ORIGINAL ARTICLE

MICROBIOLOGICAL PROFILE FROM MIDDLE EAR AND NASOPHARYNX IN PATIENTS SUFFERING FROM CHRONIC ACTIVE MUCOSAL OTITIS MEDIA

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Background: Chronic otitis media is described as a tympanic membrane perforation and ear discharge for more than six weeks duration. Ascending infection from the nasopharynx into the middle ear cleft has been attributed to prevent resolution of chronic otitis media. This research aims to determine the association between the microbiological flora of the nasopharynx with that of the middle ear in patients suffering from chronic (active) mucosal otitis media. **Methods:** Our study is a hospital-based cross-sectional survey. It was conducted from December 2015 to February 2017 at the Department of ENT, Combined Military Hospital, Abbottabad. Ear and nasopharyngeal swabs were obtained from 65 patients of chronic active mucosal otitis media and sent for microbiological analysis. Microbiological culture and sensitivity test was performed to identify the microbial spectrum of each specimen. Performa bearing the result of otoscopy, aspirate and swabs were completed for middle ear and the nasopharyngeal culture with reference to each patient. Descriptive statistics and Pearson's chi square analysis were performed using SPSS-22. **Results:** *Staphylococcus aureus* and *Pseudomonas aeruginosa* are foremost micro-organisms found in otorrhea culture isolated from patients of chronic active mucosal otitis media. Majority of the cultures from nasopharynx of these patients did not reveal any growth after incubation for 48 hours. **Conclusion:** A statistically insignificant association exists between the microbiological spectrum of the middle ear and the nasopharynx of patients suffering from chronic active mucosal otitis media. Micro organisms' exposure from a perforated tympanic membrane remains leading cause of persistent otorrhea, rather than ascending infection through the Eustachian tube.

Keywords: Otitis, otitis media; Suppurative; Culture techniques; Microbiology

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INTRODUCTION

Chronic active mucosal otitis media is the inflammation within the mucosa of middle ear and the mastoid air cells and intermittent mucopurulent otorrhea through tympanic membrane perforation lasting for more than 6–12 weeks.[1,2] The disease has a historical evidence as old as the Anglo-Saxon era.[3] Depicted by otorrhea and hearing loss due to tympanic membrane perforation; histologically, the inflammation of middle ear mucosa is characterized by oedema, sub-mucous fibrosis, hyper-vascularity and infiltration with lymphocytes, plasma cells and histiocytes. The inflammatory process is usually followed by mucosal ulceration and proliferation of blood vessels, fibroblasts and inflammatory cells, leading to granulation tissue formation.[4,5] The resulting hearing handicap from a tympanic membrane perforation and the stigma of a fetid draining ear may carry a lasting physical and psycho-social impact.[6]

Global prevalence of chronic active otitis media is 4.1%, with brunt of the condition being borne by the underdeveloped world.[7,8] Yearly estimated incidence of this otologic condition is 39 cases per 100,000 persons.[9,10] The magnitude of this condition in the general population of South East Asia is evident from a prevalence of 5.2%.[11] Otitis media is still the commonest infection to prescribe antibiotics to the paediatric population in the United States.[12]

Owing to contiguity of the respiratory mucosa, ascending infection from the lymphoid tissue of oropharynx and nasopharynx has known to predispose a central tympanic membrane perforation to persistent otorrhea.

Little work has been done in the region to ascertain a direct relationship between the nasopharyngeal colonies and the micro-organisms found in the middle ear aspirates in chronic active mucosal otitis media. Our research aims at establishing an association between the microbiological flora of the middle ear and the nasopharynx of the patients suffering from chronic active mucosal otitis media. It would help in corroborating the assumption of ascending infection through Eustachian tube, as an aetiology of chronic active mucosal otitis media in our patients.

Simultaneously, knowing the microbiological spectrum of chronic otitis media would help formulate a strategy to construct guideline for empirical therapy of this widely prevalent condition.

MATERIAL AND METHODS

After seeking approval from the hospital ethical committee and the institutional executive body, we requested all the patients of chronic active mucosal otitis media and the parents to provide us a written informed consent to be included in this cross-sectional study.

Sixty-five patients of chronic active mucosal otitis media regardless of gender, parental literacy, and socioeconomic class were included. Patients who had been operated for chronic otitis media, those with squamous variant and inactive mucosal chronic otitis media, concurrent otitis externa, traumatic tympanic membrane perforation, cleft palate, younger than 5 years of age and those who declined to consent for the project were excluded. The population of Abbottabad is 106101 as per national census of 1998. Overall prevalence of active and inactive chronic otitis media is 4.1%.[8] Keeping 'confidence level' of 95% and 'margin of error' of ±5%, the sample size of finite universe turned out to be 60.

We obtained a detailed history from adult patients and the parents or guardians of affected children. Complete ENT examination including otoscopy was performed to ascertain clinical signs of chronic active mucosal otitis media. Patients' outer ears were cleansed with sterile swab soaked in ethyl alcohol. We requested every patient (or the parents accompanying the paediatric patients) for obtaining a swab or aspirate from the discharging ear as well as from the nasopharynx with the help of a curved sterile swab-stick, in the absence of any antibiotic treatment for at least two weeks. These specimens were then sent for microbiological examination.

All the specimens and data were collected and processed systematically. Nasopharyngeal swab was cultured qualitatively as per standard protocol. All specimens were cultured on

MacConkey's and Chocolate agar. MacConkey's agar was incubated at 37 °C aerobically and Chocolate agar was incubated at 37 °C in 10% CO_2 environment. Growths obtained on all the culture media were identified by colony morphology, Gram stain, and conventional biochemical tests like catalase and coagulase for Gram positive isolates, oxidase, oxidation/fermentation, motility and API 20 E and NE galleries for Gram negative rods and API NH galleries for Gram Negative cocci.

Database was maintained in statistical program for social science IBM-SPSS version-22. Frequencies were measured using descriptive statistics. We applied Pearson's chi square test to determine the association between the two categorical (nominal) variables, i.e., microbiological spectra of otorrhea vs. the nasopharyngeal flora. The level of statistical significance in order to prove our hypothesis was 0.05.

RESULTS

Sixty-five patients belonging to both sexes, who suffered from chronic active mucosal otitis media consented us to volunteer for the research. The youngest patient was 4 years old and the oldest was 72 years of age.

Thirty-seven (52.9%) patients were male, 40% (n=28) were females. *Staphylococcus aureus* remained the predominant micro-organism found in otorrhea cultures. It was isolated from 38.5% (n=25) infected middle ear swabs. Mixed isolates revealed *Staphylococcus aureus* in co-existence with *Citerobacter freundii* in 1.5% (n=1), with *Pseudomonas aeruginosa* in 1.5% (n=1), and with *Enterococcus faecalis* in 1.5% (n=1) cultures. *Pseudomonas aeruginosa* was isolated from 26.2% (n=17) ear swab specimens. However, we found mixed flora of *Pseudomonas aeruginosa* with Klebsiella species in 1.5% (n=1) culture. *Proteus mirabilis* was found in 3.1% (n=2) otorrhea specimens. 9.2% (n=6) ears swabs revealed no growth in culture medium after incubating for a period of 48 hours. (Figure-1)

Acinetobacter baumunii, *Citerobacter freundii*, *Enterococcus faecalis*, Klebsiella species, Methycillin resistant *Staphylococcus aureus* (MRSA), *Proteus vulgaris*, *Serratia mercens*, *Serratia odorifera*, *Enterococcus faecalis* and *Streptococcus faecalis* were individual isolates obtained in identical frequency, i.e. 1.5% (n=1) cultures each out of the total subjects suffering from chronic active mucosal otitis media. (Figure-1)

Staphylococcus aureus was predominantly cultured from the nasopharyngeal swabs of patients suffering from chronic active mucosal otitis media. 10.8 % (n=7) subjects exhibited this colonization. Only 1.5% (n=1) culture yielded *Pseudomonas aeruginosa* from within nasopharynx. Nasopharyngeal swab from 87.7% (n=57) patients did not reveal any growth after 48 hours of incubation. (Figure-2). Applying Phi and Crammer's V as test of strength of association, the chi square test for independence revealed a very weak and statistically insignificant association between the micro-organisms isolated from the actively discharging middle ears, and those obtained from the nasopharynx of same patients suffering from chronic active mucosal otitis media (*p*-value 0.999). (Table-1)

Fifty-four cells (94.7%) have expected count less than 5. The minimum expected count is .02. Age and gender did not pose any significant influence on prevalence of the disease (*p*-values 0.847 and 0.376, respectively)

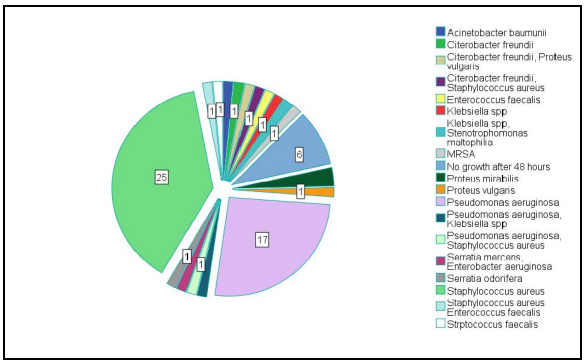

Figure-1: Middle ear isolates

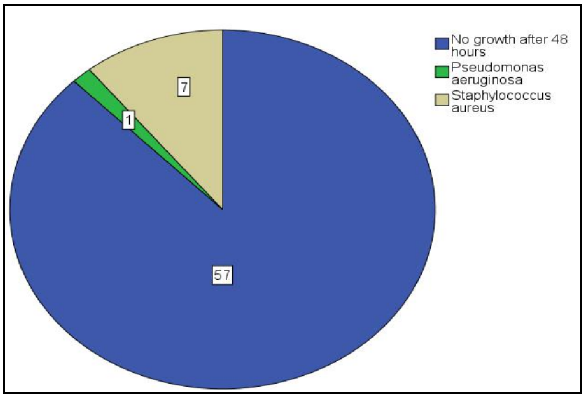

Figure-2: Nasopharyngeal isolates

Table-1: Pearson's Chi square analysis

	Value	df	Asymp. Sig. (2- sided)
Pearson Chi-Square	14.588[a]	36	.999
Likelihood Ratio	12.873	36	1.000
N of Valid Cases	65		

DISCUSSION

Histologically the mucosa of middle ear cleft is an extension of the mucosa of the nasopharynx.[13] Upper respiratory tract infections are thought to be precursor of Eustachian tube dysfunction for short intervals. This may lead to middle ear mucosal activity and subsequent bacterial infection. However, this phenomenon has not been demonstrated scientifically.[14] It is believed that chronic otitis media is a consequence of unresolved acute otitis media. Number of siblings, type of day-care, duration of breast feeding, parental socio-economic status, limited primary healthcare access and prematurity are all independent etiologic factors of acute otitis media.[8] Over 50% of cultures in active mucosal chronic otitis media in children have turned out to be anaerobes.[15] Immunization in the developed world seems to have an impact on the microbiological spectrum of otitis media. *Streptococcus pneumoniae* and *Haemophylis influenza*e outweighed the bacterial isolates from acute and chronic otitis media before year 2000 in paediatric population of the United States.[16] Though nation-wide immunization with heptavalent conjugated pneumococcal vaccine (PCV7) Prevnar could only lessen the relative risk of acute otitis media in 6–7.8% in Finland and California, however a 24% decrease in treatment failure of acute otitis media was reported by Casey and Pichichero in suburban Rochester, New York, following administration of Prevnar.[17–19] Data from Pakistan substantiates *Pseudomonas aeruginosa* to be the most prevalent strain in chronic active mucosal otitis media (38% of isolates), followed by *Staphylococcus aureus*, *Proteus mirabilis* and Klebsiella species.[7] Advent of newer 13-valent (PCV13) pneumococcal vaccines has proven to be more beneficial in eradicating otitis media in the developed world. Our results are also comparable with the multicentre research conducted in the Pakistan in 2009, whereby 40% *Pseudomonas aeruginosa* was cultured from the ear swabs of chronic active mucosal otitis media, followed by *Staphylococcus aureus* in 30.9%.[20] It is noteworthy to mention that the spectrum has also been found to vary geographically in many sub-regions of the country.[21,22] Numerous authors have determined antimicrobial susceptibility against otologic microorganism flora from patients of chronic otitis media. A strong correlation, nevertheless, exists between upper respiratory tract infections and otitis media. And association between nasopharyngeal colonization and the middle ear microorganism flora has also been demonstrated in Western and Australian literature.[23,24] These studies have proven that such colonies are in a constant state of acquisition and elimination into and out of nasopharynx. Factors responsible for this age-specific phenomenon are largely undetermined.[25] Possible colonization of nasopharynx with middle ear microorganisms is assumed to be influenced by seasonal variation, number of siblings, day-care and ongoing respiratory illness.[26–28] Simultaneously, maturation of the child's immune system with growing age is thought to be a cause of elimination of these microorganisms from the nasopharynx. Peton *et al* analysed bacterial isolates from nasopharyngeal swabs and washes from children suffering from otitis media. They also pointed out a decrease in vaccine serotypes and a relative increase in the non-vaccine serotypes in the culture with growing awareness about immunization.[29]

Our present study clearly disproves this argument that any new colonization in the nasopharynx of the patient of chronic active mucosal otitis media would influence any similar change in the middle ear microorganism flora of the same patients. It would facilitate in better understanding of development, progression and management of otorrhea in chronic active mucosal otitis media.

CONCLUSION

Micro-organisms of a chronic active mucosal otitis media doesn't show any direct association with those found in the nasopharynx of the same subjects. However, upper respiratory tract infections definitely cause mucosal oedema and impaired ciliary movement inside Eustachian tube, eventually bolstering inflammation inside the middle ear cleft.

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AUTHORS' CONTRIBUTION

SF: Proof reading. NAS: literature search, Conceptualization of study design, data analysis, data interpretation, Write-up. AA, MF: Data collection. KN: literature search

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