107	3	1	1
Nitrofurantoin	83	27	1	1
Rifampicin	98	12	2	0
Trimethoprim/Sulfamethoxazole	6	104	0	2

CoNS – Coagulase negative Staphylococcus S- Sensitive R- Resistant.

DISCUSSION

World Health Organization has listed antibiotic resistance as a growing global problem which poses a major threat to health.[1] Higher incidence of COM is common in cases due to the malnutrition, overcrowding and poor hygiene and hence is more commonly seen to occur in communities from poor socio-economic standards.[2] Both gram positive and gram negative organisms contribute to the bacteriological profile of COM infection. Proper antibiotic profile is essential for timely treatment as also to reduce the menace of antibiotic resistance. This study was therefore undertaken to define the organism profile and their resistance pattern to commonly administered antibiotics in cases of COM in a select cohort in the NCR of India.

A positive bacterial growth on culture was obtained in 466/500 (93.2%) of the samples. Pure mono-microbial cultures were obtained in 454 (90.8%) samples. Where as in remaining 12 (2.4%) patients mixed growth was obtained. No growth was seen in 34 patients (6.8%). Various studies have showed varying results on the numbers of positive culture.[3-6.] Poorey and lyer in their study reported pure growth from 82% cases, mixed growth from 10%, and no growth in 8%.[5] Prakash Rajat et al, showed lesser frequency (57.84%) of mono microbial growth.[3] Varying and complex host, environment and patient profile may affect outcome of results in these cases.

In our study, 6.8% of the cultures did not yield any microbial growths which is similar to findings in other reports in which negative cultures in their studies.[6,7] Such negative cultures may have been as a result of the modification of the bacterial flora in the affected ears by prior empirical antibiotic therapy.

Most studies revealed the disease to be prevalent in the younger age group.[3,8] However in our study, young adults were also equally affected. Mean age in our study was about 31 years. Similar results were recorded by Varunika et al and Sharma et al.[9,10]

Our study showed the disease to be common in females than males, in the ratio 1.4:1. Similar reports were obtained in the findings of other authors while Poorey et al reported the ratio to be more towards males.[3-5,11].

Pseudomonas was the commonest organism in our study followed by Staph aureus. Similar results were obtained by others studies.[9,12-15] Whereas certain reports have cited *Staphylococcus aureus* as the most predominant organism in COM.[3,16] Other bacteria isolated in our study were *Proteus* spp. (4.07%), *Klebsiella pneumoniae* (6%), *Escherichia coli* (6%), *Acinetobacter* (1.72%) and *Streptococcus viridans* (2.14%).

The variations in bacteria isolation rates of different organisms reported by different workers may be as an effect of inappropriate antibiotic uses, climatic and other geographical factors.[17] This therefore, highlights the importance of bacterial antibiotic culture sensitivity in cases of COM. Empirical use of antibiotics should be avoided and specific therapy tailor made to individual cases should be encouraged for effective antibiotic use and disease control.

Pseudomonas, infection of the middle ear cleft is generally not attributed due to invasion via the auditory tube as it is not a usual inhabitant of the upper respiratory tract. Source of infection is considered to be access via a perforation in the tympani membrane in such cases.[15] High frequency of bacteria isolated in faeces such as *E. coli*, *Klebsiella* and water borne bacteria like Pseudomonas indicates that individuals with poor hygiene are at high-risk of acquiring such infections.

Based on the antibiogram, there was high resistance to Ampicilin, Amoxycillin/Clauvalinic acid and Trimethoprim/ Sulphamethoxazole combinations across complete spectrum of bacterial isolates. Pseudomonas showed 100% sensitivity to Colistin and High Sensitivity to Piperacillin/ Tazobactam (225/252). It showed complete 100% resistance pattern to Ampicilin, Amoxycillin/Clauvalinic acid and Trimethoprim/ Sulphamethoxazole and also a high resistance to Aminogylcosides. This is in variance with other studies such as Prakash et al who showed good response of Amikacin to *Pseudomonas*.[3] This shows development of increase in resistance patterns of the organism maybe as a result of rampant misuse of these antibiotics over time. The mechanism of resistance is believed to be mediated by formation of biofilms by these organisms.[18]

Staphylococcus species showed high susceptibility to Linezolid, Vancomycin and Teicoplanin. However there was high resistance to penicillin group in our study. Similar results were obtained by other studies.[9.19] CoNS were isolated in 2 cases. All were isolated as mixed infections with *Staph aureus*. Although generally considered nonpathogenic, they may be associated in cases of immune compromised hosts wherein they then become pathogenic and can be cause of infection either singly or in combination with other organisms.[20] In our study all the CONS were in combination with Staph aureus (mixed infection).

Antibiotic commonly used as ear drops preparations such as ciprofloxacin and gentamycin, showed high resistance pattern to the microorganisms in our study. Earlier similar studies showed common antibiotic ear drops to have high sensitivity to implicated bacteria in COM.[3,21] Rampant misuse of these antibiotic drugs may have led to this high resistant state today, which is a cause for worry.

CONCLUSION

There have been rapid changes in the microbial pattern in cases of COM and their antibiotic sensitivity has been changing over time with high levels of resistance to commonly used antibiotics. Periodical assessment of microbiological profile is therefore essential for making effective protocols for cases of COM in a particular geographical location.

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