1. INTRODUCTION

*E. coli* is commensally growing bacteria found in human as well as animals. In humans, they are the major facultative aerobic organism residing in the intestine, typically with around $10^6$ to $10^9$ colony forming units per gram of stool (Adriana et al., 2012). The organism is also found in soil and water, usually as a result of fecal contamination but the pathogenic variants can cause various types of infection including gastroenteritis, urinary tract infection, meningitis, peritonitis and septicemia (Adrienne et al., 2002; Ahemed et al., 2006). Treatment to this infection is complicated due to emergence of multi drug resistance among pathogenic variants. In last 20 years of time span major increases in emergence and spread of multidrug-resistant bacteria and increasing resistance to antibiotic groups, such as fluoroquinolones and certain cephalosporins (Akram et al., 2007).

The β-lactams antibiotics, in combination with amino glycosides, are among the commonly prescribed antibiotics which are major part of empirical therapy. Because of injudicious and unnecessary use in developing countries, resistance to these drugs has become a major problem. A feature in the emergence of multidrug-resistant Gram-negative bacilli is the production of extended-spectrum β-lactamases (ESBLs) and enzymatic modification of amino glycosides, which are responsible for resistance to β-lactams antibiotics and amino glycosides, respectively (Alam et al., 2006). *CMY, CTX-M, and NDM* types of β-lactamase are mostly responsible for the emerging resistance to the β-lactams antibiotics among *E. coli* (Barry et al., 2011). The β-lactam antibiotics, especially the cephalosporin’s and b-lactam-b-lactamases inhibitor combinations are major drug classes used to treat
infections caused by *E. coli* (Adriana *et al*., 2012). Among *E. coli*, β-lactamase production remains the major contributing factor to β-lactam resistance. Extended spectrum β-lactamases are one of the major sources of resistance to oxyimino-cephalosporins in Enterobacteriaceae (Adrienne *et al*., 2002).

Most of ESBLs are mutants of TEM and SHV enzymes, but *CTX-M* enzymes are the newly emerging ESBLs (Ahemed *et al*., 2006) and are increasingly prevalent worldwide among *E. coli* bacteria. The *CTX-M* enzymes are wide group with more than 30 alleles categorized into five distinct phylogenetic groups, evolved because of genetic escape and mutation of the chromosomal beta-lactamase genes of *Kluyvera* spp (Adrienne *et al*., 2002; Ahemed *et al*., 2006). The *CTX-M* family, first described in 1992 (Akram *et al*., 2007) is known as most dominant non-TEM, non-SHV ESBL among Enterobacteriaceae.

*Escherichia coli* (*E. coli*) are a Gram-negative, facultatively anaerobic, coliform bacterium of the class *Escherichia* that is normally found in the lower digestive tract of warm-blooded living beings (endotherms). Most *E. coli* strains are non pathogenic; however some serotypes can cause actual nourishment harming in their hosts and are at times in charge of item reviews because of food contamination. The non pathogenic strains are a part of the normal flora of the gut and can yield their hosts by producing vitamin K2 and avoiding colonization of the digestive tract with pathogenic microscopic organisms having a harmonious relationship. *E. coli* is ousted into nature with fecal matter. The bacterium develops extremely in fecal
matter under oxygen consuming conditions for 3 days, however its numbers decay gradually afterwards.

*E. coli* and other facultative anaerobes constitute around 0.1% of gut flora, and fecal–oral transmission is the real course through which pathogenic strains of the bacterium cause illness. A developing assortment of research has examined naturally relentless *E. coli* which can obtain by for widen periods outside a host.

The bacterium can be developed, cultured effectively and rationally in a research center setting, has been seriously examined for more than 60 years. *E. coli* is a chemoheterotroph whose synthetically characterized medium must incorporate a source of carbon and energy (Bekele et al., 2014).

*E. coli* is the most widely considered prokaryotic model living being, and an essential species in the fields of biotechnology and microbiology, where it has filled in as the host life for the recombinant DNA technology, under ideal conditions, it takes up to 20 minutes to replicate.

It is identified as a rapidly growing family of *ESBLs* that selectively prefer to hydrolyze cephotaxime and most of them are active against ceftazidime (Alam et al., 2006). Further the incidence of Urinary tract infections (UTI) by ESBL producing *E. coli* was found to be the highest in India (60%) followed by Hongkong (48%) and Singapore (33%) (Alvarez et al., 2004). Previous studies from India have reported ESBL production varying from 28 to 84% (Von Baum et al., 2005). On the whole prevalence of ESBL producers was found to vary in different geographical regions and in different institutes. *CTX-M* enzymes have been the predominant ESBLs in Argentina for >10 years (Balcha et al., 2014) and have prevalence in many
parts of the world (Ahemed et al., 2006; Baraniak et al., 2003), including Europe (Barnes et al., 2003; Barry et al., 2011). Therefore in the present study we are predominantly focusing on prevalence of \textit{CTX-M ESBL} producing \textit{Escherichia coli} in our region.

Generally \textit{E. coli} strains don't cause disease (Global Association of Institutionalization, 2005), however harmful strains can cause gastroenteritis, urinary tract contaminations, neonatal meningitis, hemorrhagic colitis. Normal symptoms and indications incorporate extreme stomach spasm, looseness of the bowels, hemorrhagic colitis, retching and sometimes fever. In rare cases, pathogenic strains are likewise in accuse of guts rot (tissue demise) and puncturing without advancing to hemolytic-uremic disorder, peritonitis, mastitis, septicemia and pneumonia. Children are more susceptible to develop serious illness like hemolytic uremic disorder to the serious outcomes that may appear because of person infected with \textit{E. coli}. A few strains of \textit{E. coli} for instance 0157:H7 can deliver Shiga toxin. This toxin further leads to annihilation of the red platelets, which at that point stop up the body's separating structure, the kidneys, causing hemolytic-uremic disorder (HUS).Unlike commonly \textit{E. coli} that normally live in the gut, the Shiga toxin that causes inflammable reactions in target cells of the gut. In some uncommon cases (typically in kids and the elderly) Shiga toxin developing \textit{E. coli} infection may prompt hemolytic uremic disorder (HUS), which can cause kidney disorder and even death. Signs of hemolytic uremic disorder include weaken recurrence of urination, laziness and paleness of cheeks and inside the lower eyelids. In 25\% of HUS patients, entanglements of sensory system occur, which thus causes strokes because of little clot of
blood vessels in the brain, this causes the body parts controlled by this area of the brain not to work properly. Furthermore, this strain causes the development of fluid (during erratic kidney function), leading to edema around the lungs, legs and arms. This increase in fluid development particularly around the lungs hinders the functioning of the heart, causing an increase in blood pressure.

These enzymes (ESBL) have been identified in large numbers and from different regions worldwide, are significantly detected in various *E. coli* strains (Alvarez *et al.*, 2004). Due to reduced antibiotic alternate for infections caused by MDR-ESBL-producing bacteria, designing an empirical drug therapy is needed, thus antibiotic profiling will provide a guideline for proper choice of the same.

The species of *E. coli* is serologically separated in serogroups and serotypes based on its antigenic nature (substantial or O antigens, flagellar or H antigens for serotypes). Numerous strains express a second class of antigens (capsular or K antigens) are utilized as a part of serotyping. The species involve intestinal and extraintestinal pathogens. The intestinal pathogens are otherwise called diarrheagenic *E. coli* (DEC) of which six classes have been portrayed: Enteropathogenic *E. coli* (EPEC), shiga toxin producing *E. coli* (STEC) or verocytotoxins- producing *E. coli* (VTEC), enterotoxigenic *E. coli* (ETEC), enteroinvasive *E. coli* (EIEC), enteroaggregate *E. coli* (EAEC) and diffusely adhering *E. coli* (DAEC) (Kaper *et al.*, 2004; Nataro *et al.*, 1998). The extraintestinal pathogens (EXPEC) are more predominant strains incorporate those related with urinary tract infections (UPEC), neonatal meningitis (MAEC) and bacteremia.
Deliberate O serotyping of E. coli started in the mid 1930s (Nataro et al., 1998) and numerous investigations demonstrated that the O serotype of E. coli are majorly associated with pathogenesis (Wang et al., 1998). O serotyping wound up critical devices to characterize E. coli in clinical settings. It has been indicated repeatedly that antigenic typing of E. coli is valuable in epidemiological investigations (Blanco et al., 2006b).

Advances in examining and computational innovations for biosciences have been altering natural research. In last few years have seen the development of a few exceptional trial strategies, for example, DNA sequencing procedure, DNA microarray etc.

As showed by the sequencing of in excess of 1000 genomes of regular plasmids, organelles, infections and viroids, microscopic organisms, plants and creatures, including mouse (Alam et al., 2006) and human (Alvarez et al., 2004; Von Baum et al., 2005), there are hardly a few, innovative methods in obtaining the hereditary data of any living being. Although it suggests for basic applications, such data assures to convey us more like a finish understanding on how the hereditary data put away in a genome decides the practices (i.e., the phenotype) of a life form or a cell in a specific condition.

Coherent subsequent stages to recognize the qualities in a genome and to decide their capacities, specifically, by clarifying what items these qualities create and how these items associate with each other. For a specific organic framework, these downstream examinations can be requests of extent more unpredictable than sequencing the genome. To be sure, they require a wide range of devices to describe singular quality items by utilizing
biochemical, biophysical, or hereditary systems or a vast set of such sub-atomic segments by profile quality articulation at the mRNA level-utilizing DNA microarray (Adriana et al., 2012) or at the protein level-utilizing two-dimensional protein gels (Adrienne et al., 2002) or mass spectrometry (Balcha et al., 2014; Baraniak et al., 2002; Barnes et al., 2003).

Strain typing is an epidemiologically essential instrument not just to detect the cross transmission of nosocomial pathogens yet in addition for deciding the origin of infection (Balcha et al., 2014). Accessible sub-typing methods for E. coli incorporate pulse field gel electrophoresis (PFGE), plasmid profiling, ribotyping and polymerase chain response (PCR) - based typing methodology, for example, Enterobacterial Repetitive intergenic consensus (Baraniak et al., 2002). The present investigation was conveyed out to decide the hereditary assorted variety of various β-lactamase creating multidrug-safe (MDR) E. coli strains utilizing ERIC-PCR in a clinical setup. In the present scenario, pharmaceutical and biomedical sectors are facing the challenges of continuous increase in the multidrug-resistant (MDR) human pathogenic microbes. Antibiotic resistance profiles lead to fear about the emergence and reemergence of multidrug-resistant (MDR) pathogens and parasites. The main objective of this study was to disclose evolving trends of emerging antibiotic resistance in Gulbarga region. There are numerous methods of typing of organism and along with passage of time novel methods are being introduced. Molecular techniques hold great promise for detection of susceptibility and resistance to antimicrobial agents. To assess genetic diversity within the genus of E.coli, a diversity of methods has been employed. Analysis of a chromosome or extra chromosomal DNA, allow
direct comparison of genotypes between strains. Standard PCR with amplicon sizing by gel electrophoresis are especially useful for identifying genes with genetic resistance.

❖ OBJECTIVES

In the view of above we have planned the following objectives

- Isolation of and Screening of *E. coli* from clinical samples
- Characterizations of the isolates by conventional methods
- Isolation of Multi drug resistant *E. coli* through antibiogram and minimum inhibitory concentration
- Molecular typing of *E. coli* and Biocomputational analysis of *E. coli* strains