CHAPTER 2
AIMS OF THE PROJECT
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Urinary tract infections (UTIs) are significant health problems, with *Escherichia coli* as the primary pathogen in proximally 80% of cases.

UTI is frequently encountered in patients with diabetes and in those with structural and neurological abnormalities, which interfere with urinary flow. Nosocomial UTI is common following instrumentation namely, catheterization and cystoscopy.

A number of virulence determinants facilitate the ability of UPEC to colonize the urinary tract enabling them to survive and grow in urine and other extraintestinal environments and exert cytopathic effects.

Recently UTI has become more complicated and difficult to treat. Clinical experience has indicated the presence of numerous cases resistant to conventional chemotherapy. Microbial resistance rates to commonly prescribed antibiotics have increased recently.

Updated knowledge of the prevailing causal bacteria and their susceptibility patterns is important for the proper selection and use of antimicrobial drugs and for the development of an appropriate prescribing policy. Extended spectrum β-lactamase (ESBL) producing organisms pose a major problem for clinical therapeutics. Due to rising antibiotic resistance among uropathogens, it is important to have local hospital based knowledge of the organisms causing UTI and their antibiotic sensitivity patterns.

This information would be relevant not only to the local hospital but would also be a vital regional database.
The general aim of the work in this thesis was
• To identify the Uropathogenic and Enteropathogenic *Escherichia coli* from clinical samples.

The specific aims were
• To understand the different virulence markers and describe their functions.
• To compare the pathogenicity of UTI and diarrhoeal isolates of *E.coli* with respect to various identifiable markers, namely serotyping and Congo red binding.
• To characterize strains of *E.coli* using four proposed virulence factors namely hemolysin, haemagglutinin, cell surface hydrophobicity and serum resistance and compare the two pathogenic groups of *E.coli*.
• To demonstrate the multiple drug resistance in *E.coli* isolated from clinical samples and to evaluate screening procedure for ESBL.
• To identify the genetic variability of the isolates by performing whole cell protein profiles.