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ORIGINAL ARTICLE

The *Enterobacteriaceae* Isolated from Urinary Tract Infections in Kerbala City

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ABSTRACT

Objective: The goal of this study to determine the most common microorganism that causes urinary tract infection (UTI) in Kerbala city/ Iraq, and study of susceptibility of this causative agents against some antibiotics which used as treatments.

Methods: Sixty specimens were collected from urinary tract infections in Kerbala city/ Iraq from September to December 2016. The bacterial isolates were identified tested for antibiotics sensitivity test. Resistance breakpoints used were those published by Clinical and Laboratory Standards Institute (CLSI), including: Nalidxic Acid (resistance ≥ 13 mm), Trimethoprim (resistance ≥ 10 mm), Norfoxacin (resistance ≥ 12mm), Ciprofloxacin (resistance≥15mm)and Trimethoprim/sulfamethoxazole(resistance≥10mm).

Results: The most common organisms of UTI infection were *Escherichia coli* (48%), *Citrobacter* spp (22%), *Proteus* spp(12%), *Klebsiella* spp(8%), *Pseudomonas* spp(6%), *Moragenella* spp(2%) and *Providencia* spp(2%). Among all 50 isolates , 48% were resistance to Nalidxic Acid , 40% to Trimethoprim and 28% to Norfloxacinas. For the 24 *Escherichia coli* isolates, resistance rate were: Nalidxic Acid (50.0%) ,Trimethoprim (37.5 %), Norfloxacin (33.33%), Ciprofloxacin (16.67%) and Sulphamethoxaole/ Trimethoprim (58.33%).

Conclusion: From the results carried out in this study, it's concluded that *E.coli* isolates responsible for UTI infections and the higher rates of antibiotics resistance to Sulphamethoxaole/ Trimethoprim.

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INTRODUCTION

Urinary tract infections (UTIs) are among the most prevalent bacterial infections in humans [1]. UTIs have been reported to be the most common hospital acquired infection, which are associated with significant morbidity and mortality [2].

Escherichia coli—the most prominent member of the family of *Enterobacteriaceae*—is the number one cause of UTIs [1]. The predominant causative pathogen of UTIs is *Escherichia coli*, however, there have been increasing reports of other *Enterobacteriaceae* such as *Klebsiella pneumoniae* and gram negative non-fermenters such as *Acinetobacter* spp., and *Pseudomonas aeruginosa*as causes of UTIs [2].

Escherichia coli isolates from clinical specimens may be resistant to multiple antimicrobial agents and a substantial proportion of multiresistant *E. coli* isolates

carry integrons. Commensal *E. coli* isolates from humans and animals can cause extra-intestinal diseases, including urinary tract infection, pneumonia, meningitis and bacteraemia. These bacterial strains area potential reservoir for antimicrobial resistance genes and play an important role in the ecology of antimicrobial resistance of bacterial populations [3].

Increasing bacterial antibiotic resistance related to extensive use of antibiotics in human and animals constitutes a growing public health concern. Extensive antibiotic use has led to a positive selection of cells that carry efficient mechanisms of drug resistance such as mechanisms include the presence of altered target molecules or genes that modify, destroy and remove antibiotics from the cell cytoplasm [4].

Antibiotic-resistant bacteria that are difficult or impossible to treat are becoming increasingly common and are causing a global health crisis. Antibiotic resistance is encoded by several genes, many of which can transfer between bacteria. New resistance mechanisms are constantly being described, and new genes and vectors of transmission are identified on a regular basis [5].

MATERIALS AND METHODS

Bacterial Isolates

This study was conducted at Karbala city/Iraq, from September to December 2016. It involved 60 UTIs patient. Urine samples inoculated onto MacConkey's agar and EMB agar.

Isolates Identification

Isolated microbes were identified by colonial characteristic, Gram stain and conventional biochemical tests [6].

Antimicrobial Susceptibility

Antimicrobial susceptibility profiles of the isolates were performed by standard disc diffusion method on Muller-Hinton agar as recommended by the guidelines of Clinical and Laboratory Standards Institute. The 50 isolates were subjected 3 antimicrobial agents and all *E.coli* isolates were subjected to a susceptibility test against 5 antimicrobial agents. The following antimicrobial disks were used: Nalidxic Acid (NA 30µg), Norfloxacin(NOR 10µg), Trimethoprim (TMP 5µg), Ciprofloxacin(Cip 5 µg) and Sulphmethoxazole/ trimethoprim (SXT 25 µg). According to the CLSI (2016) guideline inhibition zones of all antimicrobial disks were measured and evaluated as sensitive, intermediate or resistant [7].

RESULTS

Isolation and Identification of Bacteria

Fifty *Enterobacteriaceae* isolates were studies. During the study period, 24 *E. coli*, 11 *Citrobacter* spp, 6 *Proteus* spp , 4*Klebisella* spp, 3 *Pseudomonas* spp, 1 *Morganella* spp and 1 *Providencia* spp isolates were collected from urine specimens as shown in Figure 1. The highest rate of *Enterobacteriaceae* genus was *E.coli*(24 out of 50).

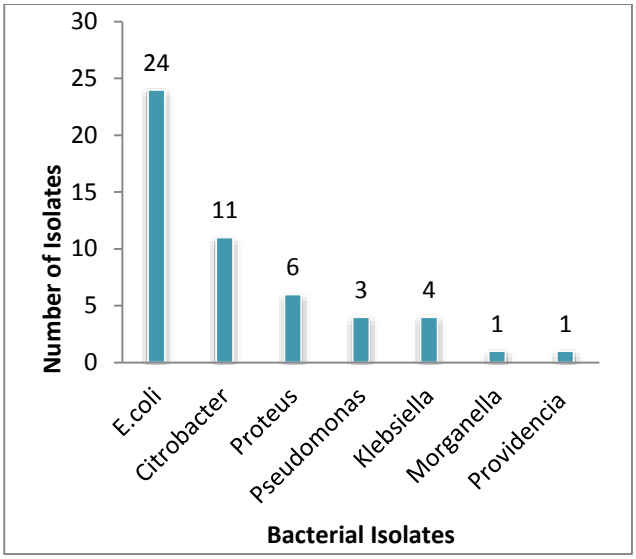

Figure 1: **Distribution of different species of *Enterobacteriaceae*.**

Antimicrobial Susceptibility Testing

Among all 50 bacterial isolates were collected from urine specimens, 24 isolates (48%) were resistance to Nalidxic Acid **(**NA, 30µg) , 20 isolates (40%) to Trimethoprim (TMP, 5 µg) and 14 isolates (28%) to Norfloxacin (NOR, 10 µg) as shown in Figure 2.

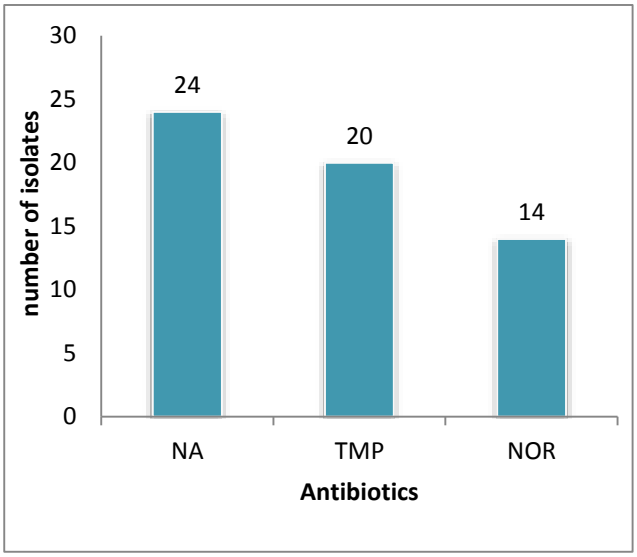

Figure 2: **Antibiotic resistance among *Enterobacteriacea* for Nalidxic Acid (NA),Trimethoprim (TMP) and Norfloxacin (NOR).**

Among 24 *Escherichia coli* isolates, resistance rate were: Nalidxic Acid **(**NA, 30µg) 12 (50.0%) ,Trimethoprim (TMP, 5 µg) 9 (37.5 %), Norfloxacin (NOR, 10 µg) 8 (33.33%) , Ciprofloxacin (Cip, 5 µg) 4 (16.67%) and Sulphamethoxaole/ Trimethoprim (SXT, 25 µg) 14 (58.33%). This study reports higher rates of antibiotics resistance to Sulphamethoxaole/ Trimethoprim**,** Figure 3.

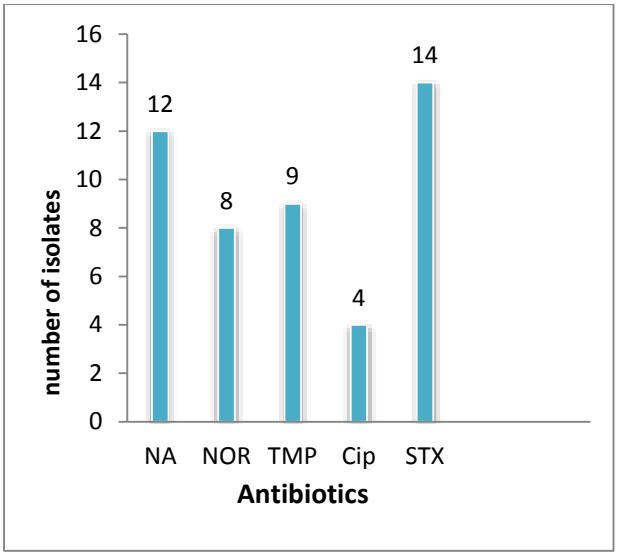

Figure 3: **Antibiotic resistance among *E. coli* for Nalidxic Acid (NA), Norfloxacin(NOR), Trimethoprim (TMP), Ciprofloxacin(Cip) and Sulphamethoxaole/ Trimethoprim (SXT).**

Discussion

This study indicate that *E.coli* is still the most common cause of UTI ,this result is in agreement with several other investigations have indicated that most common organisms of UTI infection [8,9].

The most prevalent etiological agent in UTIs in Poland was *E. coli* (73%) , followed by *Proteus* spp (8.9%) and other species of *Enterobacteriaceae* (9.6%) [10].

The emergence of MDR strains has become a serious problem and has complicated the selection of empirical treatment for UTI [11]. One of the reasons for the rapid accumulation of resistance is excessive or inappropriate use of antibiotics from patients [4]. Horizontal gene transfer and clonal expansion, are thought to account for the rise in trimethoprim–sulfamethoxazole resistance rates [12].

Conclusions

From the results carried out in this study, it's concluded that *E.coli* isolates responsible for UTI infections and the higher rates of antibiotics resistance to Sulphamethoxaole/ Trimethoprim.

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