

## **PREVALENCE OF MDR ESCHERICHIA COLI ISOLATED FROM ALL CLINICAL SPECIMENS**

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### **Abstract**

**Introduction:** Today's, multi-drug resistance (MDR) among clinical isolates of bacteria such as *E. coli* pathotypes, is major healthcare problem and is associated with increased morbidity and mortality, worldwide. A rise in bacterial resistance to antibiotics complicates treatment of infections is major concern.

**Methodology:** This study was conducted in department of Microbiology at RKDF Medical College Hospital & Research Centre, SRK University, Bhopal, Madhya Pradesh. This study included 785 cases. Among all 140 were *Escherichia coli*. Out of 140 *Escherichia coli* 122 were MDR *Escherichia coli* and rest were normal. The duration of study was over a period of two years.

**Result:** The result of this study revealed that 87.2% MDR *Escherichia coli* found and rest were non MDR *Escherichia coli*.

**Conclusion:** This study concludes that ineffectiveness of antibiotic against the bacterial strain as in resistant pattern was observed, resulting in MDR. This is due to inappropriate antibacterial treatment & misuse of antibiotic.

**Keywords:** MDR, Antimicrobial susceptibility test, *Escherichia coli*

### **Introduction**

*E. coli*, being the leader of the Enterobacteriaceae bacterial family, is classified into different pathotypes, namely intestinal and extraintestinal, based on their varying levels of pathogenicity and associated clinical symptoms. The diarrheal diseases caused by specific pathotypes of *E. coli* in the intestinal tract, known as DEC (Diarrheagenic *E. coli*), encompass several types, including enteropathogenic *E. coli* (EPEC), enterohemorrhagic *E. coli* (EHEC), enterotoxigenic *E. coli* (ETEC), enteroaggregative *E. coli* (EAEC), enteroinvasive *E. coli* (EIEC), and diffusely adhering *E. coli* (DAEC). Additionally, there are extraintestinal pathotypes of *E. coli* that lead to infections beyond the gastrointestinal tract. These include uropathogenic *E. coli* (UPEC), *E. coli* associated

with newborn meningitis (NMEC), and *E. coli* associated with sepsis (SEPEC). [1] Presently, the emergence of multi-drug resistance (MDR) among clinical isolates of bacteria, including various *E. coli* pathotypes, has become a significant healthcare challenge globally. This issue is closely linked to heightened rates of illness and death. [2] While the traditional mode of acquisition and transmission of resistance in bacteria involves chromosomal mutations, it is worth noting that resistance genes can also be transferred through extrachromosomal elements obtained from other bacteria. These elements comprise various forms of mobile DNA segments, including plasmids, transposons, and integrons. This mechanism contributes to the dissemination and spread of resistance among bacterial populations [3]. Integrons are genetic structures that possess the ability to integrate or mobilize gene cassettes that carry antibiotic resistance determinants. These gene cassettes specifically encode information related to antibiotic resistance, allowing for the exchange and acquisition of resistance genes among bacteria. [4].

The occurrence of antimicrobial resistance in *E. coli* has been documented on a global scale. The escalating rates of resistance observed among *E. coli* strains pose a significant and mounting concern in both developed and developing nations. This issue underscores the need for comprehensive strategies to address and mitigate the growing threat of antibiotic resistance. [5-6]. The increasing bacterial resistance to antibiotics presents a challenge in the treatment of infections. In many cases, up to 95% of severe symptomatic cases are treated empirically without specific identification of the causative bacteria [7]. The occurrence and susceptibility patterns of *E. coli* exhibit notable geographical variations and significant differences among diverse populations and environments. These variations highlight the importance of understanding local resistance patterns and tailoring treatment approaches accordingly. [8]. In Ethiopia, a number of studies have been done on the prevalence and antimicrobial resistance patterns of *E. coli* from various clinical sources [9-10]. The aim of this study was to determine antimicrobial susceptibility of *E. coli* from clinical sources at Dessie Regional Health Research Laboratory. So, the aim of this study is prevalence of MDR *Escherichia coli* isolated from all clinical specimens.

#### **Material & Methods:-**

**Study Area:** This study was conducted in department of Microbiology at RKDF Medical College Hospital & Research Centre, SRK University, Bhopal, Madhya Pradesh.

**Study Population:** This study included 785 cases. Among all 140 were *Escherichia coli*. Out of 140 *Escherichia coli* 122 were MDR *Escherichia coli* and rest were normal.

**Study duration:** The duration of study was over a period of two years.

**Data collection:** All specimens were collected and transported to Microbiology Laboratory aseptically. All specimens were inoculated on Blood Agar & MacConkey or CLED Agar. With the help of the standard loop method, all urine specimens were inoculated on the CLED Agar. Subsequently, the culture plates were placed in an incubator and incubated at a temperature of 37°C for duration of 24 to 48 hours. After 24-48 hour all isolates were subjected to Gram staining to differentiate Gram positive bacteria from Gram negative Bacteria. Afterthat, all gram negative bacteria were subjected to biochemical reaction and antimicrobial susceptibility test. Then MDR were isolated as per CDC guidelines. MDR defined as acquired non-susceptibility to at least one

agent in three or more antimicrobial categories.[11]

**Data analysis:** Data were analysed by using Microsoft excel.

**Result:**

TABLE:1 Distribution of cases according to Total no. of samples

| Isolates       | No. | %     |
|----------------|-----|-------|
| E. coli        | 140 | 17.8% |
| Other isolates | 645 | 82.2% |
| Total          | 785 | 100%  |

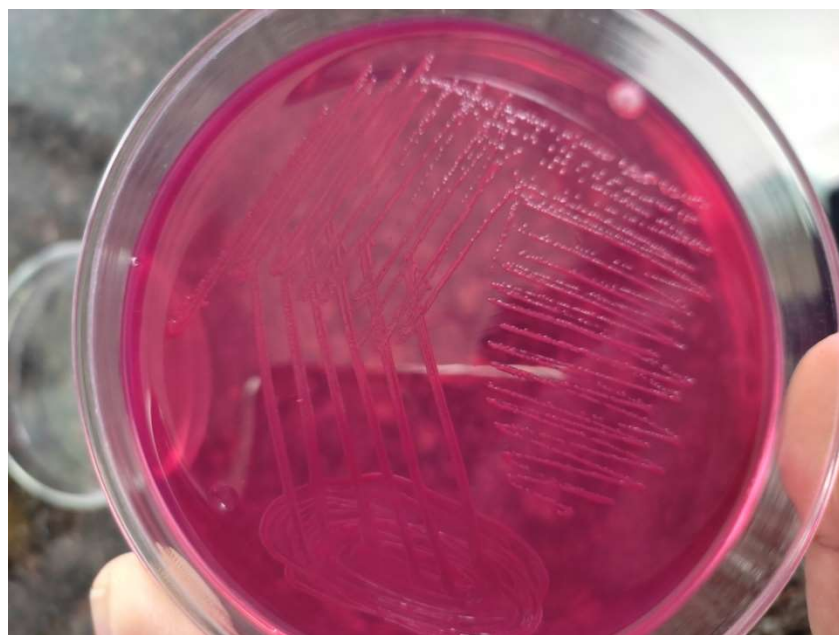
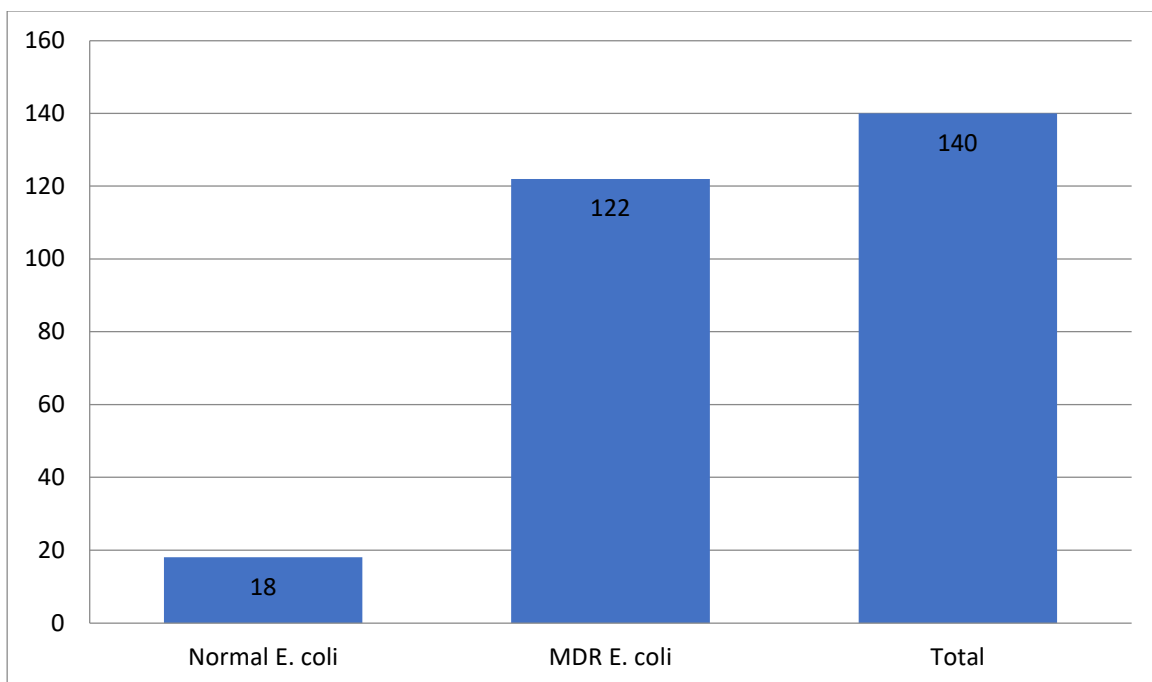


Fig:1 Lactose fermenting colonies of Escherichia coli

The above table illustrated that the distribution of isolates from all clinical samples. It was found that out of 785 cases, 140 cases of Escherichia coli and rest were found other isolates.

Fig 2:- This chart showing Distribution of cases according to MDR E. coli



The above pie chart explains that among the 140 E. coli, 87. 2% MDR Escherichia coli found and rest were non MDR E. coli.

TABLE:2 This table shows biochemical reactions of E coli.

|                |   |
|----------------|---|
| Identification |   |
| Catalase       | + |
| I              | + |
| MR             | + |
| VP             | + |
| C              | + |

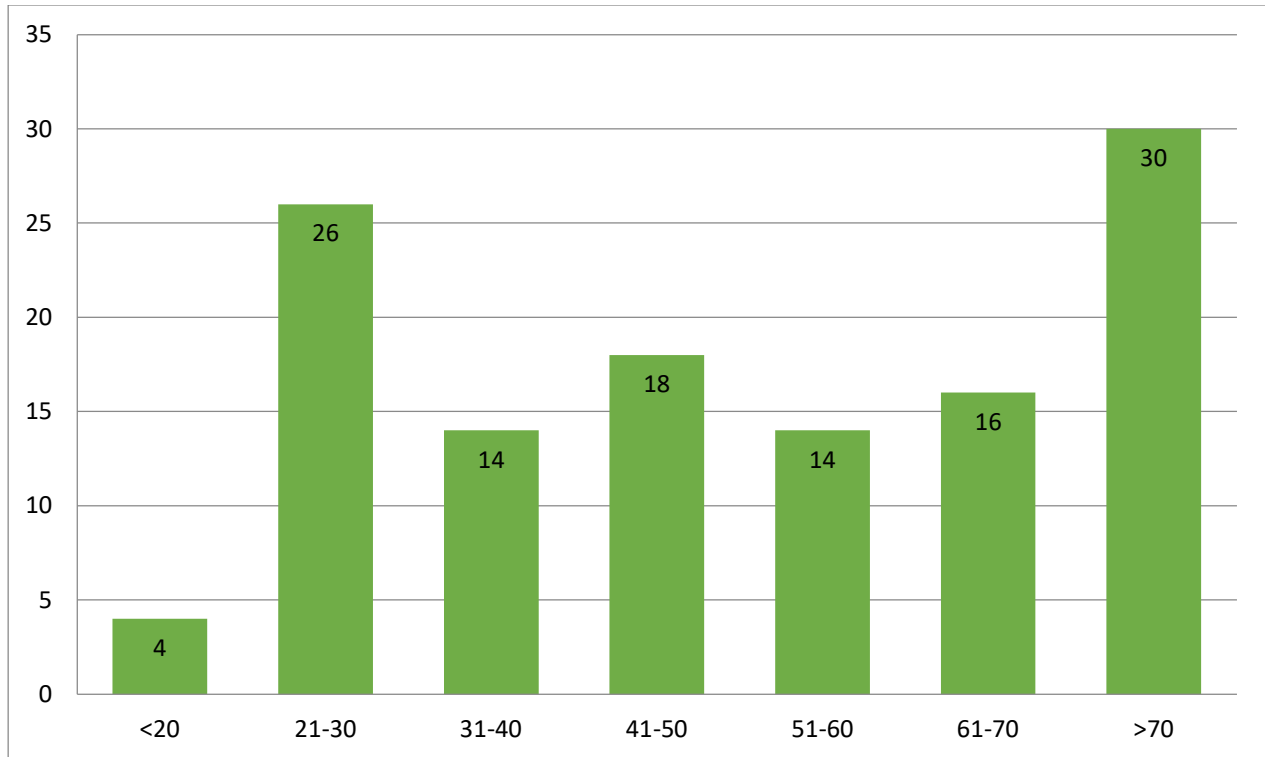
|     |   |
|-----|---|
| U   | + |
| TSI | + |
| NR  | + |

TABLE:3 Distribution of cases according to Gender

| Gender | No. | %     |
|--------|-----|-------|
| Female | 66  | 54.1% |
| Male   | 56  | 45.9% |
| Total  | 122 | 100%  |

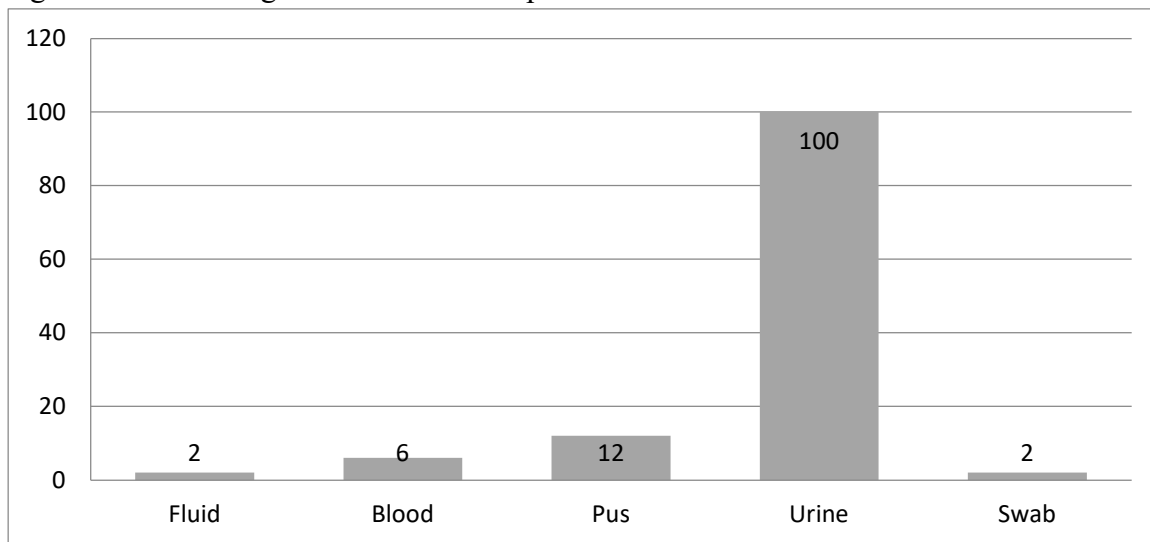
This table illustrated that the gender distribution of study subjects. It was found that out of total 122 study subjects, 66 (54.1%) were female & 56 (45.9%) were male.

Fig:-3 Chart showing age distribution



The above pie chart explain that maximum number of MDR isolates belongs to age group more than 70 years followed by 21-30 (26),41-50 (18),61-70 (16),51-60 (14),31-40(14) & >20 (4) age group.

Fig:-4 Chart showing distribution of samples



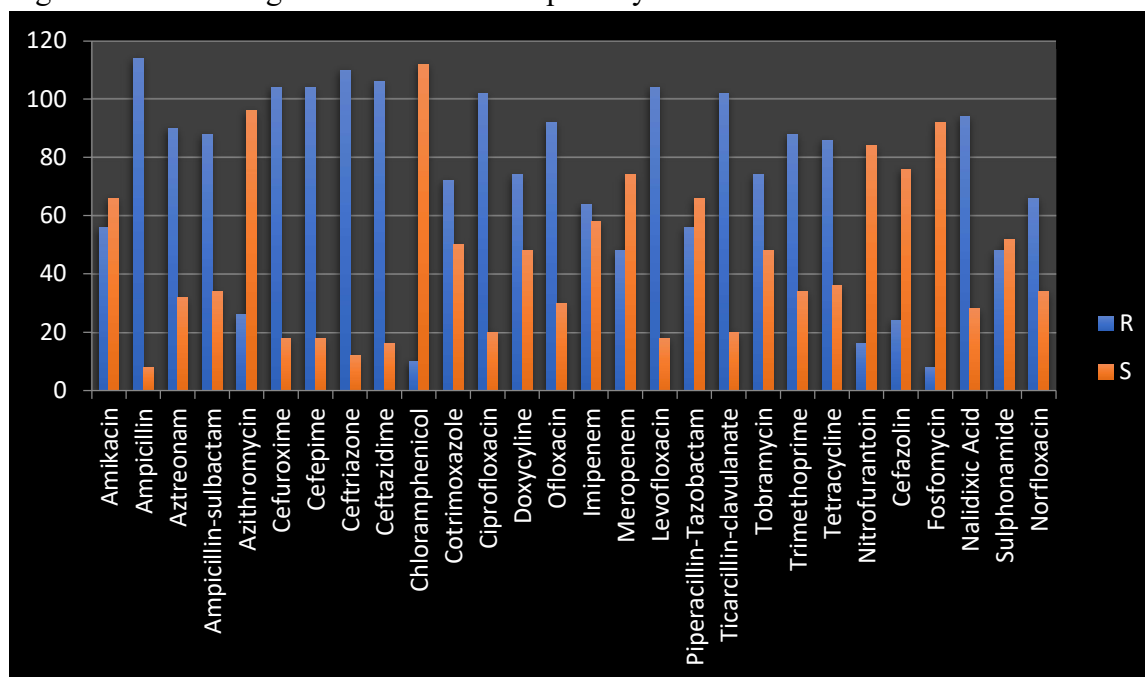
As record of the pie chart, the distributions of various samples were seen in the present study. Majority samples were urine samples followed by pus , blood, swab & fluid sample.

TABLE:4 AST PATTERN

| SR. no. | ANTIBIOTICS             | R   | %   | S   | %   |
|---------|-------------------------|-----|-----|-----|-----|
| 1       | Amikacin                | 56  | 46  | 66  | 54  |
| 2       | Ampicillin              | 114 | 93  | 8   | 6.6 |
| 3       | Aztreonam               | 90  | 74  | 32  | 26  |
| 4       | Ampicillin-sulbactam    | 88  | 72  | 34  | 28  |
| 5       | Azithromycin            | 26  | 21  | 96  | 79  |
| 6       | Cefuroxime              | 104 | 85  | 18  | 15  |
| 7       | Cefepime                | 104 | 85  | 18  | 15  |
| 8       | Ceftriazone             | 110 | 90  | 12  | 9.8 |
| 9       | Cefotaxime              | 98  | 80  | 24  | 20  |
| 10      | Ceftazidime             | 106 | 87  | 16  | 13  |
| 11      | Chloramphenicol         | 10  | 8.2 | 112 | 92  |
| 12      | Cotrimoxazole           | 72  | 59  | 50  | 41  |
| 13      | Ciprofloxacin           | 102 | 84  | 20  | 16  |
| 14      | Doxycyline              | 74  | 61  | 48  | 39  |
| 15      | Ofloxacin               | 92  | 75  | 30  | 25  |
| 16      | Imipenem                | 64  | 53  | 58  | 48  |
| 17      | Meropenem               | 48  | 39  | 74  | 61  |
| 18      | Levofloxacin            | 104 | 85  | 18  | 15  |
| 19      | Piperacillin-Tazobactam | 56  | 46  | 66  | 54  |
| 20      | Ticarcillin-clavulanate | 102 | 84  | 20  | 16  |

|    |                |     |     |    |    |
|----|----------------|-----|-----|----|----|
| 21 | Tobramycin     | 74  | 61  | 48 | 39 |
| 22 | Trimethoprim   | 88  | 72  | 34 | 28 |
| 23 | Tetracycline   | 100 | 82  | 22 | 18 |
| 24 | Nitrofurantoin | 16  | 13  | 84 | 69 |
| 25 | Cefazolin      | 24  | 20  | 76 | 62 |
| 26 | Fosfomycin     | 8   | 6.6 | 92 | 75 |
| 27 | Nalidixic Acid | 94  | 77  | 28 | 23 |
| 28 | Sulphonamide   | 48  | 39  | 52 | 43 |
| 29 | Norfloxacine   | 66  | 54  | 34 | 28 |

Fig:-5 Chart showing Antimicrobial susceptibility test







**Fig 6 : Antibiotic susceptibility pattern**

In the above table shows the Antibiotic pattern of Escherichia coli which has the susceptible pattern as follows; Amikacin (54.1%) ,Ampicillin (6.6%), Aztreonam(26.2%) Ampicillin-sulbactam (27.9%), Azithromycin (78.7%), Cefuroxime(14.8%),Cefepime(14.8%),Ceftriazone(9.8%),Cefotaxime(19.7%),Ceftazidime(13.1 %)Chloramphenicol(91.8%), Cotrimoxazole(41%), Ciprofloxacin(16.4%), Doxycycline(39.3%), Ofloxacin (24.6%),Imipenem(47.5%), Meropenem (60.7%),Levofloxacin(14.8%), Piperacillin-Tazobactam(54.1%), Ticarcillin-clavulanate(16.4%), Tobramycin(39.3%), Trimethoprim(27.9%), Tetracycline (18.1%),Nitrofurantoin(68.9%), Cefazolin(62.3%),Fosfomycin(75.4%), Nalidixic Acid(23.0%), Sulphonamide(42.6%), Norfloxacin(27.9%).

Table: 5 Chi square test

| Chi-Square Tests             |          |    |         |
|------------------------------|----------|----|---------|
|                              | Value    | df | p value |
| Pearson Chi-Square           | 839.5064 | 28 | 0.000   |
| Likelihood Ratio             | 883.4661 | 28 |         |
| Linear-by-Linear Association | 124.1745 | 1  |         |
| N of Valid Cases             | 3428     |    |         |
|                              |          |    |         |

P value is less than 5 which is highly significant.

**Discussion**

Escherichia coli are a normal flora of human intestine. It is recognized as a marker of fecal contamination in food .It is responsible for causing nosocomial infections in humans. [12] As an intestinal parasite found in both humans and animals, Escherichia coliis a prevalent pathogen

known to cause a variety of complications in humans, including UTI, bloodstream infections, wounds infection, otitis media, and other related conditions. [13-15] The issue of antimicrobial resistance in urinary tract infections is a constantly evolving and concerning problem, with particular emphasis on the rising incidence Escherichia coli infection that exhibit frequent resistance to beta-lactams and other antibiotics. [16-17]

As noted by Shah et al. (2002), Escherichia coli was most commonly identified as a pathogen in various clinical infections, including those acquired in both hospital and community settings. [18] According to Karlowsky et al. (2004), Escherichia coli exhibited a high propensity for developing resistance. [19-20] The incidence of E. coli antibiotic resistance has the rise globally, with susceptibility patterns displaying significant geographic variation, as well as variances influenced by population and environmental factors. [21-22] The lower rate of growth observed in the cultures could potentially be attributed to the inclusion of all patients, regardless of their symptoms or prior antibiotic use, or the presence of fastidious organisms that may not be detectable using routine culture media. [23-24] The present study observed that Escherichia coli among all clinical specimens was found to be 17.8% prevalent. Related result has been found by Tanzina Ak et al [25] They found 16.8% prevalence of Escherichia coli in their observations. In another studies conducted by the A M Masudul Azad Chowdhury et al, Poonam Verma & Joseph Omololu-Asoet al also found 33.3%, 32.5% & 27.5% prevalence of Escherichia coli respectively. [26-28] In contrast, Sumera Sabir's study reported a significantly high prevalence of E. coli. [29] Niraj Gupta et al. [30] reported a low incidence of Escherichia coli (5.1%) in their results.

In our study majority of specimens were collected from the rural area. In rural area the chances of open defecation could be due to poor hygiene practices. Our study's findings indicated that MDR Escherichia coli had a prevalence rate of 87.2%. There are a number of reasons for these results which are as follows; irrational use of antibiotics, easy availability of antibiotic on the counter, taking incomplete dose of antibiotic & not following the antimicrobial stewardship. The present study finding has been supported by Ibrahim ME et al, Ibrahim, D.R, Jain, P. et al. [31-34] In some other studies (Olowe O. A, Marwa E.A. Aly, Deb Pet al) researcher has been observed contradictory results. [35-36] This study determined that the antibiotic susceptibility pattern against MDR E. coli. It found that there are a number of antibiotics which were resistant to Ampicillin, Tetracycline, Ceftriaxone, Ceftazidime, Cefepime, Levofloxacin, cefuroxime, Ciprofloxacin, Ticarcillin-clavulanate, Cefotaxime, Chloramphenicol, Azithromycin, Nitrofurantoin, Cefazolin, Meropenem, Piperacillin-Tazobactam, Amikacin & Imipenem etc were found as a most susceptible antimicrobial drug among the MDR Escherichia coli in our study. Previously, Amin et al., [37] found the isolates Escherichia coli from UTI in one of his studies. It also observed that the resistant pattern were gentamicin, ceftriaxone, amikacin and ciprofloxacin and ampicillin and tetracycline respectively.

It has been reported by the Bashir et al., [38], Escherichia coli exhibited resistance against the ampicillin, Ciprofloxacin, Nitrofurantoin, Co-Trimoxazole, Amikacin.

Niranjan et al., [39] were conducted a study in India and found the resistant pattern of Escherichia coli to the ampicillin, amoxicillin clavulanic acid, cefuroxime, ceftriaxone and co-trimoxazole.

They showed susceptibility pattern as follows; amikacin, piperacillin-tazobactam, nitrofurantoin and imipenem.

In our study also reported the same antimicrobial resistant & susceptibility pattern against the E. coli. Therefore, the finding of Niranjan et al.,[39] Bashir et al.,[38] Amin et al.,[37] similar to the present study.

Nowadays, Antibiotic resistant play an vital role in upto date medicine. In 21st century, antibiotic resistance is one of the most prominent public health concern. Worldwide, the use of uncontrolled antibiotic may increase the resistance property among the bacteria.

Inappropriate antibacterial treatment & misuse of antibiotic develop the resistance among the organisms. Without the prescription of a doctor, use of antibacterial drug is an example of antibiotic misuse.

### Conclusion

This study found that the prevalence of Escherichia coli was 87.2% and MDR becomes PDR. This study concludes that ineffectiveness of antibiotic against the bacterial strain as in resistant pattern was observed. This is due to inappropriate antibacterial treatment & misuse of antibiotic, develops the resistance among the organisms. Without the prescription of a doctor, use of antibacterial drug is an example of antibiotic misuse. Excessive use of antibiotic against the organism is certainly increasing the resistance which is a serious problem over the world.

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