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Research Article

SCREENING OF MULTI DRUG RESISTANT *ESCHERICHIA COLI* FROM URINARY TRACT INFECTED PATIENTS

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ABSTRACT
Antimicrobial drug resistance is one of the major threats due to widespread use of antimicrobial drugs in general population and has been increasing in clinical significance over recent years. The prevalence of resistance to antibiotics by *Escherichia coli* is con current. A total of fifty samples were obtained from urinary tract infected patients, out of which 25 isolates of *Escherichia coli* were isolated and confirmed. All the strains were found to exhibit multiple antibiotic resistance patterns to eight antibiotics used. The present study was undertaken to accomplish isolation and characterization of multidrug resistant *Escherichia coli* and to assess the current resistant patterns of multidrug resistance among urinary isolates of *Escherichia coli*. 8 antibiotics were studied using disc diffusion Method. All the isolates were highly resistant to Tetracycline and resistant to Trimethoprim, Ofloxacin, Penicillin G, Amphicillin, Streptomycin and chloramphenicol. Many of the isolates were susceptible to Rifampicin, only 4% resistance was observed. The results demonstrate that the antimicrobial resistance of multi drug resistant *Escherichia coli* which may become endemic to the hospital environment day by day and may complicate the therapeutic management.
Key words: *E. coli,* Multidrug resistant, Urinary Tracts Infections, Antibiotics.

INTRODUCTION

Urinary tract infection remains one of the most common bacterial infections and second most common infectious disease in the community practice[9]. Approximately about 150 million people were diagnosed with urinary tract infection each year. In present scenario, the essence of antimicrobial drug resistance of major uropathogens has posed a global threat[1]. *E. coli* is a gram negative, facultative anaerobic, typically rod-shaped bacteria[8]. The pathogens causing UTIs are almost always predictable, with *Escherichia coli* the primary etiologic agent among both outpatients and inpatients[5]. Bacterial infections are usually treated with antibiotics. However, the antibiotic sensitivities of different strains of *E. coli* vary widely multi-drug resistant strains prevalent in both human and animal isolates in different parts of the world[3, 6, 7]. In the last few decades, the frequency and spectrum of antimicrobial-resistant infections have increased both in hospital and the community[2]. Antimicrobial resistance resulting in increased morbidity, mortality and health-care costs[4]. The spread of microbial drug resistance is a global public health challenge, which impairs the efficacy of antimicrobial agents and results in substantial increased illness and death rates. The resistance genes scattered throughout the bacterial kingdom and mechanisms have evolved. The emergence of *Escherichia coli* isolates with multiple antibiotic-resistant phenotypes, involving co resistance to four or more unrelated families of antibiotics has been previously reported and is considered a serious health concern.

MATERIAL AND METHODS

Culture collection and sampling

The present study included twenty five bacterial isolates out of fifty were obtained consecutively from clinical specimens in wards of hospital of tertiary care hospital of Tiruchirappalli, Tamilnadu, India. Among the 25 samples tested, 9 samples are from vaginal swabs, 16 samples from Urine (mid-stream) all are from patients suffering from urinary tract infections.

Isolation and identification of the bacteria

Clinical samples were subjected to bacteriological investigation; swabs were inoculated on Eosin - methylene blue (EMB) agar, Mac Conkey agar at 37°C overnight. Isolates that produced dry, pink colonies on Mac Conkey agar and green metallic sheen colonies on EMB were considered to be *E. coli* and maintained at 4ºC. Single colony per sample with a typical *E.coli* morphology was recovered and identified by classical biochemical methods. All the twenty five bacterial strains were subjected to different cultural and biochemical tests specific for *E.coli* according to the conventional laboratory procedures.

Antimicrobial susceptibility test

Eight antimicrobial agents were used in this study to determine the resistance pattern of identified *E.coli* by Kirby-Bauer method. The following antimicrobial disks namely Tetracycline, Trimethoprim, Rifampicin, Streptomycin, Ampicillin, PenicillinG, Ofloxacin, Chloramphenicol were tested against twenty five strains of *E.coli* and the diameters of the zones of growth inhibition were measured and expressed as diameter of the inhibition zones (mm).

RESULTS AND DISCUSSION

Urinary tract infection is one of the commonest bacterial infections. The Enterobacteriaceae are the most frequent pathogens detected, causing 84.3% of urinary tract infections[10]. The present study was conducted to achieve resistance profile of clinical isolates from hospitals against commonly prescribed antibiotics. A total of 50 samples were collected from patients with community acquired urinary tract infections. Identification was done on the basis of morphological, biochemical and phenotypic characteristics. All isolates were found to be Gram negative rods, biochemical tests confirmed that all the isolates were *E. coli* and twenty five of them were confirmed by plating on eosin methylene blue agar. The antimicrobial pattern of the tested strains showed multiple drug resistance to Tetracyline ,Trimethoprim, Rifampicin, Steptomycin, Ampicillin, Penicillin G, Ofloxacin, Chloramphenicol. Isolates showing intermediate levels of susceptibility were classified as

resistant shown in Table 1. Antibiogram for the *E.coli* isolates are shown in Figure:1 The data showed that isolates were resistant to Tetracyline-100% , Trimethoprim-72%, Rifampicin- 4%, Steptomycin, -44%, Ampicillin- 68%, Penicillin G- 76 % Ofloxacin- 80%, Chloramphenicol- 24% .The most effective *E.coli* species showing maximum resistance in the study were found to be Resistant for Tetracyline shown in figure 2. The incidence of antibiotic resistance profiles of *E. coli* evaluated in this study concludes that *E. coli* is one of the important causative agents of urinary tract infection most of the isolates showed multiple antibiotic resistance. Hence the multi resistance pattern indicates the existence of new strains prevailing in the community which results in the new drug resistance. The present study has identified the changing etiologic trends of urinary tract infections and predominant increase in development of antimicrobial resistance and suggests that adequate alternative therapy may be used to decrease the rate of resistance. Implementing antibiotic use strategies at all levels of the humans, will decrease the risk and the clinical threat of antimicrobial resistance due to use and misuse of antibiotics. Since antimicrobial resistance patterns are continually evolving and *E. coli* invasive isolates undergo progressive antimicrobial resistance, updated data on antimicrobial susceptibility profiles will continue to be essential to ensure the provision of safe and effective empiric therapies to prevent emergence and spread of antimicrobial resistance.

CONCLUSION

In recent years, *Escherichia coli* resistance has emerged as pathogens of significant clinical importance to public health. Indiscriminate use of antibiotics is the main factor resulting in this emergence, selection and dissemination of drug-resistant pathogens in human. There is a need for continuous surveillance of antimicrobial resistance trends worldwide particularly among organisms resident in the urinary tract of humans which are implicated in infectious diseases in human. Since antimicrobial resistance patterns are continually evolving *E.coli* invasive isolates undergo progressive antimicrobial resistance, continuously updated data on antimicrobial susceptibility profiles will continue to be essential to ensure the provision of safe and effective empiric therapies of antibiotic use Implementing antibiotic use strategies at all levels of the humans, will decrease the risk and the clinical threat by antimicrobial resistance due to use and misuse of antibiotics.

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Table 1: Multidrug resistant pattern of *Escherichia coli* to various antibiotics

Strain No	Source	Tetracyline 30mcg	Trimethoprim 5 mcg	Rifampicin 5 mcg	Streptomycin 10 mcg	Ampicillin 10 mcg	Penicillin G 10 mcg	Ofloxacin 5mcg	Chloramphenicol 30mcg
Ec1702	V	R	R	15	R	R	R	R	-
Ec1703	U	R	R	18	14	21	21	R	-
Ec1704	V	R	R	18	15	R	R	R	-
Ec1705	U	R	20	18	R	22	R	21	-
Ec1706	U	R	19	17	20	R	R	20	-
Ec1707	U	R	R	15	22	R	R	R	13
Ec1708	V	R	R	12	R	20	R	R	R
Ec1709	U	R	R	14	15	R	16	R	-
Ec1710	U	R	R	10	7	20	5	R	R
Ec1711	U	R	R	R	R	5	16	14	R
Ec1712	V	R	R	10	R	R	R	R	R
Ec1713	U	R	R	12	R	R	R	R	-
Ec1714	V	R	R	13	5	R	R	R	-
Ec1715	V	R	4	17	R	R	R	R	-
Ec1716	V	R	4	20	22	17	R	R	-
Ec1717	V	R	R	14	R	R	R	R	-
Ec1718	U	R	R	17	13	R	19	R	-
Ec1719	U	R	R	14	19	R	R	R	R
Ec1720	U	R	15	15	R	R	R	R	R
Ec1721	U	R	R	13	16	R	R	R	-
Ec1722	V	R	R	14	19	R	R	R	-
Ec1723	U	R	R	14	R	13	13	R	-
Ec1724	U	R	5	13	R	R	R	R	-
Ec1725	U	R	R	13	16	R	R	15	-

Isolates showing resistant to three or more antimicrobials and defined as MDR, R-Resistant, - - No disk used- Urine samples, V-Vaginal Swab.

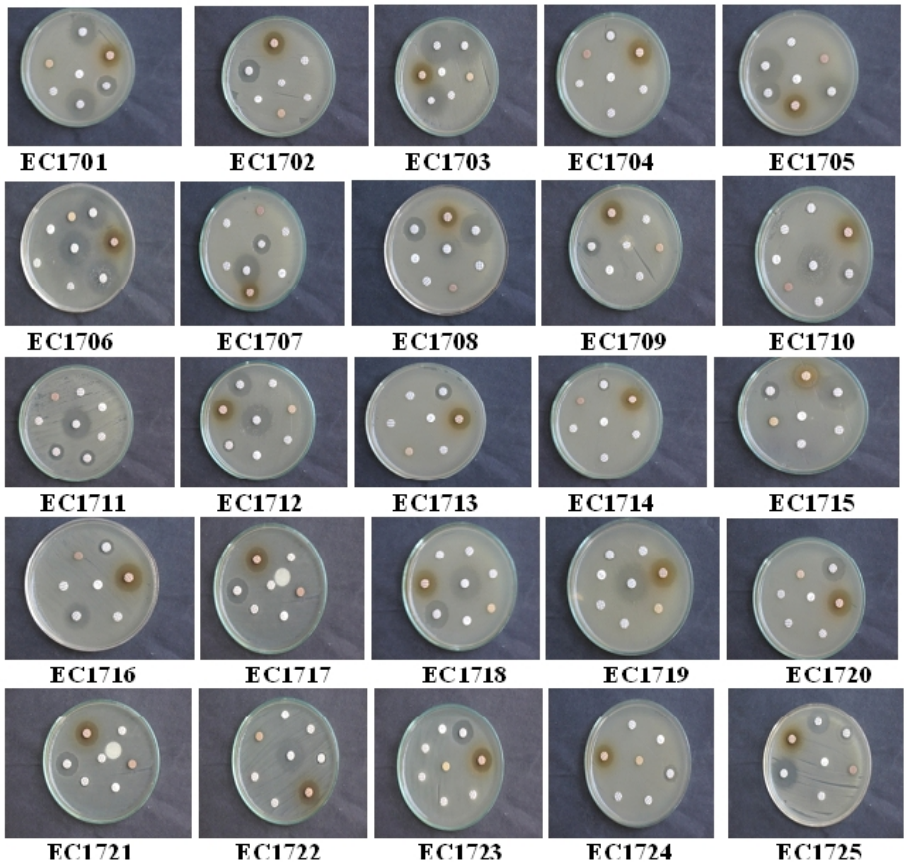


Figure 1: Antibiogram for the *E.coli* isolates

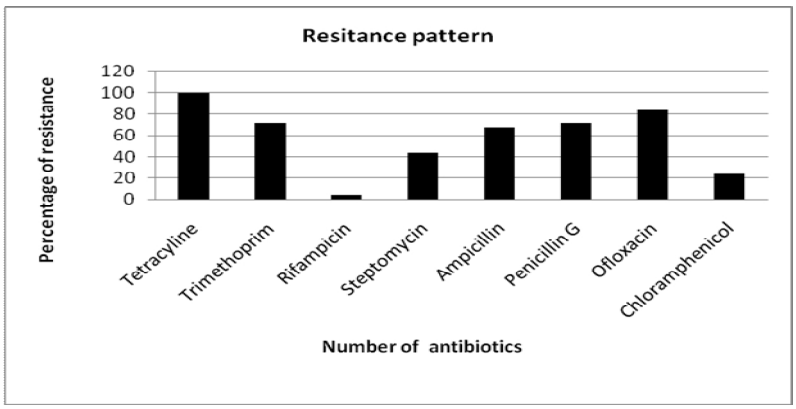


Fig.2 Resistance pattern of *E.coli* to different antibiotics

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