CHAPTER 7

CONCLUSION

Respiratory tract infection is the most common acute illness affecting pediatric population. This study focused on bacterial causes of RTI which included URI and LRI which was found to be 30.8%. The study population consisted of children from low socioeconomic status, which reflects the poor nutritional status.

Among the positives, *Streptococcus pyogenes* was found to be the most prevalent bacterial causative 30.7%. Recurrent infection with *S. pyogenes* could lead to complications like Rheumatic fever, acute glomerulonephritis, endocarditis etc. Therefore a detailed study was focused on the virulence factors, the clonal typing and antibiotic resistance pattern of *S. pyogenes*. The virulence factor such as SOF factor and Biofilm formation was studied by phenotypic method. There was no significant relatedness in biofilm formation and macrolide resistance among the isolates. More macrolide sensitive isolates were found to be biofilm formers than the resistant strains. Virulence factors like SOF factor and biofilm formation showed significant relatedness.

In the detailed studies done on GAS, all the strains were found to be sensitive to Penicillin and beta lactam antibiotics, but macrolide resistance was found to be high. In D test for MLS typing of macrolide resistance; M type was most common followed cMLS type. In molecular study done by multiplex PCR for detection of Macrolides resistant gene, *Mef A* gene and *erm B* was detected, but no *erm A* was seen. Due to the increase in macrolide resistance in GAS in this population, the situation warrants screening of resistant phenotypes and judicious use of macrolide drugs. Macrolide resistance was found in other beta hemolytic
Streptococci GCS and GGS also. There are possible chances of lateral gene transfer from GAS to GCS and GGS, which shows similar Macrolides resistance.

*emm* typing of the isolates to detect the M protein which is a virulence factor of *Streptococcus pyogenes*, will contribute to future analysis for epidemiological purpose. A high degree of diversity among the *emm* type was noted, which indicates a challenge in production of multivalent M type specific vaccine for this region. Among the 30 strains typed, 15 different *emm* types of GAS, 3 types of GGS and 1 type of GCS were found. This reveals the circulation of varied clones in the population. The 26 valent Streptococcal vaccine under trial covered only two types of *emm* identified in this study (*emm* 12 and *emm*22). This shows that inorder to produce a suitable vaccine for a population, a detailed study of emm genes circulating in that particular population is necessary. 5 types of *emm* gene isolated in this study were not reported earlier from India from respiratory tract infection, ie *emm*22, *emm* 65.1, *emm* 78.3, *emm* 124, *emm* 238.1 and stC5345.1. Many emm types which are reported only from sites other than throat, are isolated from Throat swabs in this study. To conclude, the clonal diversity among *S.pyogenes* is very vast and this report suggest periodic survey needs to be stressed for proper bacterial control.

Among the 75 positives of LRI, the most common isolate was *Pneumococci* 26.6 % (20), followed by *Klebsiella pneumoniae* 22.7% (17), *Staphylococcus aureus* 16% (12), *Hemophilus influenzae* 6.7% (5), *E.coli* 6.7% (5), GAS 9.3% (7). *Moraxella catarrhalis* 3(4%) *Pseudomonas aeruginosa* 2.7% (2), *Acinetobacter baumannii* 2.7% (2) and GGS1.3% (1) and *Enterococcus faecium* 1.3% (1). Isolation of *H.influenzae* and Pneumococci from cases of LRI is of concern, despite the era of modern vaccination. At present Hib vaccine has been introduced in the routine immunization schedule in Tamil Nadu state and the study showed reduction in *H.influenzae* infection after 2010 and the Vaccination needs to be strengthened. 20 cases of *Streptococcus pneumonia* detected, shows the need to stress on vaccination for the same.