

Antimicrobial Susceptibility Patterns of Uropathogen Isolated In Community Acquired Urinary Tract Infection (UTI) In Government Health Clinics In Klang

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Introduction

- Community acquired UTI is common and a majority of patients are prescribed with antimicrobials (1)
- There is little knowledge about antibiotic susceptibility in urine samples from patients with UTI in government health clinics especially in a local setting
- Local prevalent strains of uropathogens and its susceptible to antimicrobial is important in order to decide the antimicrobial usage
- Inappropriate antimicrobial prescription for UTIs likely drives antimicrobial resistance (2)
- Hence this study is to see the local prevalent of uropathogen and its susceptibility in order to determine the best empirical treatment option.

Method

- This is a retrospective cross sectional study on urinary samples of patients attending government health clinics in Klang, which were sent to Hospital Tengku Ampuan Rahimah (HTAR) for laboratory culture and sensitivity from January 2018 till December 2019. (universal sampling)
- The results were analysed with descriptive statistics. The Chi-square were applied for categorical variables. P-value < 0.05 is consider significant.

Results and Discussion

- Urine cultures were analysed in 412 samples
- 386 (93.7%) with complete data were used for analysis
- The majority of the UTI are caused by *Escherichia coli* (*E.coli*) (57%) followed by *Klebsiella spp* (18%), *Group B Streptococcus* (7%), *Enterococcus* (5%), and *others* (13%) (Chart 1)
- The common organisms causing UTI for all age groups and gender were *E.coli* (57.8%) and *Klebsiella species* (16.6%) which belong to Enterobacteriaceae family (Table 1). It is consistent with similar study from Singapore (3)
- Female patients have a higher prevalence of UTI (89.6%) as compared to male (10.4%). The majority of them are age < 60 years old (82.6%). (Table 1)
- A recent study from UK showed female have higher incidence of UTI (85%) compared with male with median age 54 years. (4)
- Our study showed that *E.coli* were susceptible to Nitrofurantoin (96.2%), and Amoxicillin-Clavulanate (85.5%) (Table 2)
- As for *Klebsiella species* was susceptible to Trimethoprim Sulfamethoxazole (83.8%), Ciprofloxacin (82.4%), and Amoxicillin-Clavulanate (79.7%) (Table 2)
- The limitation of this study is the samples were collected in a single centre which may not reflect the general population

Chart 1. Distribution Of Uropathogens That Cause UTI (n=412)

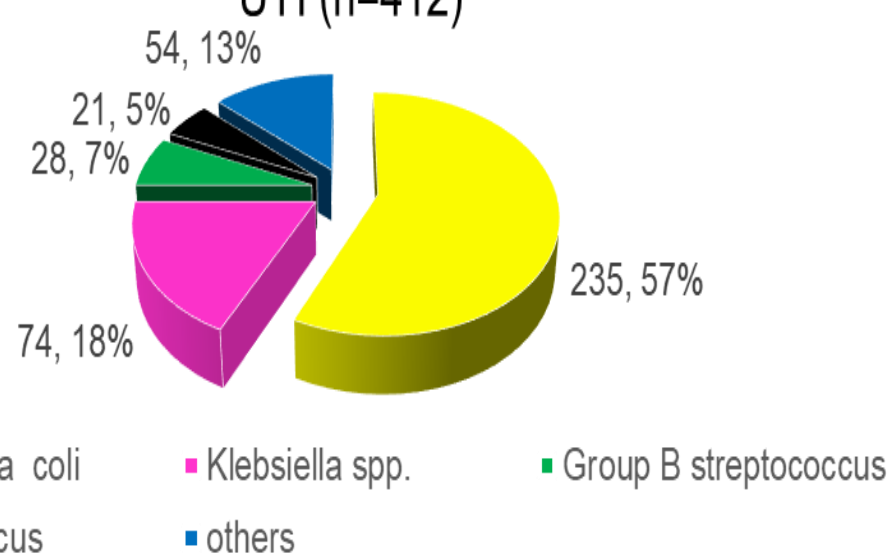


Table 1. Distribution Of Uropathogens That Cause Community Urinary Tract Infections In Patients by Genders and Age Groups (N=386)

Organism	Total	Male (n=40)	Female (n= 346)	Age <60 (n=319)	Age > 60 (n=67)
Escherichia coli	223 (57.8%)	19 (47.5%)	204 (59%)	178 (55.8%)	45 (67.2%)
Klebsiella spp.	64 (16.6%)	5 (12.5%)	59 (17%)	57 (17.9%)	7 (10.4%)
Group B streptococcus	27 (7%)	1 (2.5%)	26 (7.5%)	27 (8.5%)	0 (0%)
Enterococcus	18 (4.7%)	3 (7.5%)	15 (4.3%)	16 (5%)	2 (3%)
others	54 (14%)	12 (30%)	42 (12.1%)	41 (12.8%)	13 (19.4%)

Table 2. Susceptibility Of E.Coli And Klebsiella To The Antimicrobial Testing Panel Which Commonly Available In Primary Care (n= 309)

Antimicrobial	Antimicrobial susceptibility (%)		
	Total	E.Coli (n=235)	Klebsiella spp (n=74)
Amoxicillin-Clavulanate (AmC)	84.1	85.5	79.7
Ampicillin Sulbactam (SAM)	72.8	72.8	73
Cefuroxime (CXM)	48.5	49.8	44.6
Ciprofloxacin (CIP)	69.9	66	82.4
Nitrofurantoin (NIT)	87.7	96.2	60.8
Trimethoprim Sulfamethoxazole (SXT)	75.4	72.8	83.8
Ampicillin (AMP)	34.4	43	6.76

Conclusion

- Enterobacteriaceae family (*E.coli* and *Klebsiella species*) is the common organism causing UTI among patients attending government health clinics
- For *E.coli*, it was susceptible to Nitrofurantoin and Amoxicillin-Clavulanate
- Klebsiella species* were susceptible to Trimethoprim Sulfamethoxazole, Ciprofloxacin, and Amoxicillin-Clavulanate
- The local prevalence of uropathogen and antimicrobial susceptibility should be updated periodically in order to ensure optimal empirical antibiotic use, and opportunities for improvement of antimicrobial stewardship

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