



GENOTYPIC STUDY OF UROPATHOGENIC ESCHERICHIA COLI STRAINS FIMH GENE ISOLATED FROM PATIENTS WITH URINARY TRACT INFECTION

Microbiology

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ABSTRACT

Our aim is to study the genotypic of uropathogenic Escherichia Coli strains isolated from patients with urinary tract infection by using PCR methods. Urinary tract infection is one of the most common infections among male and female of all age groups affecting 150 million people worldwide. This study was carried out in the Department of Microbiology, Meenakshi Medical College Hospital and Research Institute, Kanchipuram from March 2017 to March 2018. Totally 500 urine samples were collected and among these 280 were culture positive, out of which females were 221 and male were 59 of varying age groups between 0 – 70 yrs of age. Out of 500 urine samples collected 280 were culture positive. Among them 221 were females and 59 were males. *E. Coli* was significantly present in culture compared with other Bacteria. This study emphasizes the fact that genotypic pattern of UTI can guide the clinicians in choosing the right antibiotics for treatment so that misuse of antibiotics may be prevented.

KEYWORDS

Urinary Tract Infection, *E. Coli*, Genotypic pattern of UTI

I. INTRODUCTION

Urinary tract infections (UTIs) account for about 30%-40% of all hospital associated infections and are important since they increase mortality, and morbidity, duration of hospital stay and health costs^{1,3}. The most important risk factor for developing a UTI is urinary catheterization. It is estimated that 15%-25% of all the patients hospitalized in health centers undergo urinary catheterization at least once during their hospital stay and it is reported that the frequency of urinary catheterization has increased in the past 20 years.

Patients admitted to intensive care units (ICU) are the most appropriate candidates for UTIs due to their more frequent necessity of urinary catheterization and longer duration of catheter use^{1,2,3,4}.

Perineal care after indwelling urinary catheter insertion is important for the prevention of catheter associated urinary tract infection (CAUTIs) because the incidence of bacteriuria increases among patients with indwelling urinary catheters who have bacterial colonization around the urinary tract.

Early diagnosis and rapid administration of antimicrobial therapy to patients with UTIs has been shown to reduce mortality and morbidity⁵. The choice of antimicrobial therapy for septicemia must therefore include knowledge of the extent of resistance among common pathogens associated with CAUTIs.

Hence, this study was conducted to investigate the frequency of bacterial pathogens causing intra vascular catheter associated UTIs in our hospital and their antibiotic sensitivity pattern.

II. MATERIALS AND METHODS

The present study was carried out period from March-2017 to April 2018 in MMCH&RI Kanchipuram. Ethical clearance was obtained from institution ethical committee samples were collected from various ICUs and processed.

Study period: March -2017 to March -2018

INCLUSION CRITERIA: Adult patients admitted to ICU's who have been catheterized for more than 48 hrs showing clinical signs of sepsis including signs of urinary tract infection, Lower abdominal pain & burning micturition, Fever, Hypothermia, chills, rigors, hypotension tachycardia and achypnea.

EXCLUSION CRITERIA: All catheterized patients in ICU's without any signs of sepsis.

Collection of urine: It was collected by standard aseptic procedures

PCR Technique:

PCR is the ability to monitor the progress of the PCR as it occurs (i.e. in

real time). Data is therefore collected throughout the PCR process, rather than at the end of the PCR. This completely revolutionizes the way one approaches PCR based quantitation of DNA and RNA. In real-time PCR, reactions are characterized by the point in time during cycling when amplification of a target is first detected rather than the amount of target accumulated after a fixed number of cycles. The higher the starting copy number of the nucleic acid target, the sooner a significant increase in fluorescence is observed. In contrast, an endpoint assay (also called a —plate read assay) measures the amount of accumulated PCR product at the end of the PCR cycle.

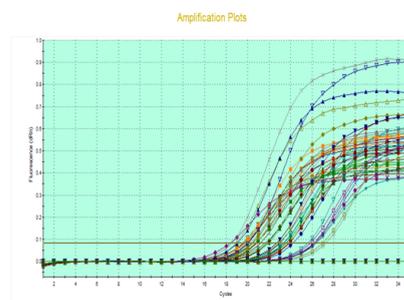
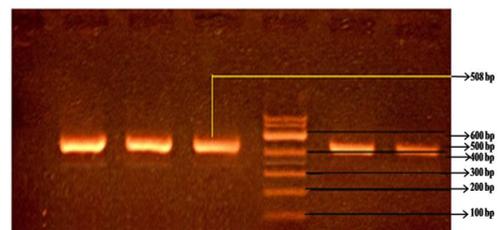
III. RESULTS

Detection of fimH gene in Escherichia coli by PCR amplification

All the bacterial isolates were identified using biochemical tests and screened by PCR. The fimH gene was amplified using specific primers and appeared as a band of about 508 bp on polyacrylamide gel (Figure.1). The FimH gene was found in 87 isolates out of 100 isolates.

Primer name	sequence (5'-3')	Gene Bank data base
fimH	TGCAGAAAGGATAAGC CGTGG	KJ190185
fimH	GCAGTCACCTGCCCTCC GGTA	

FIGURE.1. fimH gene band



I. DISCUSSION

Uropathogenic *E. coli* strains have many virulence factors which enhance their capacity to colonize in the urogenital tract. Attachment to the urothelial cell surface is mediated by FimH adhesion, placed at the tip of the type 1 fimbriae, which prevents bacterial washout by urine flow and starts bacterial invasion. Since the FimH virulence factor associated with UTI cases was not widely determined from the UPEC isolated from ICU patients, Iran, the prevalence of the fimH gene was examined.

The presence of the fimH gene was confirmed by PCR and the results indicated that the fimH gene was present in 87 of the 100 isolates of hospitalized ICU patients. This showed that most of the UPEC strains had the fimH gene with 508bp and our results were almost in accordance with the results of previous literature. Tarchouna et al.⁶ reported that among the studied virulence genes of UPEC strains, the fimH gene was the most prevalent virulence gene and was found in 87% of the UTI isolates. Garofalo et al.⁷ studied 18 UPEC isolates collected from females and found that the fimH gene was the most prevalent virulence factor and 100% of the isolates had that gene. In another study, Watts et al.⁸ demonstrated that the fimH gene was the most frequent virulence gene and was detected in 98% of *E. coli* strains isolated from patient with UTIs. Mladin et al.⁹ evaluated the distribution of virulence genes among the studied UPEC and showed that the prevalence of different virulence genes varied from 10% for the cnf gene to 80% for the fimH gene. In addition, Arabi et al.¹⁰, investigated the frequency of FimH and other adhesions genes in UPEC and determined the fimH gene frequency as 87.7%.

II. CONCLUSION:

In the present study we recommend for the multicentric, large scale study in various geographical locale, on the prevalence and antibiotic resistance pattern of *E. coli* both in genotypic method and surveillance study to know the epidemiological pattern and to formulate antibiotic policy as well as infection control measures against these infections.

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