ABSTRACT

Respiratory tract infection is the most common acute illness in pediatrics, ranging from self limited infection like common cold to life threatening infections like pneumonia and epiglottitis. Respiratory disease have over taken diarrhea as most frequent cause of death among children in developing countries with *Streptococcus pneumonia* being one of the most pathogenic species. The prevalence of various bacteria differs from region to region, different seasons and different age group. Most of the acute RTI respond well to antibiotics, however over use and misuse of antibiotics for upper RTI in children is wide spread, leading to résistance. Therefore it is necessary to study the susceptibility pattern of these isolates to routinely used antibiotics.

This study was carried out in SRM hospital in children of age group 0 to 14 years presenting chief complaints of respiratory tract infection (RTI). In URI, for patients with tonsillitis and pharyngitis, throat swab was taken. In LRI, sputum, Pleural fluid, Tracheal aspirate was collected. In children with pneumonia, in addition to sputum, blood was also collected. All the samples were processed according to standard microbiological protocol. Antibiotic sensitivity testing was carried by Kirby Bauer’s disc diffusion method, according to CLSI guidelines. MIC testing and Macrolide resistant gene detection was done for Erythromycin resistant isolates.
In URI, 36.28% (156/430) was positive for bacterial growth and *S. pyogenes* was the most common isolate 14.9% followed by GGS 8.8%, GCS 6.7% and *Staphylococcus aureus* 4.2%. There were 4 isolates of *Moraxella catarrhalis*, 2 isolates of *Hemophilus influenzae* and 1 isolate of *Streptococcus pneumoniae*. Total Bacterial isolates from 320 cases of LRI was 23.4%(75) which included *Klebsiella pneumoniae* 5.3%(17), *Streptococcus pneumoniae* 6.6%(20), *Staphylococcus aureus* 3.7%(12), GAS 2.2%(7), *Hemophilus influenza* 1.6%(5), *E.coli* 1.6%(5) *Moraxella catarrhalis* 0.9% (3), *Pseudomonas aeruginosa* 0.6%(2), *Acinetobacter baumannii* 0.6%(2) and 1(0.3%) isolate of *Enterococcus faecium* was isolated. Among 32 blood samples taken from cases of Pneumonia, only 7(21.87%) were positive for bacterial culture which included 4 isolates were *S. pneumoniae*, and one each of GAS, GGS and *Enterococcus faecium*.

Detailed study was done on *S.pyogenes*. Double Disc diffusion test were performed for all Erythromycin resistant isolates. GAS showed 55% M type, followed by 40% cMLS and 5% iMLS. GCS showed equal number of cMLS and M type. GGS showed 54.54% cMLS followed by 36.36% Mtype and 9.09% iMLS. Detection of Macrolide resistance genes was attempted by multiples PCR in selected 11 GAS strains. 5 each of cMLS and M type resistance and 1 strain of iMLS type resistance were included in the study. Among 5 M type, 4 were positive for *mef* A gene, but 1 showed positive for *erm* B. All the 5 cMLS type were positive for *erm* B gene. The iMLS which came positive by Phenotypic method D test could not be proved by molecular method, as it gave negative for all 3 genes.
Among the 29 beta hemolytic streptococci typed, 24 GAS had 15 different emm types were identified: emm 12.40, emm 22, emm25.1, emm42, emm 65.1, emm 78.3, emm81.11, emm106, emm 113, emm118, emm118.5, emm124, emm152, emm183.2 and emm238.2. The four Group G Streptococcus were found to be stG6792.3, stG6792.2, stG6792 and Group C Streptococcus was found to be stC5345.1. Biofilm formation and Serum opacity factor was screened for all the 71 isolates of GAS by micro titer plate. 25/71 (29.6%) isolates showed positive for Biofilm formation and 38/71 (53.52%) isolates were positive of SOF production. According to 2X2 Fischer’s contingency table test, the association between SOF and Biofilm formation was statistically found to be highly significant and, the association between the Macrolide resistance and Biofilm formation was found to be statistically not significant.