Bacterial pathogens implicated in causing urinary tract infection (UTI) and their antimicrobial susceptibility pattern in Ethiopia.

Patógenos causantes de infección del tracto urinario (ITU) y sus patrones de susceptibilidad antimicrobiana en Etiopía.

Theodros Getachew
Ethiopian Health and Nutrition Research Institute, PO Box 57326, Addis Ababa, Ethiopia

tedi.getachew@yahoo.com
Bacterial pathogens implicated in causing urinary tract infection (UTI) and their antimicrobial susceptibility pattern in Ethiopia.

ABSTRACT
Introduction: Urinary Tract Infection (UTI) is one of the most common infectious disease ranking next to upper respiratory tract infection is the cause of morbidity and mortality in human. They are mostly caused by bacteria. However, studies conducted in Ethiopia are few and are not extensive. Therefore, studying bacterial pathogens causing UTI and their drug susceptibility patterns is of a highest priority. Material & Methods: A total of 3228 urine samples were collected from 2004 to 2009. Fresh midstream urine samples were aseptically collected in sterile containers. Each sample was cultured onto 5% sheep blood agar and CLED agar plates using a calibrated loop, delivering 1ul of the sample. This was incubated at 37°C aerobically overnight. Bacterial isolates were identified using standard biochemical tests and antimicrobial susceptibility pattern was determined using the Kirby – Bauer’s disk diffusion method followed CLSI guidelines. Result & discussion: From a total of 3228 urine samples significant bacterial growth was obtained from 651 samples. The gram positive and negative bacteria accounted 17.7% and 80.2% respectively, the rest 2.2% are yeasts. The majority 475(72.9) of the isolates were from women while the remaining 176 (27.1) were from men. A wide spectrum of uropathogens was isolated, of which 359 (55.1 %) were Escherichia coli, 107 (16.4 %) Klebsiella species, 66 (10.1 %) streptococcus species, 49(7.5%) staphylococcus species, 14 (2.2 %) citrobacter species, 14 (2.2 %) candida species, 13 (2 %) enterobacter species, 11 (1.7 %) pseudomonas and the rest 2.8% are 5 proteus species, 5 salmonella species, 4 acinetobacter species and 4 M. morganii. Resistance rate to Gram-negative bacilli were 96 % to amoxicilline-clavulanic acid, 66.9 % to tetracycline, 61.4 % to ampicillin, 64.7 % to trimethoprim-sulfamethoxazole, 37.6 % to chloramphenicol, 34 % to norfloxacin and 22.4 % to ceftriaxone. Among Gram-positive, 45.1 % were resistant to penicillin, 25.8 % to chloramphenicol, 21.1 % to erythromycin and 9.1 % to clindamycine. Conclusions: High prevalence of drug-resistant urinary tract pathogens, particularly to amoxicilline-clavulanic acid, tetracycline, ampicillin and co-trimoxazole suggests cautious use of antibiotic therapy for the treatment. Finally, we suggest that empirical antibiotic selection should be based on knowledge of the local prevalence of bacterial organisms and antibiotic sensitivities rather than on universal guidelines.

Keywords: UTI ; antimicrobial susceptibility pattern; Ethiopia

INTRODUCTION
Urinary tract infection (UTI) is one of the most common infections encountered and treated worldwide. The spectrum of etiologic agents causing urinary tract infections and their antimicrobial resistance pattern have been continuously changing over the years, both in community and in hospitals. Trimethoprim-sulfamethoxazole (TMP-SMX) is the current treatment of choice in community associated UTI. Due to rising antibiotic resistance among uropathogens, it is important to have local hospital based knowledge of the organisms causing UTI and their antibiotic sensitivity patterns. This information would be relevant not only to the local hospital but would also be a vital regional database. UTI is frequently encountered in patients with diabetes and in those with structural and neurological abnormalities, which interfere with urinary flow. Nosocomial UTI is common following instrumentation namely, catheterization and cystoscopy. Almost all known bacterial pathogens have been incriminated as possible causative agents of this clinical syndrome. Many other antibiotics like amoxicillin, amoxicillin/clavulanic acid, cephalaxin and ciprofloxacin are also often used in the empirical
therapy for community associated UTI. However, as with many community acquired infections, antimicrobial resistance among the uropathogens that cause UTI is increasing. For rational empirical therapy of community associated UTI, it is necessary to consider the spectrum of uropathogens and their antimicrobial susceptibility pattern time to time, as it may vary institutionally and geographically.

Urinary tract infection (UTI) is one of the most common infections encountered and treated worldwide. Increasing resistance in bacterial pathogens is of world-wide concern. They are mostly caused by bacteria. The prevalence of antimicrobial resistance in both out and hospital patients with UTI is increasing and can vary according to geographical and regional location. Urinary tract infections (UTIs) are one of the most frequent infections in children. At least 8% of girls and 2% of boys will have a urinary tract infection (UTI) in childhood, and between 30% and 40% will have another episode within two years.

Several studies has demonstrated that the geographical variability of pathogen occurrence in cases of UTI among inpatients and outpatients populations is limited by the predominance of gram-negative species usually Enterobactericeae and particularly E. coli and Enterobacter spp. in various regions of the world.

However, Pseudomonas aeruginosa and Enterococcus spp. are usually ranked among the top five pathogens and the resistance patterns of these pathogens can vary significantly between hospitals, countries and continents. Antimicrobial resistance among urinary tract isolates has recently been reported with an increased frequency all over the world.

However, no studies are conducted in Ethiopia. Therefore, studying bacterial pathogens causing UTI and their drug susceptibility patterns is of a highest priority.

Objective of the research
General objective
To describe the spectrum of bacteria implicated in causing UTI and their antimicrobial susceptibility patterns from patients attending in Ethiopian Health and Nutrition Research Institute, Ethiopia.

Specific objective
- To have local knowledge of the most prevalent organisms causing UTI.
- To provide local knowledge of UTI causing bacterial antibiotic resistance patterns.
- Based on the study to revise the empirical antibiotic prescriptions for bacterial UTI.

MATERIALS AND METHODS
A retrospective review of the microbiology laboratory record of three thousand two hundred twenty eight urine samples was collected from 2004 to 2009. Fresh midstream urine samples were aseptically collected in sterile universal container and transported to the laboratory within 30 minutes. Each sample was cultured onto 5% sheep blood agar and cystine lysine electrolyte deficient (CLED) agar plates using a calibrated loop, delivering 1ul of the sample. This was incubated at 37°C aerobically overnight. Symptomatic UTI was defined as a positive urine culture of >10^5 CFU/mL. Bacterial isolates were identified using standard biochemical tests and antimicrobial susceptibility pattern was determined using the Kirby – Bauer’s disk diffusion method following clinical and laboratory standard institute (CLSI) guideline. Data is analyzed by SPSS software.

RESULTS
From a total of 3228 urine samples significant bacterial growth was obtained from 651 samples. The gram positive and negative bacteria accounted 17.7 % and 80.2 % respectively, the rest 2.2 % are yeasts. The majority 475 (72.9 %) of the isolates were from women while the remaining 176 (27.1 %) were from men. A wide spectrum of uropathogens was isolated, of which 359 (55.1 %) were Escherichia coli, 107 (16.4 %) Klebsiella species, 66 (10.1 %) streptococcus species, 49 (7.5 %) staphylococcus species, 14 (2.2 %) citrobacter species, 14 (2.2 %) candida species, 13 (2 %) enterobacter species, 11 (1.7 %) pseudomonas and the rest 2.8 % are 5 proteus species, 5 salmonella species, 4 acinetobacter species and 4 M. morganii. Resistance rate to Gram-negative bacilli were 96 % to amoxicilline–clavulanic acid, 66.9 % to tetracycline, 64.7 % to trimethoprim-sulfamethoxazole, 61.4 % to ampicillin, 37.6 % to chloramphenicol, 34 % to norfloxacin, 34.5 % to nalidixic acid, 22.4 % to ceftriaxone and 10.4 % to nitrofurantoin. Among Gram-positive, 45.1 % were resistant to penicillin, 25.8 % to chloramphenicol, 21.1 % to erythromycin and 9.1 % to clindamycin.

DISCUSSION
This study shows the distribution and antimicrobial resistance pattern of uropathogens isolated from patients referred to Ethiopian Health and Nutrition Research Institute, Ethiopia. In our study, Escherichia coli remain the most important uropathogen causing community associated UTI and was isolated in 55.1 % cases. Isolation of Escherichia coli as the predominant pathogen of community associated UTI has been extensively reported in many studies.22,23 Although, the decline in E. coli isolation (55.1 %) rate in our setting remains unclear. But, similar low rate isolation E. coli have also been reported by investigators from developed and developing countries.22,24 K. pneumoniae was the second most common pathogen (16.4 %).

Resistance rates among common uropathogens to many commonly used antimicrobial agents have increased over the years and theses resistance rates vary from country to country.25 In our country set up the least effective drugs are amoxicilline–clavulanic acid, tetracycline, trimethoprim-sulfamethoxazole and ampicillin. Our result shows that the choice of antibiotics for empirical treatment of enterobactericea which causes UTI is nitrofurantoin, nalidixic acid, norfloxacin and chloramphenicol.

CONCLUSION
High prevalence of drug-resistant urinary tract pathogens, particularly to amoxicilline-clavulanic acid, tetracycline, ampicillin and co-trimoxazole suggests cautious use of antibiotic therapy for the treatment. Finally, we suggest that empirical antibiotic selection should be based on knowledge of the local prevalence of bacterial organisms and antibiotic sensitivities rather than on universal guidelines

REFERENCES


