Scientific Foundation SPIROSKI, Skopje, Republic of Macedonia
Open Access Macedonian Journal of Medical Sciences. 2023 Feb 23; 11(A):117-121.
https://doi.org/10.3889/oamjms.2023.10701
eISSN: 1857-9655
Category: *A - Basic Sciences*
Section: *Microbiology*

Since 2002

Bacterial Profile of Chronic Kidney Failure Patients and their Sensitivity to Meropenem at General Hospital

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Edited by: Slavica Hristomanova-Mitkovska
Citation: Isnawati A, Prayitno L. Bacterial Profile of Chronic Kidney Failure Patients and their Sensitivity to Meropenem at General Hospital. Open Access Maced J Med Sci. 2023 Feb 23; 11(A):117-121. https://doi.org/10.3889/oamjms.2023.10701
Keywords: Chronic kidney failure; Bacterial profilel; Resistance; Meropenem
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Received: 17-Jul-2022
Revised: 27-Sep-2022
Accepted: 16-Feb-2023

Funding: This research did not receive any financial support
Competing Interests: The authors have declared that no competing interests exist

Abstract

BACKGROUND: Patients with chronic kidney disease (CKD) tend to have low immunity so they are easily infected. Treatment using meropenem is relatively safe but must be based on antibiotic sensitivity testing to prevent resistance.

AIM: The aim of the study was to determine the bacterial profile and its sensitivity to the antibiotic meropenem in patients with end-stage chronic renal failure.

METHODS: This was a quantitative, descriptive, and cross-sectional research. Data derived from medical records of selected hospitals. The sample was based on inclusion and exclusion criteria with ICD10 N18.0 and N18.5 codes in January–December 2016. Data are processed with descriptive statistics.

RESULTS: There were 39 CKD patient at Hospital X and 29 respondents at Hospital Y that received meropenem. There were only 14 CKD patients at hospital X and 22 CKD patients at hospital Y with culture tests and results. There were nine samples in Hospital X and 29 samples in Hospital Y that showed bacterial growth. There were 31 (81.58%) g negative bacteria, 6 (15.79%) g positive bacteria, and 1 (2.63%) aerob bacteria. *Citrobacter* from samples of pus and *Acinetobacter baumannii* (×1) from urine samples were resistant to meropenem.

CONCLUSION: The majority of bacterial culture results are Gram-negative. *Eschericia coli* bacteria are the most commonly Gram-negative bacteria. *Citrobacter* bacteria and *A. baumannii* bacteria are resistant to meropenem.

Introduction

Kidney disease is an irreversible condition in kidney function. In very bad condition, it requires permanent renal replacement therapy, that is: Dialysis and kidney transplantation [1]. Chronic kidney disease (CKD) is a state of chronic inflammation. Chronic inflammation weakens the body's immune response to infections. Hence, CKD patients are at an increased risk of infections. Urinary tract infection (UTI) is one of the most common types of community-acquired infection. There [2]. Infections in CKD patients must be treated first because infections can make kidney disease worse [3].

Meropenem at the recommended dose is a safe antibiotic. It is widely used for infection CKD patients. Patients with renal replacement therapy or creatinine clearance (CrCl) of <70 mL/min had high rates of target attainment with the standard dosing regimens. There was a low number of patients with a CrCl >100 mL/min that achieved the target concentrations with the maximum recommended dosage. Patients with impaired renal function only required therapeutics drug monitoring if toxic side effects were noted. Hence, it can be used [4]. It also can be used for febrile neutropenia, sepsis, and other severe infections. The maximum used is 7 days/patient. After the antibiotic sensitivity culture are obtained, it will be replaced with first-line or narrow-spectrum antibiotic [5]. In the previous study, seven types of bacteria were identified, namely, *Eschericia coli*, *Streptococcus*, *Staphylococcus*, Gram-negative *Cocci*, Gram-positive *Coccus*, *Seratia marcesnes*, and *Bacillus subtilis*. The most common type of bacteria found in hemodialysis CKD patients was *B. subtilis* (50%). The most common type of bacteria found in non-hemodyliasis CKD patients was *E. coli* (25%) [6]. Based on the information above, CKD patient is prone to infection so it is important to know its bacterial profile. Although Meropenem is safe, it must be used based on antibiotic sensitivity test results to prevent antimicrobial resistant. Therefore, this study is important because it determines the bacterial profile and sensitivity to the antibiotic meropenem especially in patients with end-stage chronic renal failure in a general hospital. We get data from research "Analysis of Cost Effectiveness of the Use of Meropenem Based on Sensitivity Test Results Compared Not Based on Antibiotic Sensitivity Test Results in Patients with Chronic Renal Failure in Hospitals" [3].

Methods

This study was quantitative and descriptive research. The method was cross-sectional. The research location was selected based on predetermined criteria. There were two selected government teaching hospitals. We did it from April to December 2017. The research population was medical data of patients with chronic kidney failure with ICD10 codes N18.0 and N18.5 who went to selected hospitals in January–December 2016. Research sample was patient medical data with chronic kidney failure that complied with inclusion and exclusion criteria. Inclusion criteria were adult (≥18 years), hospitalized at least 3 days, patients diagnosed infection with leukocyte parameters and changes in "vital signs," patient chronic with end stage kidney failure, patient received meropenem therapy, and complete laboratorium data. Exclusion criteria were patient force to go home and critical patient. Based on inclusion and exclusion criteria, we get 39 respondents at hospital X and 29 respondent at hospital Y. Based on the completeness of the data in the medical record, there were only 14 (35,9%) respondents at Hospital X who tested for bacterial culture after or before administration of meropenem. Meanwhile, in Hospital Y, there were 22 (75.9%) respondents who were tested for bacterial culture after and before administration of meropenem. There were only nine bacterial growth at hospital X and 29 bacterial growth at hospital Y. We analyzed data on bacterial profiles and their sensitivity to meropenem. Sources of research data came from the patient registration unit and medical records, pharmacy installations, hospital information systems (SIRS/INSTI), and hospital finances. The data obtained were processed by descriptive statistics.

Results

Based on Table 1, the number of culture tests in both hospitals was greater than the number of respondents. It could be happen because some respondents conducted more than one culture test. Culture tests do not always result in bacterial growth. The number of culture tests with bacterial growth in Hospital X (9) was less than Hospital Y (29). There were 31 (81.58%) g negative bacteria, 6 (15.79%) g positive bacteria, and 1 (2.63%) aerob bacteria.

Table 1: Number of respondents with culture tests and results

S. No.	Parameter	Hospital X	Hospital Y
1	Number of responden	14	22
2	Number of culture test	25	42
3	Number of bacterial growth	9	29
4	Number of non bacterial growth	15	13

Based on Table 2, there were four samples that were tested for pus culture. Bacterial growth occurred in three samples. The results of bacterial cultures were *Proteus*, *Citrobacter,* and *E. coli*. All of them were gram negative bacteria. The other sample showed no bacterial growth.

Table 2: Bacterial profile of respondents at X hospital

S. No.	Culture sample	Bacterial growth		
		No	Yes	
		Number	Number	Bacterial
1	Pus	1	3	*Eschericia coli, Proteus, Citrobacter*
2	Blood	11	2	*Staphylococcus capitis; Aeromonas sobria*
3	Urin	2	4	*Staphylococcus haemolyticus, Eschericia coli* (2×), Bakteri Aerob
4	Sputum	1	-	-

There were 13 samples that were tested for blood culture. Bacterial growth only occurred in two samples. The results of bacterial cultures were *Staphylococcus capitis* and *Aeromonas sobria*. They were (50%) Gram-negative and (50%) g positive bacteria. Other samples showed no bacterial growth.

There were six samples that were tested for urine culture. Bacterial growth occurred in four samples. The results of bacterial cultures were *E. coli* (×2), *Staphylococcus haemolyticus* (×1), Aerobic Bacteria (×1). Hence, there were 2 (50%) g negative bacteria, 1 (25%) g positive bacteria and 1 (25%) aerobic bacteria. Other samples showed no bacterial growth. Antibiotic sensitivity test was carried out on the growth of *E. coli* and *S. haemolyticus.* There was only one sample of sputum culture test and it was performed before administration of meropenem. The results of the culture test showed no bacterial growth.

Based on the results of the antibiotic sensitivity test, only *Citrobacter* from the pus sample was resistant to meropenem. *Citrobacter* was g negative bacteria. Five samples were stated to be still sensitive to meropenem. Urine samples with the growth of aerobic bacteria and *E. coli* bacteria were not tested for antibiotic sensitivity. Urine samples with the growth of *S. haemolyticus* were not sensitivity tested to meropenem.

Based on Table 3, the bacterial culture samples at Hospital Y came from 14 blood, one pus, seven sputum, 16 urine, three chateter urine, and one wound swab. Not all samples tested contained bacterial growth. There was one sample had the growth of *Candida tropicalis* fungus. Samples with bacterial growth came from five blood samples, 13 urine samples, and three sputum samples, one wound swab sample,

Table 3: Bacterial profile of respondents at Y hospital

S. No.	Culture Sample	Bacterial growth		
		No	Yes	
		Number	Number	Bacterial
1	Urin	3	13	*Eschericia coli* (7×); *Acinetobacter baumannii* (2×); *Klebsiella pneumoniae* (2×); *Achromobacter xylosoxidan* (1×); *Enterococcus faecalis* (1×)
2	Urin chateter	1	2	*Enterococcus faecium* (1×); *Eschericia coli* (1×)
3	Sputum	0	7	*Klebsiella pneumoniae* (3x); *Acinetobacter r* (1×); *Acinetobacter* (1×); *Pseudomonas aeruginosa* (1×); *Eschericia coli* (1×)
4	Blood	9	5	*Staphylococcus capitis* (1×); *Staphylococcus epidermidis* (1×); *Klebsiella pneumoniae* (1×); *Eschericia coli* (1×); *Burkholderia cepacia* (1×)
5	Pus	0	1	*Eschericia coli* (1×)
6	Swab	0	1	*Eschericia coli* (1×)

two chateter urine samples, and one pus sample. There were 25 (86.21%) g negative bacteria and 4 (13.79%) g positive bacteria.

The bacteria that grew in the blood samples were *Burkholderia cepacia*, *E. coli*, *Klebsiella pneumoniae*, *Staphylococcus epidermidis*, and *S. capitis*. There were 3 (60%) g negative bacteria and 2 (40%) g positive bacteria.

The bacteria that grew in the urine sample were *E. coli* (7×), *Achromobacter xylosoxidan*, *K. pneumoniae*, *Acinetobacter baumannii* (2×), *Klebsiella*, and *Enterococcus faecalis*. There were 12 (92.31%) g negative bacteria and 1 (7.69%) g positive bacteria.

The bacteria that grew in the sputum samples were *Pseudomonas aeruginosa*, *E. coli*, *Acinetobacter*, *K. pneumoniae* (2×), *Klebsiella, and Acinetobacter*. All of them were gram negative bacteria.

The bacteria that grows in the wound swab were *E. coli*. It is Gram-negative bacteria. The bacterium that grows in the pus sample was *E. coli*. It is Gram-negative bacteria.

Bacteria that grow in chateter urine samples were *E. coli* and *Enterococcus faecium*. There were 1 (50%) g negative bacteria and 1 (50%) g positive bacteria.

In Hospital Y, all samples with bacterial growth were tested for antibiotic sensitivity. Based on the results of antibiotic sensitivity tests, only *A. baumannii* bacteria from urine samples were resistant to meropenem. *A. baumannii* was Gram-negative bacteria. Twenty samples were declared still sensitive to meropenem. Seven other samples were not sensitivity tested to meropenem, including: Urine sample of chateter with growth of *E. faecium*, sputum sample with growth of *Acinetobacter*, blood sample with growth of *S. capitis*, blood sample with growth of *S. epidermidis*, urine sample with growth of *K. pneumoniae*, blood samples with the growth of *B. cepacia*, and sputum samples with the growth of *P. aeruginosa*.

Discussion

Based on research data, there were only nine samples in Hospital X that showed bacterial growth from 25 samples. While in Hospital Y, there were 29 samples that showed bacterial growth from 42 samples. Other study stated that the results of the culture showed that 16 (34.8%) of the culture treatments were identified as microbes and 30 (66.2%) of the culture results showed that no microbes were identified [7]. Bacterial growth was not only influenced by the presence of bacteria, but was also influenced by temperature, pH, oxygen, osmotic pressure, and surrounding chemical elements such as C, H, N, S, and P. Besides that, it also required micro elements such as Zn, Fe, and Cu [8].

Based on research data, At Hospital X, there were four g-positive bacteria and six g-negative bacteria. At Y Hospital, there were four g positive bacteria and 25 g negative bacteria. Another study stated that there were 21 types of bacteria from 111 samples. There were 70.7% g-negative and 29.3% g-positive bacteria [9]. Another study had different result. There were 36 g positive bacteria and 22 g negative bacteria from 58 samples [10]. It was also in line with Chudlori *et al*. (2012) [11] and Verma (2012) [12]. Chudlori's research (2012) found 66.04% g negative bacteria [11]. Verma's (2012) research found 60% g negative bacteria [12]. It could happen because Gram-negative bacteria were more often resistant. It would complicate therapy so that Gram-negative bacteria were more often found. Bacterial resistance is due to irrational use of antibiotics.

There are several factors that can influence the shift in bacterial patterns, that is: differences in immune responses, population genetic factors, differences in the way of microbiological analysis, differences in levels of education, and health services as well as changes in the pattern of antibiotic use (inappropriate administration of antimicrobials in empirical therapy and inappropriate infection control strategies) [13]. Hence, the differences in the types of bacteria could possibly be caused by several factors including research methods, research tools and media used, room and air conditions, and the quantity of bacterial colonies that grew differently.

Based on blood sample research data, there were five g negative and three g positive bacteria. The results of Gram-negative bacteria cultures were *B. cepacia*, *E. coli*, *K. pneumoniae*, and *A. sobria* (×2). The results of the Gram-positive bacteria were *S. epidermis* and *S. capitis* (×2). Another study stated that in blood specimens, they found *Staphylococcus* coagulase negative bacteria (3), *P. aeruginosa* (1), *K. pneumoniae* (1) [7]. *Aeromonas* bacteria were emerging pathogens that caused various diseases to humans, that is,: gastroenteritis, septicemia, and wound infections. It could infect to both immunocompromised and immunocompetent patients [14], [15]. *Staphylococcus* coagulase negative bacteria were frequently found on skin, blood cultures, or other samples. Six species was associated to higher clinical significance, namely, *S. epidermidis*, *Staphylococcus saprophyticus*, *S. haemolyticus*, *S. capitis*, *Staphylococcus hominis,* and *Staphylococcus lugdunensis* [16].

Based on sputum sample research data, there were six cultures of Gram-negative bacteria, that is, *P. aeroginosa*, *Acinetobacter*, *K. pneumoniae*, *Klebsiella*, *Acinetobacter*, and *E. coli*. Other study stated that out of 2318 samples, 694 (29.93%) sputum samples at 95% confidence interval (737.21–650.79) were reported as culture positive. *Klebsiella* was the most common isolate followed by *Pseudomonas*, *E. coli*, *Acinetobacter*, *Staphylococcus aureus*, *Candida* *albicans*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, and others. Imipenem and vancomycin showed the most sensitivity toward Gram-negative and Gram-positive bacteria, respectively [17]. Other study stated that Gram-negative bacteria were pathogenic bacteria that caused acute respiratory infection, such as *P. aeruginosa*, *K. pneumoniae*, *Enterobacter aerogenes,* and *Proteus mirabilis* [18].

Based on urine sample research data, there were seven cultures of Gram-negative bacteria, two cultures of Gram-positive bacteria, and an aerobic bacteria. The results of Gram-negative bacteria culture were *P. aeroginosa*, *Acinetobacter*, *K. pneumoniae*, *Klebsiella*, *Acinetobacter*, and *E. coli*. The results of Gram-positive bacteria were *E. faecalis* and *S. haemolyticus*. *E. coli* was bacteria that most often grow in urine samples. Other study also stated that the most common type of bacteria causing UTI was Gram-negative bacteria. The most common Gram-negative bacteria were *E. coli* [19]. Other study also stated that the bacteria in the urine culture were *E. coli*, *Streptococcus* spp, *Staphylococcus* spp, *Coccus* Gram negative, *Coccus* Gram positive, *S. marcesnes,* and *B. subtilis* [20].

Based on chateter urine sample research data, there were one g negative bacteria and one g positive bacteria, that is: *E. coli* and *E. faecium*. Other study also state that the most common bacterial isolates were *E. coli* 17/42 (40.5%), *Klebsiella* species 9/42 (21.4%), and *Enterococcus* species 5/42 (11.9%) [21].

Based on pus sample research data, there were three g negative cultures only. The results of the culture of Gram-negative bacteria were *E. coli* (2×), *Proteus*, and *Citrobacter*. Another study stated that the most common pus-producing bacteria were *Staphylococcus aureus*, *Klebsiella* spp., *Pseudomonas* spp., *E. coli*, and *Streptococcus spp*. *Staphylococcus aureus* is the most common bacteria that produces pus in wounds [22].

Based on wound swab sample research data, the bacteria were *E. coli*. Another study stated that the swab results for diabetic ulcers were *P. aeruginosa* and *E. coli* [7]. Based on the PCR results, the most bacterial growth in surgical wounds was *P. aeruginosa* in 6 samples (46.1%), followed by *E. coli* in 2 samples (15.4%) and *Enterobacter hormaechei*, *Alkaligenes faecalis*, *Enterobacter cloacae*, *Bacteroides fragilis*, and *P. mirabilis*, each with 1 sample (7.7%) [23].

Based on the results of the antibiotic sensitivity test at Hospital X, only *Citrobacter* from the pus sample was resistant to meropenem. Based on the results of the antibiotic sensitivity test at Hospital Y, only *A. baumannii* from urine samples was resistant to meropenem. Other study also shown that most *A. baumannii* was resistant to carbapenems such as doripenem, ertapenem, meropenem, and imipenem [24]. According to research by Sieniawski *et al*. in hospitals in Asia and the Middle East (2013) found that *A. baumannii* caused the most infections [25]. *A. baumannii* was an opportunistic pathogen that often causes severe infections or nosocomial infections, especially in long hospitalized immunocompromised patient [26].

Conclusion

The majority of bacterial cultures were Gram-negative bacteria. Based on the results of the bacterial sensitivity test, it was found that only *Citrobacter* bacteria from pus samples and *A. baumannii* bacteria from urine samples were resistant to meropenem. Meropenem is broad spectrum carbapenem antibiotic. Hence, it must be used wisely based on antiobiotic sensitivity test.

Acknowledgment

The authors would like to thank to those who have contributed to this research, namely: Head of the Center for Humanities and Health Management, Head of the Center for Health Resources and Services, Bpk. Dr. Karyana, dr. Maria Shinta Dame Parhusip, Sp.PK., Dr. dr. Laurentia Konadi, MS., Sp.GK., Dr. Ingan Tarigan, SKM., M.Kes., Dra. Selma Siahaan, M.Si., Dr. Masdalina Pane, and M.Kes. Other parties that cannot be mentioned one by one who greatly helped the process of collecting data for this research.

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