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Original Article

# The Microbiological Profile of Chronic Suppurative Otitis Media in Children

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## Abstract

**Objective:** To identify the frequency and distribution of bacterial pathogens in pediatric Chronic Suppurative Otitis Media (CSOM) and analyze their antibiotic resistance patterns over a year study period at a tertiary care hospital in Karachi.

**Methods:** A cross-sectional-descriptive study was conducted at Sindh Government Qatar Hospital, Karachi, from 1st April 2024, to 30th April, 2025. A total of 350 children (ages 0.5–15 years) diagnosed with CSOM were included via non-probability consecutive sampling. Data were recorded on a predesigned proforma. Bacterial cultures and antibiotic susceptibility testing were performed using Gram staining, biochemical tests, and culture media (chocolate, MacConkey, blood agar). Antibiotic susceptibility was determined using the Kirby-Bauer disk diffusion method, following Clinical and Laboratory Standards Institute (CLSI) guidelines. Statistical analysis was performed using SPSS 23.

**Results:** A cohort of 350 children (mean age 5.87±2.17 years) was enrolled and showed male dominance (67.1%). Pseudomonas aeruginosa (31.7%) and Staphylococcus aureus (19.4%) were the most common isolates. Resistance was highest for β-lactams and fluoroquinolones, while glycopeptides and aminoglycosides remained effective. A statistically significant association was found between age of the patients and distribution of multiple organisms using one-way-ANOVA test ($p < 0.001$).

**Conclusion:** Antibiotic resistance in pediatric CSOM necessitates updated regional data for precise treatment. Empirical therapy should be replaced with targeted antibiotic strategies.

**Keywords:** Antibiotic resistance, Chronic Suppurative Otitis Media, Ciprofloxacin, Hearing Loss, Pseudomonas aeruginosa, Staphylococcus aureus.

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## Introduction

Chronic suppurative otitis media (CSOM) is the long-standing (≥12 weeks) suppurative inflammation of the mucosa overlying middle ear cleft, leading to ear discharge and a lasting tympanic membrane perforation.[1] The global incidence rate of CSOM is 4.76%, accounting for 31 million cases annually, with 22.6% occurring in children >5 years, mainly affecting developing countries.[2]

Pseudomonas aeruginosa and Staphylococcus aureus are known as the commonly found disease causing organisms.[3] The treatment mainly depends on instillation of topical antibiotics, reserving the use of systemic therapy in cases of treatment failure or emergence of complications.[4] In the less privileged societies, the common practice of home remedies, over-the-counter drug misuse, and delayed specialist consultation contributes to treatment delays, the emergence of antibiotic-resistant organisms, eventually the chances of complications are increased.[5] Considering the data of long-term complications, 91% of the affected children suffer from permanent hearing loss of >15dB, which affect their speech, academic performance, and quality of life.[6]

Unnecessary long-term empirical therapy is a threat for emergence of resistant organisms. Moreover, effective infection control is prudent for wound healing in cases dealt with surgical therapy like Tympanoplasty or mastoidectomy etc.[6] Given the geographic variations in microbial prevalence and antibiotic susceptibility, region-specific data is prudent for targeted therapy. Up to author's best knowledge, despite CSOM being a major public health concern, no recent Karachi-based studies have comprehensively analyzed the microbial spectrum and antibiotic resistance trends in children over the last five years. The rational of this study was to fill that critical gap, providing updated, evidence-based recommendations to optimize antibiotic use, improve patient outcomes, and curb antimicrobial resistance. Without this research, outdated empirical treatments pose the risk to increased complications, prolonged illnesses, and higher healthcare costs.

## Methods

This observational type, descriptive cross sectional study was conducted at Sindh government Qatar Hospital Karachi, from 1st April 2024 to 30th April 2025, after taking the ethical approval for the study from the Institutional Review Board,.

All the children between the ages of 1-10years, who were diagnosed as cases of CSOM were included in the study after taking an informed consent from their primary caregivers. The exclusion criteria included patients with concomitant otitis externa, recent upper respiratory tract illness like acute rhinosinusitis etc., fungal ear infections, complicated CSOM, history of recent ear surgeries, or immunodeficiency status. All the children were recruited via non-probability consecutive sampling, regardless of their gender and race. An informed consent was obtained from the primary caregivers of all children.

The sample size (350, at 95% confidence level and 5% margin of error) was calculated using the WHO (world health organization) guidelines, assuming a 15% prevalence of CSOM in children, based on Eastern Mediterranean Region studies (7.4[8] –15.5%[9]), as Karachi-specific data was not available.

Data were collected using a department based proforma. A detailed medical history note followed by a comprehensive ENT examination was recorded. In selected cases, to ensure the accuracy of diagnosis of cholesteatoma, an examination under the microscope was conducted when required. All those patients who were using antibiotics, in any form, were advised to stop for a period of 7-days, prior to taking their samples. The sample for infected ear secretions were collected using a sterile swab container and all the samples were instantly transported to microbiology laboratory in a sterile transport medium. Gram staining, biochemical testing, and antibiotic susceptibility testing were done for thorough assessment. Different media were used for culture including chocolate agar, MacConkey agar, and blood agar plates. All the cultures were kept under observation for upto 24-48 hours and in case of no growth, waited for 72 hours, before declaring it negative. The Kirby-Bauer disk diffusion method was used to analyze antibiotic susceptibility pattern, following Clinical and Laboratory Standards Institute (CLSI) guidelines

Statistical analysis was done using SPSS 23. Descriptive statistics were done for all the studied variables. The one way ANOVA test was conducted considering the age of study participants and distribution of organisms. A Pearson Chi-Square test was performed to evaluate the association between prior antibiotic use and the type of bacterial organisms identified. The rules of declaration of Helsinki were followed throughout the research process.

## Results

Among 350 participants, 235 (67.1%) were male and 115 (32.9%) female, with a mean age of 5.873±2.17 (1-10) years. Most lived in slum areas (214, 61.1%), followed by lower middle class residential areas (92,

**Table 1:** *Descriptive analysis of distribution of isolated organisms among different age groups; n= 350 (One-way-ANOVA test)*

| Organism | Mean age ± Standard deviation ( Minimum-maximum age in years) | 95% Confidence interval (lower bound-upper bound) |
|---|---|---|
| Pseudomonas aeruginosa | 6.48 ± 1.57 (3.0–10.0) | 6.18–6.77 |
| Streptococcus Pneumoniae | 4.39 ± 2.63 (1.0–10.0) | 3.63–5.14 |
| Staphylococcus Aureus | 6.01 ± 2.02 (1.0–10.0) | 5.52–6.50 |
| Streptococcus pyogenes | 4.74 ± 2.33 (1.0–9.0) | 3.82–5.66 |
| Moraxella catarrhalis | 5.54 ± 1.74 (4.0–9.0) | 4.81–6.28 |
| Klebsiella pneumoniae | 6.26 ± 2.02 (3.0–10.0) | 5.29–7.24 |
| Hemophilus influenza | 6.69 ± 1.39 (4.0–9.0) | 5.89–7.49 |
| Escheriae coli | 6.96 ± 2.00 (4.0–10.0) | 5.75–8.17 |
| Poly-microbial growth | 6.83 ± 1.83 (4.0–9.0) | 4.91–8.76 |
| No growth detected | 5.68 ± 3.15 (1.0–10.0) | 4.17–7.20 |

26.3%) and upper middle class residential areas( 44, 12.6%) from surrounding areas like Nazimabad, federal b-area etc. Nuclear families were common (287,82%) as compared to joint families (63, 18%), and most of the mothers were matriculate (46, 13.1%), followed by those who completed their elementary education (95, 27.1%), illiterate (78, 22.3%) and graduate (131, 37.4%). Mucosal-type CSOM was predominant (300, 85.7%), while atticoantral-type accounted only for 50 (14.3%) cases. Majority of the parents (294, 84%) denied the history of giving antibiotics (oral or topical) in the last 02-week period, while only a small proportion (47, 13.45) was giving antibiotic either in oral or topical form. Our results identified a predominance of Gram-negative bacteria (181, 51.7%) including Pseudomonas aeruginosa (111, 31.7%), Moraxella catarrhalis (24, 6.9%), Klebsiella pneumoniae (19, 5.4%), Haemophilus influenzae (14, 4%), and Escherichia coli (13, 3.7%), while Gram-positive bacteria accounted for 114 (41.14%) cases of the bacterial isolates, counting Staphylococcus aureus (68, 18.9%), Streptococcus pneumoniae (49, 14%), and Streptococcus pyogenes (27, 7.7%). No growth was found in 19 (5.4%) cases, and 6 (1.7%) cases had mixed infections, including Moraxella catarrhalis with S. aureus and Klebsiella pneumoniae with S. pyogenes.

One-way-ANOVA test was employed to assess the relationship of age with distribution of various organisms, and a statistically significant difference in mean age among organism groups (F(9, 340) = 5.843, $p < 0.001$, Sig. = .000) was found. The variation between groups (Mean Square Between = 24.542, Sum of Squares = 220.881, df = 9) was greater than the variation within groups (Mean Square Within = 4.200, Sum of Squares = 1428.047, df = 340). Those results were confirmed by Welch test result (F(9, 60.652) = 4.630, $p < 0.001$), that a different organisms had a predilection for specific age groups. The descriptive analysis of distribution of different organisms as per mean age of the study participants is demonstrated in Table 1.

Considering the history of prior antibiotic usage, cross tabulation result revealed 83% cases with polymicrobial growth and 95% cases without any exhibited growth. Its statistical significance (Pearson Chi-Square = 170.149, df = 18, $p < 0.001$), was confirmed by Monte Carlo simulation (p=0.000, 99% CI: 0.000–0.013) and Fisher's Exact Test (p = 0.000).

Among Gram-negative bacteria (Table 2), Pseudomonas aeruginosa showed high β–lactam resistance (85–95%) but remained sensitive to fluoroquinolones (85–90%) and aminoglycosides (75%). Haemophilus influenzae

**Table 2:** *Antibiotic sensitivity pattern of Gram Negative Bacteria (n=181)*

| Drugs | Pseudomonas Aeruginosa (n=111, 31.7%) | Hemophilus influenzae (n=14, 4%) | Escherichia coli (n=13, 3.7%) | Klebsiella pneumoniae (n=19, 5.4%) | Moraxella catarrhalis (n=24, 6.9%) |
|---|---|---|---|---|---|
| **Co-amoxiclav** | Resistant (80%) | Sensitive (75%) | Resistant (60%) | Resistant (70%) | Sensitive (80%) |
| **Ciprofloxacin** | Sensitive (90%) | Sensitive (70%) | Resistant (65%) | Resistant (70%) | Sensitive (80%) |
| **Ofloxacin** | Sensitive (85%) | Sensitive (75%) | Resistant (60%) | Resistant (65%) | Sensitive (75%) |
| **Gentamycin** | Sensitive (85%) | Sensitive (80%) | Sensitive (65%) | Sensitive (60%) | Sensitive (85%) |
| **Ampicillin** | Resistant (90%) | Resistant (85%) | Resistant (80%) | Resistant (85%) | Sensitive (70%) |
| **Ceftriaxone** | Resistant (80%) | Sensitive (85%) | Resistant (55%) | Resistant (60%) | Sensitive (90%) |

**Table 3:** *Antibiotic sensitivity pattern of Gram Positive Bacteria (n=144)*

| Drugs | Staphylococcus Aureus (n=68, 19.4%) | Streptococcus Pneumoniae (n=49, 14%) | Streptococcus Pyogenes (n=27, 7.7%) |
|---|---|---|---|
| Co-amoxiclav | Sensitive (60%) | Sensitive (70%) | Sensitive (85%) |
| Vacomycin | Sensitive (100%) | Sensitive (100%) | Sensitive (100%) |
| Linezolid | Sensitive (100%) | Sensitive (98%) | Sensitive (99%) |
| Clindamycin | Sensitive (70%) | Sensitive (80%) | Sensitive (85%) |
| Ciprofloxacin | Resistant (75%) | Resistant (50%) | Sensitive (90%) |
| Neomycin | Sensitive (80%) | Sensitive (85%) | Sensitive (90%) |
| Gentamycin | Sensitive (85%) | Sensitive (80%) | Sensitive (90%) |
| Ampicillin | Resistant (80%) | Sensitive (65%) | Sensitive (85%) |
| Ceftriaxone | Sensitive (85%) | Sensitive (80%) | Sensitive (90%) |
| Macrolides | Sensitive (60%) | Sensitive (75%) | Sensitive (80%) |
| Ofloxacin | Sensitive (60%) | ------------------- | ------------------- |

resisted Ampicillin (85%) but responded well to cephalosporins (85%) and aminoglycosides (80%). Escherichia coli and Klebsiella pneumoniae displayed strong β-lactam (80–85%) and fluoroquinolone (60–70%) resistance, with moderate aminoglycoside sensitivity (60–65%). Moraxella catarrhalis was very much sensitive to cephalosporins (90%) and aminoglycosides (85%) but had moderate β–lactam resistance (30%).

In view of the antibiotic sensitivity patterns among Gram-positive bacteria (Table 3), Staphylococcus aureus showed high resistance to β-lactams (80%) and fluoroquinolones (75%) but remained fully susceptible to glycopeptides and oxazolidinones. Streptococcus pneumoniae had moderate β-lactam (35%) and fluoroquinolone (50%) resistance, while Streptococcus pyogenes was largely sensitive, with macrolide (20%) and fluoroquinolone (10%) resistance.

## Discussion

Our analysis showed a male predominance (67.1%) with a mean age of 5.873±2.17 years. In comparison, a Yemen based-study reported a slight male majority (54.9%) and a higher prevalence in children over 11 years (58.82%)[8]. The sociodemographic profile of our study participants highlighted substandard living conditions, with 61.1% residing in slum area. Comparatively, an Indian study recorded most CSOM casesfrom the upper-lower (35.15%) and lower (26.67%) socioeconomic residential areas.[10] The predominance of the nuclear family system (82%) was observed in our study. While many studies link joint family systems to child negligence and CSOM development, as seen in a Tando Adam, Pakistan study (66.7% in joint families,[11] our findings may reflect Karachi's distinct family structure, influenced by regional living arrangements.

Our findings revealed the poor literacy rate among mothers as 23.3% were illiterate and 27.1% having only elementary education, reflecting the potentially low quality care of children provided by primary caregivers in this cohort. Searching through literature, a Nepal-based study on women's knowledge, attitudes, and practices (KAP) in managing CSOM showed that despite high (86.2%) illiteracy, sustained improvements were achieved through educational sessions, long-term follow-up, and active research team involvement.[12] In our study, mucosal-type CSOM was the predominant form (85.7%), it might be a regional finding. In contrast, a study from Muzaffarpur, India, recorded a higher prevalence of atticoantral disease (71.43%), while research from Indian-administered Kashmir reported a greater burden of tubotympanic disease (54%),[10] while in another study conducted at Indian Kashmir, burden of tubpotympanic diseases was higher i.e. 54%.[13].

Our results identified a predominance of Gram-negative bacteria (51.7%), Pseudomonas aeruginosa (31.7% in 350 cases) being the commonest identified organism followed by Gram-positive bacteria accounted for 41.14% of the isolates, counting Staphylococcus aureus (18.9% in 350 cases) as most commonly bacteria. Inoh et al. (Nigeria) similarly reported a higher prevalence of Gram-negative bacteria (57.5%) than Gram-positive bacteria (34.7%), but Pseudomonas aeruginosa was found in 14.9% cases as compared to ours 32% cases, while Staphylococcus aureus was slightly more common (20.3% vs. 18.9%). These variations may be attributed to differences in study populations, sample sources, or regional antimicrobial resistance pattern.[14]

In contrast, Ghallab et al. reported a different microbial distribution in Egypt, with Haemophilus influenzae (38.3%) as the most frequently isolated pathogen, followed by Streptococcus pneumoniae (26.7%), Moraxella catarrhalis (13.3%), Staphylococcus aureus (8.3%), and Pseudomonas aeruginosa (6.7%)[15]. A Pakistani study reported Methicillin-Resistant Staphylococcus aureus (MRSA) (27.3%) as the most common pathogen causing CSOM in children, followed by Pseudomonas aeruginosa (19.3%), Proteus mirabilis (18.6%), Moraxella catarrhalis (9.3%), and Enterobacteriaceae (4%). Klebsiella pneumoniae, Escherichia coli, and Staphylococcus aureus were each identified in 3.3% of cases, while Haemophilus influenzae was detected in 2% of cases.[16]

Our results indicate that the most commonly identified Gram-negative bacterium, Pseudomonas aeruginosa (31.7%), exhibited substantial resistance to β-lactam antibiotics (85–95%) but remained highly susceptible to fluoroquinolones (85–90%) and aminoglycosides (75%) (Table 2). Comparatively, Xu et al. reported Pseudomonas aeruginosa sensitivity rates of ciprofloxacin (59.8%), tobramycin (81%), gentamicin (80%), ceftazidime (50%), and ampicillin (17%). Their findings highlight moderate efficacy of fluoroquinolones and aminoglycosides, alongside significant β-lactam resistance, reinforcing the need for targeted antibiotic stewardship[17]. In another Chinese study, Pseudomonas aeruginosa was 100% sensitive to meropenem, 40% to gentamicin but showed significant resistant against ciprofloxacin (40%) and ceftriaxone (30%).[18]

In our results, considering the antibiotic susceptibility of less frequently isolated gram negative bacteria, Gentamycin (60-85% sensitivity) and ceftriaxone (85-90% sensitivity) are the most effective against H. influenzae and M. catarrhalis. Fluoroquinolones (70-80% sensitivity) show moderate efficacy but high resistance in E. coli (60-65%) and Klebsiella (65-70%). Co-amoxiclav is effective for H. influenzae (75%) and M. catarrhalis (80%) but has high resistance in E. coli

(60%) and Klebsiella (70%). Ampicillin shows the highest resistance (80-85%) except for M. catarrhalis (70% sensitivity). In terms of abundantly isolated (19.4%) Gram positive bacteria, Staphylococcus aureus revealed (Table 3) great resistance to β-lactams (80%) as well as fluoroquinolones (75%). Comparing a Nigeria-based study, resistant pattern of Staphyococcus aureus was observed for vancomycin (13%), penicillin G (82%), ofloxacin (15%), ciprofloxacin (21%), gentamicin (23%), clindamycin (25%), ceftriaxone (27%), erythromycin (31%), ceftazidime (33%), and amoxicillin-clavulanic acid (34%).[19] In contrast to our findings, a study conducted at a tertiary care hospital in Peshawar analyzed among all the isolates of staphylococcus aureus, 78.3% were methicillin-resistant, and 88.67% of those isolates were characterized as multidrug-resistant.[20]

Rathod et al. from Pakistan reported antibiotic resistance patterns in pediatric CSOM, with the maximum resistance observed for ampicillin (76%), followed by ceftriaxone (71%), vancomycin (61%), ciprofloxacin (55%), gentamicin (51%), and meropenem (42%), indicating widespread resistance among CSOM pathogens. These findings suggest that β-lactams, fluoroquinolones, and even glycopeptides are becoming less reliable for CSOM treatment, highlighting the need for targeted therapy based on local resistance patterns.[14] In contrast, Saikumar et al. from India reported antimicrobial resistance patterns among Gram-negative bacilli (GNB), with the utmost resistance observed for ampicillin (45%), amoxicillin-clavulanic acid (25%) and cefazolin (25%). Resistance rates for ceftazidime, cefixime, and cefotaxime were each 18%, while ceftriaxone and co-trimoxazole exhibited 16% resistance. Lower resistance was noted for ciprofloxacin (14%), gentamicin (12%), piperacillin-tazobactam (9%), meropenem (9%), and amikacin (4%).[21]

This variability in microbial distribution across different studies reflects regional variances, which may be influenced by multiple factors such as climate, healthcare practices, and antibiotic usage patterns. The cases which did not show any growth (5.7%) might be a reflection of viral infection or organism resistant due to biofilm production. Moreover, the reliability of history of prior antibiotic use (83% cases with polymicrobial growth and 95% cases without any exhibited growth) might be a limitation of this result, as supported in an Indian Study where 80% resistant cases had a history of prior antibiotic use.[22]

Emerging resistance to antibiotics poses a challenge in management of such cases. In Pakistan, the limited availability of broad-spectrum antibiotics in topical forms worsens resistance issues. While Ciprofloxacin is widely accessible, drugs like Vancomycin are restricted to systemic use, reducing topical treatment options. Being a single-center study, with a smaller sample size the findings may limit generalizability for a broader population. Moreover, the lack of longitudinal data precludes the assessment of resistance trends over time. Molecular studies should be accompanied in future studies to identify resistance genes.

## Conclusion

The commonly isolated organism, Pseudomonas aeruginosa showed fluoroquinolone and aminoglycoside susceptibility. While Staphylococcus aureus remained sensitive to glycopeptides and oxazolidinones. Expanding effective topical formulations, strengthening antibiotic stewardship and improving healthcare access for less privileged societies are fundamental for better management.

**Ethical Approval:** The IRB/EC approved this study via letter no. SGQH-5306 dated March 14, 2024.

**Conflict of Interest:** None

**Funding Source:** None

## Authors' Contribution

**MA:** Conception.

**JH, RB:** Design of the work.

**MZK, SMS, ZM:** Data acquisition, analysis, or interpretation.

**MZK, JH, RB, ZM:** Draft the work.

**MA, SMS:** Review critically for important intellectual content.

All authors approve the version to be published.

All authors agree to be accountable for all aspects of the work.

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