Conclusion

Fluoroquinolones are one of the most promising and encouraging contemporary anti infective chemotherapeutic agents exhibiting broad spectrum and potent activity. These agents have ideal properties such as excellent bioavailability, good tissue penetrability and a moderately low level of adverse and toxic effects. They have been found effective in the treatment of various infectious diseases, including urinary tract infection, gonococcal infections, osteomyelitis, enteric infections or respiratory tract infections, and as prophylaxis in neutropenic patients, surgery or to prevent spontaneous bacterial peritonitis in cirrhotic patients. They are the most commonly used oral antibiotics in this part of the world. This drug is frequently misused due to self medication, over the counter availability and suboptimal dose administration. This situation has led to the carriage of quinolone resistance within normal flora beside their wide dissemination in community settings as well as hospital environment. The present study provides an insight into different quinolone resistance mechanisms in Enterobacterial clinical isolates in southern region of Assam. The high prevalence of plasmid mediated quinolone resistant determinants in clinical and environmental isolates is at an alarming rate and poses a serious threat.

Thus the study may be concluded with the following comments:

- An overall fluorquinolone resistant phenotype was observed to be highest in respect of norfloxacin (66.9%). This higher rate is very alarming which suggests that a thorough review on quinolone therapy is need of the hour.
- Plasmid mediated quinolone resistance was the predominant mechanism, which poses the potential risk of horizontal expansion.
- Quinolone resistance determinants were also reported among environmental enterobacterial isolates. Presence of these plasmid mediated quinolone resistance determinants in environmental isolates particularly

aac(6) Ib-cr genes is indicative of its ability of persistence, thus causing potential health hazard. Proper measures should be adopted in public health and hygiene management so as to trace and prevent the propagation of these resistance genes within environmental reservoirs.

- The aac(6')-Ib-cr gene has spread rapidly among Enterobacteriaceae, and although only conferring a low-level resistance, it may create an environment facilitating the selection of more highly resistant determinants, especially those harboring topoisomerase mutations. So the presence of heterogeneous resistance mechanism can lead to worrisome condition at the nosocomial level and community acquired infection. So aac(6')-Ib-cr harboring strains should be promptly detected and reported so that the treatment with non-hydrophilic FQs, such as levofloxacin and ofloxacin may be initiated. Therefore, a gene specific treatment may be initiated and it will be a new approach to minimize treatment failure.
- To the best of our knowledge presence of *qnr*D in clinical isolates as well as environmental isolates this appears to be the first report from this country. Thus it underscores the necessity of molecular epidemiological investigation in this region. Isolates harboring *qnr*D and *aac(6')-Ib-cr* genes showed association with integron which played an important role in the capture and persistence of these genes which are broadly disseminated among diverse host ranges.
- The results of the present study suggest that acquisition of new pattern of mutations in *gyrA* and *parC* genes plays a significant role in the development of high-level resistance to quinolones among Enterobacteriaceae. Additional investigations are required to prevent the dissemination and emergence of newer mutations in community and nosocomial pathogens which may compromise future treatment options.

A unique finding of this study is the selection of plasmid mediated quinolone resistance determinants by the isolates with a bias towards particular group of quinolone antibiotics. This study demands urgent need for review in fluroquinolone therapy and their prophylactic use in both community and

hospital acquired infections. More molecular epidemiological investigations must be carried out to correlate the maintenance and persistence of resistance gene within a host when a quinolone treatment is initiated. Thus, the study presents a scenario of plasmid selection, host selection and plasmid host coselection due to quinolone stress and their role in horizontal expansion.

The present study provided an epidemiological, diagnostic and therapeutic insight into quinolone resistant enterobacteriaceae which will benefit public health management, infection control policy and future new drug discovery research.