Clinical Characteristics and Microbiological Profiles of Community-Acquired Intra-Abdominal Infections

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ABSTRACT

***Background*:** *Intra-abdominal infections (IAIs) have different aspects to consider. One important aspect is the microbiological analyses, especially in the era of broad spread of resistant microorganisms. The study was designed to describe the clinical characteristics and microbiological profiles of community acquired IAIs.*

Method: *An observational study was performed on medical records of 12 months period (January to December 2013) in a General Hospital, Karawaci, Tangerang. Adult patients undergoing surgery for IAIs with positive microbiological culture and identification of microorganisms were included. Data collected were clinical characteristics and microbiological profiles and wereanalyzed statisticallyusing the SPSS version 17.*

Results: *In 12 months period of study, 17 patients of IAIs with a total of 17 intra peritoneal specimens were collected. A total of six microorganisms were cultured. All the IAIs were monomicrobial, with aerobic microorganism dominantly Gram-negative bacilli. The dominant microorganism was Escherichia coli (E. coli), found in 58.8% of IAIs. The most common site was appendix (41.2%), and none from small intestine. The susceptibility test found that piperacillin tazobactam, tigecycline, meropenem and amikacin were the most active antimicrobial against E. coli. Multi-drug resistant (MDR) E. coli in this study was 40%. The MDR E. coli had 66.6% resistance to levofloxacin and ciprofloxacin, 66.6% susceptibility to ceftriaxone and ceftazidime, and 100.0% susceptibility to amikacin.*

Conclusion: *The most common site of community-acquired IAIs was appendix (41.2%). E. coli is still a dominant microorganism with the MDR E. coli proportion of 40%.*

Keywords: *intra-abdominal infections, clinical characteristics, microbiological profiles*

ABSTRAK

Latar belakang: *Infeksi intra abdomen (IIA) memiliki berbagai aspek. Salah satunya adalah analisis mikrobiologi, khususnya di era resistensi mikroorganisme. Penelitian ini dirancang untuk menggambarkan karakteristik klinis dan profil mikrobiologi IIA komunitas.*

Metode: *Penelitian observasional dilakukan dari data rekam medis pasien selama periode 12 bulan (Januari sampai Desember 2013) di rumah sakit umum, Karawaci, Tangerang. Pasien dewasa yang menjalani pembedahan karena IIA dengan kultur mikrobiologik yang positif dan mikroorganisme yang teridentifikasi diikutsertakan. Data yang dikumpulkan adalah karakteristik klinis dan profil mikrobiologik. Data dianalisis secara statistik menggunakan SPSS versi 17.*

Hasil: *Selama periode 12 bulan didapatkan 17 pasien IIA dengan total 17 spesimen intra peritoneal. Didapatkan enam mikroorganisme. Semua IIA monomikrobial, dengan mikroorganisme aerobik terutama basil Gram-negatif. Mikroorganisme yang dominan adalah Escherichia coli (E. coli) pada 58.8% IIA. Lokasi yang umum adalah apendiks (41.2%), dan tidak ada dari usus halus. Tes sensitivitas mendapatkan bahwa piperacillin tazobactam, tigecycline, meropenem dan amikacin adalah antimikrobial paling aktif terhadap E. coli. Multi-drug resistant (MDR) E. coli pada studi ini 40%. MDR E. coli 66.6% resisten terhadap levofloxacin dan ciprofloxacin,*

66.6% sensitif terhadap ceftriaxone dan ceftazidime, dan 100.0% sensitif terhadap amikacin.

***Simpulan*:** *Lokasi tersering IIA komunitas adalah apendiks (41,2%). E. coli masih merupakan mikroorganisme yang dominan, dengan proporsi MDR E. coli 40%. Profil mikrobiologik IIA pada penelitian ini serupa dengan penelitian-penelitian lainnya.*

Kata kunci: *infeksi intra abdomen, karakteristik klinis, profil mikrobiologi*

INTRODUCTION

Intra-abdominal infections (IAIs) are complex disease entity with different aspects to consider. Several reports have emphasized the role of appropriate empirical antibiotic therapy to improve clinical success rates, reduce length of stay and decrease overall cost of hospitalization in IAIs.[1-4] The results of the microbiological analyses are important for the therapeutic strategy, especially in the initial empirical antimicrobial therapy.

Many studies have found the variation of resistance according to the isolated microorganisms and the antibiotic used to provide guidance in choosing empirical antimicrobial therapy for selected infections.[5-7] In the era of the broad spread of resistant microorganisms such as nosocomial and community extended-spectrum β-lactamase (ESBL) Enterobacteriaceae, multi drug resistance (MDR) *Escherichia coli (E. coli)*, community-acquired methicillin-resistant *Staphylococcus aureus* (MRSA), β lactam- and vancomycinresistant enterococci (VRE), epidemiological studies are of great importancein choosing the appropriate empirical antibiotic and adjusting the initially inappropriate or de-escalation of antibiotics. This observational study was done to describe the clinical characteristics, and microbiological profiles of community-acquired IAIs.

METHOD

An observational study was performed on medical records of 12 months period (January to December 2013) in a General Hospital, Karawaci, Tangerang. Adult patients undergoing surgery for IAIs with positive microbiological culture (intra-abdominal sample) and identification of microorganisms were included. Data collected were clinical characteristics of patients (age, sex, comorbidities, type of infection, type of peritonitis, localization of lesions), and microbiological profiles (microorganisms identification and antibiotic susceptibilities of bacterial isolates). Nosocomial infections were excluded. Nosocomial IAIs was defined as an infection absent upon admission that became evident 48 hours or more after admission inpatients hospitalized for a reason other than IAIs.[8] Patients with post-operative infections were considered as nosocomial cases. Comorbidities included chronic kidney disease, chronic heart failure, diabetes mellitus, hypertension, malnutrition and malignancy. Microbiological analyses and susceptibility testing were performed using the VITEK 2 Compact and according to the recommendations of the Clinical Laboratory and Standards Institute (CLSI).[8,9] Multidrug resistance (MDR) was defined as resistance to three or more groups of antimicrobials. After entry into a computerized database, the data was analyzed statistically using the software package SPSS version 17. Results are expressed as median (range), mean and standard deviation for continuous variables, and the number with the corresponding percentage for qualitative variables. The epidemiology of the microorganisms isolated inintra-abdominal samples and their susceptibility to antibiotics is described and analyzed.

RESULTS

In 12 months period of study on January to December 2013 17 patients of IAIs were included. Male to female ratio was 1.3 : 1. Median age was 44 year old with range 4–78 year old. Among these patients, a total of 17 intra peritoneal specimens were collected. The clinical characteristics of patients are described in Table 1.

Table 1.Clinical characteristics of patients

Clinical characteristics	Frequency n (%)
Co-morbidities	
Chronic kidney disease	0 (0.0%)
Chronic heart failure	0 (0.0%)
Diabetes mellitus	2 (11.8%)
Hypertension	0 (0.0%)
Malnutrition	1 (5.9%)
Malignancy	1 (5.9%)
Type of peritonitis	
Generalized	7 (41.2%)
Localized	10 (58.5%)
Localization of lesions	
Appendix	7 (41.2%)
Colon	3 (17.6%)
Small intestine	0 (0.0%)
Biliary tract	1 (5.9%)
Urinary tract	4 (23.5%)
Reproduction system	2 (11.8%)

A total of 6 microorganisms were cultured. All the IAIs were monomicrobial, with aerobic microorganism dominantly Gram-negative bacilli. No anaerobic microorganism was found.The dominant microorganism was *E. coli*, found in 58.8% of IAIs. According to the localization of infections, the most common site was appendix (41.2%), and none from small intestine. Microorganisms isolated from patients with IAIs are described in Table 2 and their localizations are described in Table 3. Antimicrobials susceptibilities (% susceptible) of bacteria isolated from patients with IAIs are described in Table 4.

The susceptibility test found that piperacillin tazobactam, tigecycline, meropenem and amikacin were the most active antimicrobial against *E. coli*. MDR *E. coli* in this study were 40%, the MDR *E. coli* found to be resistant to the commonly used antimicrobials of amoxicillin, trimethoprim-sulfamethoxazole, and ciprofloxacin.

Table 2. Microorganisms isolated from patients withintra-abdominal infections

Microorganisms	Frequency n (%)
Aerobes	
Gram-negative bacilli	
Escherichia coli	10 (58.8%)
Morganella morganii ssp	1 (5.9%)
Acinetobacter baumannii	2 (11.9%)
Pseudomonas aeruginosa	1 (5.9%)
Gram-positive cocci	
Streptococcus spp.	1 (5.9%)
Staphylococcus aureus	2 (11.8)

In this study, MDR *E. coli* had 66.6% resistance to levofloxacin and ciprofloxacin, 100.0% resistance to amoxicillin, 66.6% susceptibility to ceftriaxone and ceftazidime, 66.6% resistance to gentamicin and 100.0% susceptibility to amikacin. Antimicrobials susceptibilities of *E. coli* isolated from patients with IAIs are described in Table 5. Patients with MDR *E. coli* are no. 1–6.

Table 3. Microorganisms isolated from patients with intra-abdominal infections according to localization of infections

Localization	*Escherichia coli* (n = 10)	*Morganella morganii ssp.* (n = 1)	*Acinetobacter baumannii* (n = 2)	*Pseudomonas aeruginosa* (n = 1)	*Streptococcus spp.* (n = 1)	*Staphylococcus aureus* (n = 2)
Appendix	7	0	0	0	0	0
Biliary tract	0	0	0	0	1	0
Colon	1	1	1	0	0	0
Reproduction system	2	0	0	0	0	0
Urinary tract	0	0	1	1	0	2

Table 4. Antimicrobials susceptibilities of bacteria isolated from patients with IAIs

Antimicrobial agent	Susceptible (%)					
	Escherichia coli (n = 10)	*Morganella morganii ssp.* (n = 1)	*Acinetobacter baumannii* (n = 2)	*Pseudomonas aeruginosa* (n = 1)	*Streptococcus spp.* (n = 1)	*Staphylococcus aureus* (n = 2)
Amoxicillin	10.0	0.0	NA	NA	NA	0.0
Ampicillin sulbactam	50.0	0.0	50.0	0.0	100.0	100.0
Piperacillin tazobactam	100.0	100.0	50.0	100.0	100.0	100.0
Cefotaxime	80.0	100.0	50.0	NA	NA	100.0
Ceftriaxone	80.0	100.0	0.0	0.0	NA	100.0
Ceftazidime	80.0	100.0	50.0	100.0	0.0	100.0
Cefepime	80.0	50.0	0.0	100.0	NA	100.0
Gentamicin	60.0	100.0	50.0	100.0	100.0	100.0
Amikacin	100.0	100.0	100.0	100.0	0.0	NA
Ciprofloxacin	60.0	100.0	50.0	100.0	100.0	100.0
Levofloxacin	60.0	100.0	0.0	100.0	NA	100.0
Co–trimoxazole	20.0	100.0	100.0	0.0	NA	100.0
Imipenem	100.0	NA	50.0	100.0	100.0	100.0
Meropenem	90.0	100.0	100.0	100.0	100.0	100.0
Aztreonam	70.0	100.0	0.0	0.0	NA	NA
Tigecycline	100.0	0.0	100.0	0.0	NA	100.0

Table 5. Antimicrobials susceptibilities of *Eschericia coli* isolated from patients with IAIs

Sex	Age	Amoxicillin	Ampicillin subactam	Piperacillin Tazobactam	Cefotaxime	Ceftriaxone	Ceftazidime	Cefepime	Gentamicin	Amikacin	Ciprofloxacin	Levofloxacin	Co – trimoxazole	Imipenem	Meropenem	Aztreonam	Tigecycline
M	44	R	S	S	S	S	S	S	R	S	R	R	R	S	S	S	S
F	19	R	R	S	R	R	R	R	R	S	R	R	R	S	S	R	S
F	52	R	S	S	R	R	R	R	S	S	R	R	R	S	S	R	S
M	4	R	R	S	S	S	S	S	S	S	R	R	R	S	S	S	S
F	6	R	R	S	S	S	S	S	R	S	S	S	R	S	S	S	S
M	54	R	R	S	S	S	S	S	R	S	S	S	R	S	S	S	S
M	13	S	S	S	S	S	S	S	S	S	S	S	S	S	R	R	S
F	28	R	S	S	S	S	S	S	S	S	S	S	R	S	S	S	S
M	45	R	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S
M	13	R	R	S	S	S	S	S	S	S	S	S	R	S	S	S	S

M: male; F: female; R: resistant; S: sensitive

DISCUSSION

Several epidemiological studies on microbiological profiles of IAIs at single centre or international level have been published recently.[1,2,5-7] The microbiological profile of IAIs is the summary of transient or persistent normal gastrointestinal flora with potentially pathogenic microorganisms, including the Gram-positive, Gram-negative, anaerobic bacteria and fungal. The microbiological profile is of great importance inchoosing the appropriate empirical antibiotic and adjusting the initially inappropriateor de-escalation of antibiotics.

About 20–25% of cultures in secondary peritonitis were negative, 25% were monomicrobial and 50% were polymicrobial.[5,6] To conclude, IAIs are polymicrobial with an aerobic and anaerobic component, with the aerobic component inducing local or systemic inflammation, and the anaerobic component inducing abscess formation.[7] In this study, no culture was negative and all IAIs were monomicrobial. The possible explanation is most of the IAIs were community-acquired from appendicitis.

In studies of community-acquired IAIs, *E. coli* were found in more than 50% isolates.[1,3] *E. coli*, *Streptococcus spp.* and *Bacteroides fragilis (B. fragilis)* were the most frequently isolated microorganisms.[4-6] This study also found *E. coli* as the most frequent microorganism in IAIs (58.8%), followed by *Acinetobacter baumannii* and *Staphylococcusaureus* (11.8% and 11.8% respectively).

Location of the lesions of secondary peritonitis influences the spectrum of pathogens involved, as gastro-duodenal, small intestine, appendix and colorectal have a different flora in terms of microorganism species and density.[10] Gram-negative and anaerobic bacteria are dominant in IAIs from colorectal or appendix. Gram-positive bacteria and yeasts are dominant in IAIs from gastroduodenal. There is a relative balance between the four groups of microorganisms in IAIs from small intestine.[11] In this study the dominant microorganism was *E. coli* (58.8%), a Gram-negative bacteria, as the most common site of infection was appendix (41.2%). *E. coli* was found in all IAIs originating from appendix.

MDR *E. coli* in this study were 60%, whereas studies in Africa and South America showed prevalence of 70-90%, and studies in Europe and USA showed lower prevalence.[12-17] The emergence of different MDR *E. coli* phenotypes with resistance to three or more groups of antimicrobials has been reported in other studies and considered as a serious health problem.[15-17] The MDR *E. coli* in this study was found to be multi-resistant to the commonly used antimicrobials of amoxicillin, trimethoprim-sulfamethoxazole, and ciprofloxacin. These resistance profiles were common and could be associated with a number of known acquired resistance genes.[3] In this study, MDR *E. coli* has 66.6% resistance to levofloxacin and ciprofloxacin. In a study in Sudan, MDR *E. coli* showed high resistance to ofloxacin and ciprofloxacin (55.9 % and 57.4% respectively).[13] The hypothesized causes were the inappropriate use of fluoroquinolones for humans and prolonged use of low dose of the more potent fluoroquinolones such as ciprofloxacin.[18,19] The study in Sudan showed high resistance to 2nd and 3rd generation cephalosporins, whereas this study showed 66.6% susceptibility to ceftriaxone and ceftazidime. The hypothesized cause wasthe presence of ESBL in these strains.[13,20] In according to other studies[13,14,21] MDR *E. coli* in this study showed 100.0% susceptibility to amikacin. The hypothesized cause is that amikacin is a very powerful antimicrobial used only in hospital settings and not as first-line antimicrobial.[13] Other microorganisms in this study were not evaluated due to few numbers. The weakness of this study is, that as an observational study on medical records there were no standards to some data. The significance of susceptibility test from studies involving fewer than 30 organisms is difficult to interpret.[22]

CONCLUSION

This study concluded that the most common site of community-acquired IAIs was appendix and *E. coli* is still a dominant microorganism in community-acquired IAIs. Microbiological profiles of IAIs in this study were similar to other studies.

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