SCRENNING 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. Antibiotics were studied using disc diffusion Method. All the isolates were highly resistant to Tetracycline and resistant to Trimethoprim, Ofloxacin, Penicillin G, Ampicillin, 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. 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. E. coli is a gram negative, facultative anaerobic, typically rod-shaped bacteria. The pathogens causing UTIs are almost always predictable, with Escherichia coli the primary etiologic agent among both outpatients and inpatients. 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. The last few decades, the frequency and spectrum of antimicrobial-resistant infections have increased both in hospital and the community. Antimicrobial resistance resulting in increased morbidity, mortality and health-care costs. 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 4°C. 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. 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 Tetracycline, Trimethoprim, Rifampicin, Streptomycin, 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
Tetracycline 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
prevention of drug 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.

**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

| Table 1: Multidrug resistant pattern of *Escherichia coli* to various antibiotics |
|---------------------------------|-----------------|-----------------|---------------|-----------------|-----------------|-----------------|-----------------|
| Strain No | Source | Tetracyline 30mcg | Trimethoprim 5 mcg | Rifampicin 5 mcg | Steptomycin 10 mcg | Ampicillin 10 mcg | Penicillin G 10 mcg | Ofloxacin 5mcg | Chloramphenicol 30mcg |
| Ec7102 | V | R | R | 15 | R | R | R | - | |
| Ec7103 | U | R | R | 18 | 14 | 21 | 21 | R | - |
| Ec7104 | V | R | R | 18 | 15 | R | R | R | - |
| Ec7105 | U | R | 20 | 18 | R | 22 | R | 21 | - |
| Ec7106 | U | R | 19 | 17 | 20 | R | R | 20 | - |
| Ec7107 | U | R | 15 | 22 | R | R | R | 13 | |
| Ec7108 | V | R | R | 12 | 20 | R | R | R | |
| Ec7109 | U | R | R | 14 | 15 | R | 16 | R | - |
| Ec7110 | U | R | R | 10 | 7 | 20 | 5 | R | R |
| Ec7111 | U | R | R | R | 5 | 16 | 14 | R | R |
| Ec7112 | V | R | R | 10 | R | R | R | - | |
| Ec7113 | U | R | R | 12 | R | R | R | - | |
| Ec7114 | V | R | R | 13 | 5 | R | R | - | |
| Ec7115 | V | R | 4 | 17 | R | R | R | - | |
| Ec7116 | V | R | 4 | 20 | 22 | 17 | R | R | - |
| Ec7117 | V | R | R | 14 | R | R | R | - | |
| Ec7118 | U | R | R | 17 | 13 | R | 19 | R | - |
| Ec7119 | U | R | 14 | 19 | R | R | R | - | |
| Ec720 | U | R | 15 | 15 | R | R | R | R | |
| Ec721 | U | R | R | 13 | 16 | R | R | R | - |
| Ec722 | V | R | R | 14 | 19 | R | R | R | - |
| Ec723 | U | R | R | 14 | R | 13 | 13 | R | - |
| Ec724 | U | R | 5 | 13 | R | R | R | - | |
| Ec725 | 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.

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**REFERENCES**

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

![Antibiogram](image)

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

![Resistance Pattern Graph](image)

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