**Introduction**

*Escherichia coli*, one of the first enteric bacilli to be described and cultured, is a normal inhabitant of the intestinal tract of humans and animals\(^1\). Even after more than a century after its discovery, there still exist misconceptions regarding the various strains of *E. coli* and the infections that they cause. There is a significant genetic diversity between different strains. Such differences determine whether strains are able to cause disease and, if so, whether they can cause gastroenteritis or extraintestinal infection. From a genetic and clinical perspective, *E. coli* strains of biological significance to humans may be broadly categorized as (1) commensal strains, (2) intestinal pathogenic strains, and (3) extraintestinal pathogenic strains\(^2\).

Extraintestinal infections (EIs) due to *E. coli* are common in all age groups and can involve almost any organ or anatomical site. Typical EIs include urinary tract infection (UTI), meningitis (mostly in neonates and after neurosurgery), diverse intra-abdominal infection, pneumonia (particularly in hospitalized and institutionalized patients), intravascular-device infection, osteomyelitis, and soft-tissue infection. Bacteremia can accompany infection at any of these sites.\(^3\) Extraintestinal pathogenic *E. coli* (ExPEC) strains have acquired genes encoding diverse virulence factors that enable them to cause infections outside of the gastrointestinal tract, in both normal and compromised hosts. Characteristic virulence traits that are present in most ExPEC include various adhesins (e.g. P and type I fimbriae), factors to avoid or subvert host defence systems (e.g. capsule, lipopolysaccharide), mechanisms for nutrient acquisition (e.g. siderophores), and toxins (e.g. hemolysin, cytotoxic necrotizing factor).\(^4\)

In recent years, extraintestinal *E. coli* infection and a high level of drug resistance among such ExPEC is often seen in India. Physicians have noticed patients suffering with extraintestinal *E. coli* infections showing features of systemic inflammatory response syndrome, organ failure, features of HUS and ARDS. The treatment of *E. coli* infections is increasingly becoming difficult because of the multi-drug resistance exhibited by the organism. As multi-drug resistance has spread, we are already coming across infections that cannot be cured with any available antibiotics. The progression of antimicrobial resistance among microorganisms is both unavoidable and persistent, and the key factors are misuse of antimicrobials to treat human and animal infections.
Several Indian studies (Sharma et al., Raksha et al., Naveen et al.) have characterized the ExPEC isolates based on their phenotypic properties but none of the studies have included molecular characterization of the virulence traits of such strains. Although several Indian studies (Goyal et al., Mohamudha et al., Deshpande et al.) did molecular characterization of antimicrobial resistance genes, none of the studies have addressed clinical outcome adequately. However, extensive laboratory data (Johnson et al., Drews et al.) as well as clinical data supported by molecular methods are available on the virulence and resistance of ExPEC from developed countries. From a developing country like India where there is limited data regarding the exact role of virulence traits of the infecting extraintestinal E.coli strains, we wanted to correlate the phenotypic and genotypic characteristics of extraintestinal E.coli virulence genes, their ability to develop multidrug resistance and clinical outcome of patients infected by such strains. The knowledge of clinical details, virulence properties, the drug resistance patterns of ExPEC strains in a geographical area will help in the formulation of an appropriate hospital antibiotic policy which can assist clinicians in controlling these infections. Hence we proposed to conduct a clinic-microbiological study of extraintestinal pathogenic Escherichia coli strains isolated from patients admitted in tertiary care hospitals at Mangalore.