

Abstract of the study

Worldwide emergence of drug resistant clones of *Escherichia coli*, for example ST131 is a global problem (Petty et al., 2014). This has grabbed the attentions of researchers and clinicians throughout the world. Based on different studies, it is believed that if urgent steps are not taken to combat these antimicrobial resistant infections, then such infections may lead to 10 million deaths annually by the year 2050 (O'Neill, 2016) of which 3 million deaths alone would be due to drug resistant *E. coli*. Huge studies implicate the requirement of worldwide global analysis, to have an idea of the underlying molecular adaptations these strains are undergoing, to delineate their rapid evolution, effect of selective pressures of different compounds present in the environment, which all contribute to their evolution and enable them to show such drug resistant phenotype. One such study, was undertaken in this thesis, to understand the genotypes (chromosomal and plasmid borne) and effect of selective pressures of heavy metals in influencing multidrug resistant phenotype. Our study has revealed presence of diverse array of resistance genes and active efflux which together play a fundamental role in conferring antimicrobial resistance in clinical *E. coli* strains isolated from Indian scenario. Since efflux was found functional strains with low MIC which did not harbor resistance genes, it would be appropriate to conclude that active efflux remains the primary mechanism for antimicrobial resistance in *E. coli*. Metals showed ability to promote horizontal gene transfer (HGT) of antibiotic resistance genes, which makes it worrisome as they may promote HGT of resistance genes present in environment from commensal and environment bacteria. The study showed plasmids play an important role in contributing and disseminating antibiotic resistance in *E. coli*.