

การตรวจหาชิ้นที่สร้างเอนไซม์ carbapenemases ในเชื้อ *Acinetobacter baumannii*



นางนภาพรรณ ปุณกบุตร

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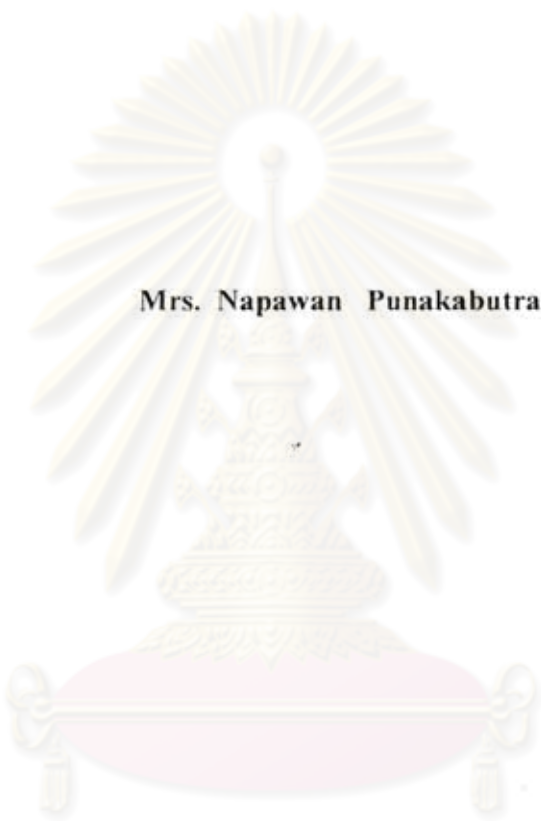
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**DETECTION OF CARBAPENEMASE GENES IN
*ACINETOBACTER BAUMANNII***



Mrs. Napawan Punakabutra

**A Thesis Submitted in Partial Fulfillment of the Requirements
for the Degree of Master of Science Program in Medical Microbiology**

(Interdisciplinary Program)

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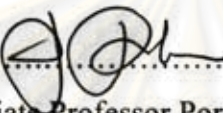
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นภาพรณ ปุณณบุตร : การตรวจหาชิ้นที่สร้างเอนไซม์ carbapenemases ในเชื้อ *Acinetobacter baumannii*. (Detection of Carbapenemase Genes in *Acinetobacter baumannii*) อ. ที่ปรึกษาวิทยานิพนธ์หลัก : ดร. ธนิษฐา นัครสุวรรณ , อ.ที่ปรึกษาวิทยานิพนธ์ร่วม : อ. นิพนธ์ อุดมสันติสุข, 167 หน้า.

Carbapenems เป็นยาที่นิยมใช้ในการรักษาการติดเชื้อ *Acinetobacter baumannii* ที่คือต่อยาหลายชนิด อย่างไรก็ตาม มีรายงานการดื้อยาของกลุ่ม carbapenems ในเชื้อชนิดนี้ทั่วโลก การศึกษานี้มีวัตถุประสงค์เพื่อตรวจหาชิ้นที่สร้างเอนไซม์ carbapenemases ในเชื้อ *A. baumannii* และตรวจหาความชุกของการดื้อยา กลุ่ม carbapenems โดยทำการศึกษาในเชื้อ *A. baumannii* จำนวน 501 สายพันธุ์ซึ่งเพาะแยกได้จากผู้ป่วยในโรงพยาบาลจุฬาลงกรณ์ ระหว่างเดือนมกราคม ปี พ.ศ.2547 ถึงเดือนสิงหาคม ปี พ.ศ.2550 จากการทดสอบความไวรับของเชื้อด้วยวิธี Agar dilution พบว่า อัตราการดื้อยา imipenem และ meropenem คือ 82.4% และ 81.8% ตามลำดับ เชื้อที่ดื้อยาของกลุ่ม carbapenems ทุกสายพันธุ์มี carbapenemase activity เมื่อทดสอบโดยวิธี modified Hodge test ไม่พบเอนไซม์ Metallo- β -lactamases เมื่อทดสอบด้วยวิธี imipenem-EDTA double-disk synergy test การตรวจคัดกรองชิ้นที่สร้างเอนไซม์ carbapenemases ในเชื้อทั้งหมด 501 สายพันธุ์ได้แก่ $bla_{OXA-like}$, $bla_{IMP-like}$ และ $bla_{VIM-like}$ ด้วยวิธี PCR พบยีน $bla_{OXA-23-like}$, $bla_{OXA-24-like}$, $bla_{OXA-51-like}$ และ $bla_{OXA-58-like}$ แต่ไม่พบยีน $bla_{IMP-like}$ และ $bla_{VIM-like}$ โดยเชื้อ *A. baumannii* ทุกสายพันธุ์มียีน $bla_{OXA-51-like}$ ซึ่งสายพันธุ์ที่พบยีน $bla_{OXA-51-like}$ เพียงชนิดเดียวจะไวต่อยาของกลุ่ม carbapenems ในขณะที่สายพันธุ์ที่พบยีน $bla_{OXA-51-like}$ ร่วมกับยีน $bla_{OXA-like}$ ชนิดอื่นๆ ได้แก่ $bla_{OXA-23-like}$, $bla_{OXA-24-like}$ และ $bla_{OXA-58-like}$ จะคือต่อยา carbapenems การศึกษาครั้งนี้เชื้อ *A. baumannii* ที่คือยาของกลุ่ม carbapenems พบยีน $bla_{OXA-51-like}$ ร่วมกับยีน $bla_{OXA-23-like}$ มากที่สุด (93.2%) เมื่อทำการวิเคราะห์ลำดับ นิวคลีโอไทด์ของยีน $bla_{OXA-23-like}$, $bla_{OXA-24-like}$, $bla_{OXA-51-like}$ และ $bla_{OXA-58-like}$ ในเชื้อ *A. baumannii* ชนิดละ 10 สายพันธุ์ พบว่าเป็นชนิด bla_{OXA-23} (100%), bla_{OXA-72} (100%) และ bla_{OXA-58} (100%) ตามลำดับ พบความหลากหลายในยีนกลุ่ม $bla_{OXA-51-like}$ โดยพบเป็น bla_{OXA-68} 5 สายพันธุ์ (50%), bla_{OXA-66} 2 สายพันธุ์ (20%), bla_{OXA-64} 1 สายพันธุ์ (10%), bla_{OXA-67} 1 สายพันธุ์ (10%) และ $bla_{OXA-51-like}$ ชนิดใหม่ซึ่งยังไม่เคยมีรายงานมาก่อน 1 สายพันธุ์ (10%) โดยลำดับนิวคลีโอไทด์และกรดอะมิโนของเอนไซม์ชนิดใหม่นี้มีความเหมือนกับลำดับนิวคลีโอไทด์และกรดอะมิโนของ $bla_{(OXA-51)}$ และ OXA-51 99%

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NAPAWAN PUNAKABUTRA : DETECTION OF CARBAPENEMASE GENES IN *ACINETOBACTER BAUMANNII*. THESIS PRINCIPLE ADVISOR : TANITTHA CHATSUWAN, Ph.D., THESIS COADVISOR : NIBONDH UDOMSANTISUK, 167 pp.

Carbapenems are among the drugs of choice for treatment of multidrug-resistant *Acinetobacter baumannii* infections. However, emergence of carbapenem resistance in *A. baumannii* has been reported worldwide. The present study identified carbapenemase genes in *A. baumannii* and investigated the prevalence of carbapenem resistance of the 501 *A. baumannii* isolated from patients at the King Chulalongkorn Memorial Hospital, Bangkok during January 2004 to August 2007. The minimal inhibitory concentrations (MICs) of imipenem and meropenem were determined by agar dilution. Resistance rates were 82.4% and 81.8% for imipenem and meropenem, respectively. All carbapenem-resistant isolates had carbapenemase activity by modified Hodge test. Metallo- β -lactamases were not detected in any isolate when screened by imipenem-EDTA double-disk synergy test. Screening for carbapenemase genes in the 501 *A. baumannii* by PCR revealed the presence of *bla*_{OXA-23-like}, *bla*_{OXA-24-like}, *bla*_{OXA-51-like} and *bla*_{OXA-58-like} and the absence of *bla*_{IMP-like} and *bla*_{VIM-like}. All 501 *A. baumannii* isolates carried the *bla*_{OXA-51-like} gene. The isolates carrying only *bla*_{OXA-51-like} were susceptible to carbapenems whereas the isolates carrying *bla*_{OXA-51-like} together with other *bla*_{OXA-like} including *bla*_{OXA-23-like}, *bla*_{OXA-24-like} and *bla*_{OXA-58-like} were resistant to carbapenems. The presence of *bla*_{OXA-51-like} together with *bla*_{OXA-23-like} were detected in the majority of carbapenem-resistant *A. baumannii* isolates (93.2%), suggesting that *bla*_{OXA-23-like} plays a major role in carbapenem resistance. DNA sequences of the entire *bla*_{OXA-23-like}, *bla*_{OXA-24-like}, *bla*_{OXA-51-like} and *bla*_{OXA-58-like}, each from 10 representative isolates, were analyzed. The results revealed that the *bla*_{OXA-23-like}, *bla*_{OXA-24-like} and *bla*_{OXA-58-like} from their 10 representative were *bla*_{OXA-23}, *bla*_{OXA-72} and *bla*_{OXA-58} respectively, whereas those of the *bla*_{OXA-51-like} were *bla*_{OXA-68} (5 isolates), *bla*_{OXA-66} (2 isolates) and *bla*_{OXA-64}, *bla*_{OXA-67} and a novel *bla*_{OXA-51-like} (1 isolate each). Nucleotide and amino acid sequences of this novel enzyme showed 99% identity to *bla*_{OXA-51} and OXA-51.

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ABBREVIATIONS

A	adenosine
AC	amoxicillin
Ala (A)	alanine
Asn (N)	asparagine
Asp (D)	aspartic acid
Arg (R)	arginine
bp	base pair
C	cytidine
CO ₂	carbon dioxide
CH	clarithromycin
CLSI	Clinical and Laboratory Standards Institute
°C	degree Celsius
Cys (C)	cysteine
dATP	deoxyadenosine 5'-triphosphate
dCTP	deoxycytidine 5'-triphosphate
ddATP	dideoxyadenosine 5'-triphosphate
ddCTP	dideoxycytidine 5'-triphosphate
ddGTP	dideoxyguanosine 5'-triphosphate
ddTTP	dideoxythymidine 5'-triphosphate
DDW	double distilled water
ddNTPs	dideoxynucleotide-tri-phosphate
dGTP	deoxyguanosine 5'-triphosphate
DNA	deoxynucleic acid
dNTPs	deoxynucleotide-tri-phosphate
dTTP	deoxythymidine 5'-triphosphate
DW	distilled water
EDTA	ethylenediamine tetraacetic acid
<i>et al.</i>	<i>et alii</i>
E-test	epsilometer test
g	gram
G	guanosine
Gly (G)	glycine

Glu (E)	glutamic acid
Gln (Q)	glutamine
HCl	hydrochloric acid
HPLC	high performance liquid chromatography
hr	hour
His (H)	histidine
i.e.	id test
Ile (I)	isoleucine
Lys (K)	lysine
Leu (L)	leucine
M	molar
mg	milligram
MgCl ₂	magnesium chloride
MIC	minimum inhibitory concentration
min	minute (s)
mL	milliliter
mM	millimolar
mmol	millimole
Met (M)	methionine
NaCl	sodium chloride
Na ₂ HPO ₄	sodium phosphate dibasic, anhydrous
NaOH	sodium hydroxide
NARST	National Antimicrobial Resistance Surveillance Center Thailand
Phe (F)	phenylalanine
PCR	polymerase chain reaction
<i>Pfu</i>	<i>Pyrococcus furiosus</i>
pmol	picomol
Pro (P)	proline
sec	second
Ser (S)	serine
T	thymidine
TAE	tris-acetate-EDTA
Thr (T)	threonine

Tris	Tris-(hydroxymethyl)-aminoethane
Trp (W)	tryptophan
Tyr (Y)	tyrosine
U	unit
μg	microgram
μL	microliter
μM	micromolar
UV	ultraviolet
V	volt



ศูนย์วิทยทรัพยากร
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CHAPTER I

INTRODUCTION

Acinetobacter baumannii is an opportunistic pathogen that is frequently involved in nosocomial infection. *A. baumannii* is mostly a cause of infection in all systems such as septicemia, urinary tract infection, ventilator-associated pneumonia and skin infection following hospitalization of patients with more severe illness or immunocompromised patients. Carbapenems such as imipenem and meropenem are drugs of choice for treatment of *A. baumannii* infection, but carbapenem resistance in this species is now observed increasingly worldwide and also to be multidrug-resistance strains.

Carbapenems are member of β -lactam antibiotics, act cytostatically on bacteria by inactivating peptidoglycan transpeptidases known as penicillin-binding proteins (PBPs) that catalyse the cross-linking of the peptidoglycan polymers in the bacterial cell wall. Primary cause of carbapenem resistance in *A. baumannii* is β -lactamase production such as carbapenemase enzymes to destroy β -lactam ring structure of drug, resulting in loss of efficiency. Other resistance mechanisms are attributed to reduced affinity of PBPs for carbapenems, increased efflux of the β -lactam antibiotics, decreased permeability of the outer membrane or to a combination of several mechanisms.

The β -lactamases can be classified into four different molecular groups, A, B, C and D according to amino acid sequence identities. Class A, C and D β -lactamases use a catalytically active serine residue for inactivation of the β -lactam drug, while molecular class B β -lactamases are metallo-enzymes requiring zinc for their catalytic activity. Carbapenemase production is the major mechanism of carbapenem resistance in *A. baumannii*. Most of these enzymes are members of class D β -lactamase (oxacillinase), followed by class B metallo- β -lactamase such as IMP-type and VIM-type and rarely found in class A β -lactamase (1).

Carbapenems such as imipenem and meropenem are drugs of choice for treating penicillin- and cephalosporin-resistant *A. baumannii*. Reports of carbapenem-resistance *A. baumannii* have been increasing over the last few years. In Taiwan, the proportion of *A. baumannii* resistant to carbapenems rose from 5.88% in 1993 to 21.5% in 2000 (2). In 1999, carbapenem-resistance *A. baumannii* was 53% in USA and 34% in Spain during 1997 to 1999 (3, 4). Furthermore, there were many reports about carbapenem-resistance *Acinetobacter* spp. worldwide such as Greece (5), Turkey (6, 7), Croatia (8), Italy, England (9), Germany, Poland, China, Brazil, France (10, 11), Argentina (12), Romania (13), etc.

Most of carbapenemase enzymes that found in *A. baumannii* are OXA-type carbapenemase (oxacillinase), whereas metallo- β -lactamases such as IMP-type and VIM-type have been rarely identified. First carbapenem-hydrolyzing oxacillinase (CHDLs) encoding gene was reported in *A. baumannii* in 1995. This enzyme, originally named ARI-1, was identified in Scotland and it was renamed OXA-23 following its genetic and biochemical reaction (14). After that, there were many reports about OXA-type carbapenemases produced by *A. baumannii* around the world. OXA enzymes can be subclassified into eight subgroups by amino acid identities. Four of the eight subgroups, OXA-23 like, OXA-24 like, OXA-51 like and OXA-58 like, have been identified in *A. baumannii*. The first subgroup encompasses the OXA-23, -27 and -49, which were reported in Brazil (15), Korea (16), China (17), Singapore (18), Scotland (14), South America (19), United Kingdom (20), Australia (21) and Tahiti (11). The second subgroup encompasses the OXA-24 to -26, -33, -40 and -72, which were reported in Spain (22), Belgium (23) and France (24). The Third subgroup consists of the OXA-51 family, including OXA-51, OXA-64 to -71, OXA-75 to -80, OXA-82 to -84, OXA-86 to -95, OXA-99, OXA-100, OXA-104, OXA-106 to -113, OXA-115 to -117, OXA-128, OXA-130 to -132. They were reported in Argentina (25-27), Spain (25), Hong Kong (25), Singapore (25), South Africa (25), France (28), Poland (29), United Kingdom (30), Greece (31, 32) and Turkey. The fourth subgroup encompasses the OXA-58, -96 and -97, which were reported in South Europe (13), France (33), Singapore (18) and Tunisia (34). For IMP-type, there were reported in *Acinetobacter* spp. IMP-1 were reported in Japan (35), Korea (36, 37) and Italy (38). IMP-2, IMP-4, IMP-5, IMP-6 and IMP-11 were

reported in Italy (39), Hong Kong (40), Portugal (41), Brazil (42) and Japan (43), respectively. For VIM-type, VIM-2 were reported in *A. baumannii* in Korea (36, 44). VIM-1 and VIM-2 were reported in *Acinetobacter* spp. in Italy (41) and Korea (36, 45), respectively whereas SIM-1 was reported in South Korea (46).

In Thailand, there was no evidence of carbapenem resistance in *Acinetobacter* spp. at Siriraj Hospital in 1998 (47). In 1999, *Acinetobacter* spp. were 21% resistant to imipenem at Vajira Hospital (48). In 2007, imipenem resistance rate of *A. baumannii* collected from Chiang Mai University Hospital were 35.5% (49). At the same period, the imipenem resistance rate of 2,130 *A. baumannii* isolated from clinical specimens at Songklanagarind Hospital was 34.7%. The 61.9% of these imipenem-resistance *A. baumannii* isolates were isolated from respiratory tract, and frequently found in ICU. Moreover, 14.8% of all imipenem-resistance *A. baumannii* isolates were resistant to all routine tested antibiotics (50). In 2003, the imipenem resistance rate of *A. baumannii* was 61% at Police General Hospital (51). Sixty-eight percent of *A. baumannii* isolated from Siriraj Hospital in 2006 were resistant to carbapenems and 57% were resistant to all antimicrobials currently available in Thailand (52). The data from the National Antimicrobial Resistance Surveillance Center Thailand (NARST) showed that imipenem resistance in *Acinetobacter calcoaceticus-baumannii* complex increased from 2% in 1998 to 57% in 2006 (53).

The emergence of carbapenem resistance in *A. baumannii* has become a global concern including Thailand. In Thailand there are few studies on mechanisms of carbapenem resistance in *A. baumannii*. The purpose of this study is to determine carbapenemase genes including *bla*_{OXA-23-like}, *bla*_{OXA-24-like}, *bla*_{OXA-51-like}, *bla*_{OXA-58-like}, *bla*_{IMP-like} and *bla*_{VIM-like} in carbapenem-resistant *A. baumannii* and investigate the prevalence of carbapenem resistance in *A. baumannii* isolated from Thai patients between January 2004 and August 2007.

CHAPTER II

OBJECTIVES

- I. To examine carbapenemase genes (*bla_{OXA}* , *bla_{IMP}* , *bla_{VIM}*) in carbapenem-resistant *A. baumannii*.
- II. To investigate the prevalence of carbapenem resistance in *A. baumannii* isolated from Thai patients.



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CHAPTER III

LITERATURE REVIEW

1. BACTERIOLOGY

Genus *Acinetobacter* is currently classified in the Phylum Proteobacteria, Class Gammaproteobacteria, Order Pseudomonadales, Family Moraxellaceae. There are three genera in this family including *Moraxella*, *Acinetobacter* and *Psychrobacter*. Species in genus *Acinetobacter* are strictly aerobic non lactose fermentative gram negative coccobacillus but occasionaly are difficult to destain. Individual cell is 1 to 1.5 μm by 1.5 to 2.5 μm in size and frequently arrange in pairs. They are non motile, oxidase-negative, catalase positive and do not reduce nitrate to nitrite. Colonies on MacConkey agar are smooth, opaque, colorless or slightly pinkish colonies. All strains grow between 20°C and 30°C. Most strains have optimal temperature at 33-35°C and grow in defined media containing a single carbon and energy source. They use ammonium or nitrate salts as the source of nitrogen. D-Glucose is the only hexose utilized by some strains, whereas the pentose D-ribose, D-xylose and L-arabinose can also be utilized as carbon sources by some strains.

Studies based on DNA-DNA hybridization, showed that there were at least 32 genomic species and 17 of them have been assigned species name as described in Table 1. Genomespecies 1, 2, 3 and 13 of Tjernberg and Ursing are closely related and difficult to separate in the clinical laboratory, referred to as the *A. calcoaceticus*-*A. baumannii* complex (54). Strains belonging to genomic species 2 (*A. baumannii*), 3, and 13 have been found most frequently to be associated with hospital infection and epidemic outbreaks (55-57).

Acinetobacter spp. are generally considered to be nonpathogenic to healthy individuals. However, *A. baumannii* persists in hospital environments and causes severe, life-threatening infections in compromised patients. This organism is resistant to multiple antimicrobial agents and has high capacity for survival on most both

moist and dry environmental surfaces, including respiratory therapy equipment and human skin. It can also be isolated readily from nonclinical sources such as soil, water, sewage and a variety of different foodstuffs. In addition, this organism is also part of the normal oropharyngeal flora of a small number of healthy people and can proliferate to large numbers during hospitalization. These factors have led to an increased concern regarding hospital-acquired infections due to *A. baumannii*.

2. EPIDEMIOLOGY

2.1 Hospital-acquired *A. baumannii* infection

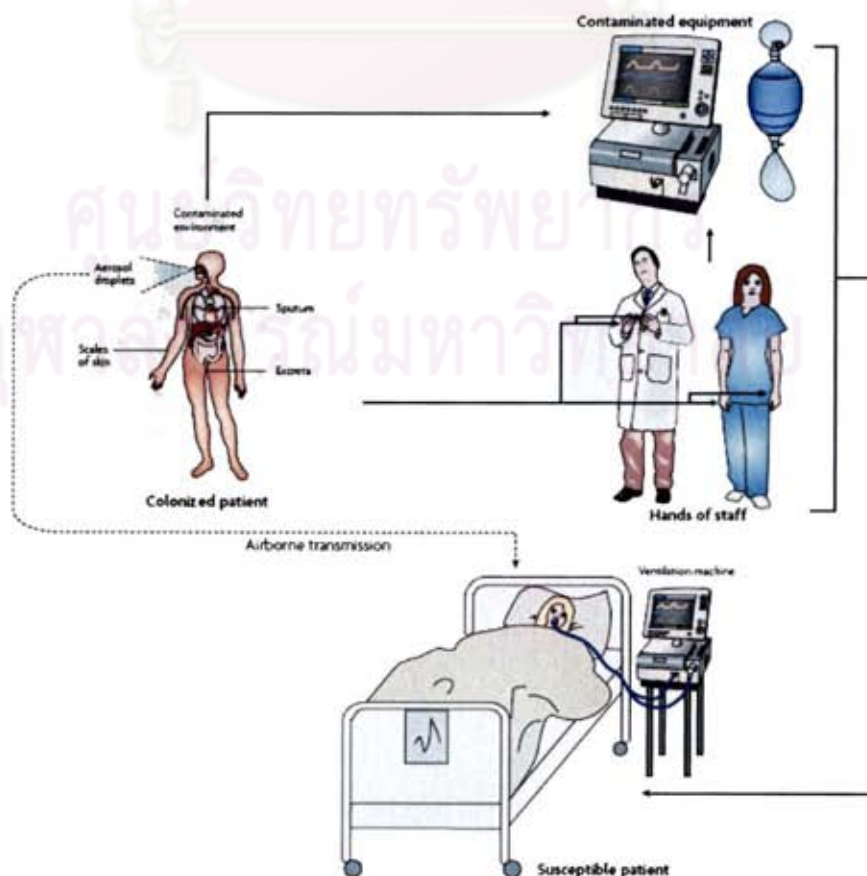
Hospital-acquired *A. baumannii* infection includes ventilator-associated pneumonia, skin and soft-tissue infections, wound infections, urinary-tract infections, secondary meningitis and bloodstream infections. The most frequent clinical manifestations of nosocomial *A. baumannii* are ventilator-associated pneumonia and bloodstream infections. A scheme that explains the dynamics of *A. baumannii* epidemiology in a hospital is shown by Figure 1 (58). *A. baumannii* can spread from the colonized patient to the environment and other susceptible patients via excreta, aerosol droplets and scale of skin. The most common mode of transmission is from the hands of medical staff. Organisms can survive in dry environment. During outbreak, it has been recovered from various patient's environments including bed curtains, furniture and medical equipment. The medical equipments such as mechanical ventilation, indwelling devices (intravascular catheters, urinary catheters and drainage tubes) are the most common contaminated by *A. baumannii*.

The potential risk factors for the acquisition of *A. baumannii* infection include host factors such as major surgery, major trauma especially in burn trauma, prematurity in newborns. The exposure related factors are previous stay in an ICU, the length of stay in hospital or ICU, residence in a unit that *A. baumannii* is endemic, exposure to contaminated medical equipment, the number of invasive procedures, previous antimicrobial therapy and deficiency in the implementation of infection

control guidelines. These factors explain the difficulty of controlling *A. baumannii* infection in hospitals.

The clinical impact of nosocomial *A. baumannii* infection has been debated. Cisneros *et al.* and Seifert *et al.* showed high mortality rates in patients who had *A. baumannii* bacteraemia or pneumonia (59, 60). Falagas *et al.* also concluded that an increase in attributable mortality ranging from 7.8 to 23% was associated with *A. baumannii* infection (61, 62). However, this organism mainly affects patients that severe underlying disease and prognosis. It has been argued that the mortality in patients with *A. baumannii* infection caused by their underlying disease rather than by *A. baumannii* infection. Study by Blot *et al.* showed no significant difference between the mortality rate of *A. baumannii* bacteraemia in ICU patients and control group that were 42.2% and 34.4%, respectively ($P = 0.378$) (63). Similar to the study by Garnacho *et al.*, there was no significant difference between the mortality rate of ventilator-associated pneumonia caused by *A. baumannii* and control group that were 40% and 28.3%, respectively ($P = 0.17$) (64).

Figure 1. Overview of the dynamics between patients, bacteria and the hospital environment (58).



2.2 Community-acquired *A. baumannii* infection

A. baumannii is an important cause of community-acquired pneumonia. The evidence of community-acquired *A. baumannii* infection is increasing. High incidence of bacteraemia and high mortality ranging from 40 to 64% (58). The incidence of community-acquired *A. baumannii* infection has been reported almost exclusively in tropical climates, especially in Southeast Asia and tropical Australia (65, 66). In Israel, *A. baumannii* showed a 31-fold increase when it was hospital-acquired bacteraemia and a 13-fold increase when it was community-acquired bacteraemia by an infection control surveillance program at the Assaf Harofeh Medical Center (AHMC) in 1997-2004 (67). In northern Australia, 10% of all community-acquired bacteremic pneumonia were caused by *A. baumannii* and 21% by gram-negative bacteria in 1992 (68). There were case reports of community-acquired pneumonia caused by *A. baumannii* from countries in tropical or subtropical regions such as Australia (68), Kuwait (69), Taiwan (70) and Thailand (71-73). The prevalence of infection occurred in warm and humid environment might be due to its appropriated condition for growth. The risk factors for community-acquired *Acinetobacter* pneumonia have been associated with underlying conditions such as alcoholism, smoking, chronic obstructive pulmonary disease (COPD) and diabetes mellitus.

3. PATHOGENESIS AND VIRULENCE FACTORS OF *ACINETOBACTER BAUMANNII*

Acinetobacter baumannii is an opportunistic pathogen. Colonization with *A. baumannii* is more common than infection. However it can be severe when an infection is developed. The factors that contribute to *A. baumannii* environment persistence and host infection and colonization are summarized in Figure 2 (58). Adherence to host cell such as bronchial epithelial cells and skin is the first step in the colonization process. *A. baumannii* can survive and grow on host skin and mucosal surface because it can resist to inhibitory agents and conditions that are exerted by these surfaces. In addition, it can resist to desiccation, disinfectants and

antibiotics and can use various substrates for growth, resulting in survival in the environment. Growth on mucosal surfaces and medical devices, such as intravascular catheters and endotracheal tubes, can result in biofilm formation, which enhanced the risk of bloodstream and airway infections (74). Biofilm formation might have been regulated by quorum sensing, the presence of which has been inferred from the detection of a genes that is involved in autoinducer production (75). Virulence factors that could have a role in *A. baumannii* are described below.

1. Adherence of bacterial cell to epithelial cell

Adherence of bacteria to epithelial cells is considered to be an essential first step in colonization and subsequent infection (76). This organism can survive and grow on host skin because organism can resist to inhibitory agents and protective conditions of skin (such as desiccation, low pH, the resident normal flora and toxic lipids). Organism also can survive and grow on mucus membrane because it can resist to the presence of mucus, lactoferrin, lactoperoxidase and the sloughing of cells (58). In addition, the pili and hydrophobic sugars in the O-side-chain moiety of lipopolysaccharide (LPS) might promote adherence to host cells (77-80). Studies by electron microscopy demonstrated that pili on the surface of *Acinetobacter* interact with human epithelial cell. Moreover, there were thread-like connections between these bacteria in early phase of biofilm formation (81).

2. Biofilm formation

Biofilm formation is important pathogenic feature, especially in intravascular line infections and ventilator-associated pneumonia. *A. baumannii* can grow on mucosal surfaces and medical devices such as intravascular catheters and endotracheal tubes by biofilm formation, resulting in enhancing the risk of infection in bloodstream and airways. Study by Rodriguez-Bano demonstrated that all catheters related urinary tract or bloodstream infections and shunt-related meningitis were caused by biofilm forming strains. They also found that previous aminoglycoside use was associated with biofilm-forming isolates (82). *A. baumannii* isolates carrying *bla_{PER-1}* showed a significantly higher ability for epithelial cell

adherence and biofilm formation than isolates without *bla*_{PER-1} (83). Similar to the study by Sechi *et al.*, PFR-1 production in *A. baumannii* was found to be related to cell adhesion (84). In the other hand, treatment with EDTA caused a 55%-65% reduction in biofilm formation by detachment of biofilm cells and inhibit bacterial growth (83). Organisms that caused many device-related and chronic infections and formed biofilm in or on these devices were difficult to eradicate because organisms in biofilm were usually resistant to numerous antimicrobial agents and products of the immune system (85, 86). Similar to the study by Lee *et al.*, multidrug-resistant isolates of *A. baumannii* were reported to form large amounts of biofilm and showed a significant correlation with epithelial cells adherence (83). In addition, the ability of bacterial cells to transfer gene horizontally is increasing within biofilm communities, resulting in the spread of antibiotic resistance (86, 87). So, the high ability to colonize of *A. baumannii* combined with its resistance to multidrugs will contribute to the organism's survival and further dissemination in the hospital.

3. Potential toxic role of lipopolysaccharide

The lipopolysaccharide (LPS) is involved in resistance to complement in human serum and acts in synergy with the capsular exopolysaccharide. The endotoxic potential of *A. baumannii* LPS is able to stimulate inflammatory signaling via Toll-like receptor (TLRs). Whole UV-killed cells of *A. baumannii* could stimulate both TLR2- and TLR4-dependent signaling, whereas pure endotoxins induced signaling only TLR4 (88). In addition, capsular polysaccharide blocks the access of complement to microbial cell wall and prevent the triggering of the alternative pathway of complement activation. Stimulating in innate immune response by the endotoxins and capsular polysaccharide may contribute to the pathology of *A. baumannii* infection.

4. The outer membrane protein

The outer membrane protein A, AbOmpA, previously called Omp38, has been associated with the cytotoxicity induction. AbOmpA is a 38 kDa porin, which is a trimeric porin with a pore size of 1.3 nm and acts as a general diffusion pore. Choi

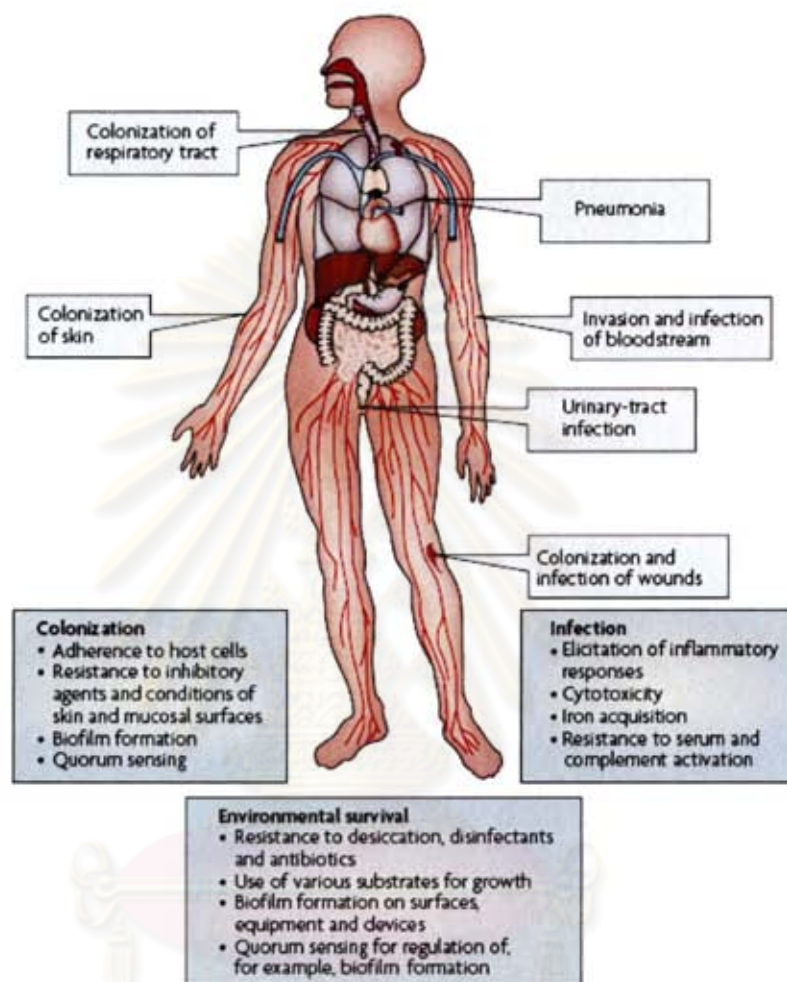
et al. found that this protein was a potent cytotoxin that induced apoptosis of human laryngeal epithelial cell, Hep-2 (89, 90). AbOmpA entered to the Hep-2 cell and was localized to the mitochondria, resulting in releasing of proapoptotic molecules such as cytochrome *c* and apoptosis-inducing factor (AIF) into the cytosol as a consequence of mitochondrial disintegration. This event activated caspase-3 followed by degradation of DNA approximately 180 bp in size. AIF activated caspase-independent apoptosis and degraded chromosomal DNA approximately 50 kb in size, which resulting in large-scale DNA fragmentation. Apoptosis of epithelial cells may disrupt the mucosal lining and resulting in invading of bacteria or bacterial products to deep tissues.

5. Siderophores synthesis

A. baumannii is able to utilize host resources for its survival in human. Iron is an important resource that is not readily available in human, rather it is found to be complexed with iron-binding molecules, including heme and lactoferrin (91, 92). Siderophores are low-molecular-mass ferric binding compounds that can uptake iron in iron-limiting conditions. The bacteria can survive and multiply under iron-limiting conditions by expressing this active system, siderophores synthesis. Siderophores are classified into four categories by their chemical structures (91, 93). Yamamoto *et al.* demonstrated the structure of acinetobactin, the siderophore secreted by *A. baumannii* 19606 had a phenolate group as the iron-binding site (94). Acinetobactin formed complex with ferric and this complex were transported into bacterial cell across the bacterial membrane via the FatA-like protein (95). Other bacteria that has siderophores synthesis is *Vibrio anguillarum*, which secreted anguibactin for iron acquisition.

Over all together, the ability of *A. baumannii* to adapt in variable conditions together with antibiotic resistance and effective stress-response mechanisms might explain the success of *A. baumannii* infection.

Figure 2. The factors that contribute to *A. baumannii* environment persistence and host infection and colonization (58).



4. DIAGNOSIS OF *A. BAUMANNII* INFECTION

Infection or colonization with *A. baumannii* is usually diagnosed by culture of blood, sputum, urine, wound, sterile body fluid, ect. on routine medium. There are several methods for identifying *A. baumannii*, including phenotypic and genotypic identification as described below.

Phenotypic Identification

A. baumannii is gram negative coccobacilli usually diploid form. Colonies growing on MacConkey agar may have a slightly pinkish tint. This organism does not produce cytochrome oxidases and oxidize glucose with production of acid. It can grow at 37°, 42° and 44°C. *A. baumannii* can decarboxylate arginine and use malonate as a carbon source. It does not produce urease enzyme and cannot reduce nitrate to nitrite and nitrogen gas. The biochemical scheme of genus *Acinetobacter* is shown in Table 3 (54). Phenotypic identification methods take a long time for identification and can not discriminate some genomospecies that are highly related (57, 96). Genomospecies 1 (*A. calcoaceticus*), 2 (*A. baumannii*), 3 and Tjernberg and Ursing 13 are often similar and belong to *A. calcoaceticus* - *A. baumannii* complex (ACB complex). These organisms cannot be differentiate by phenotypic tests. So, genotypic identification has been used for classifying the members of genus *Acinetobacter*.

Genotypic Identification

In 1986, Bouvet and Grimont classified the genus *Acinetobacter* to 12 DNA groups or genomospecies by DNA-DNA hybridization tests (97). Genomospecies 1, 2, 4, 5, 7 and 8/9 were designated *A. calcoaceticus*, *A. baumannii*, *A. haemolyticus*, *A. junii*, *A. johnsonii* and *A. lwoffii*, respectively. The others were designated by group number, genomospecies 3, 6 10, 11 and 12. In the following years, *A. radioresistens* was described and demonstrated to correspond to Bouvet and Grimont's genomospecies 12 by Nishimura *et al.* (98). By using DNA-DNA hybridization, Tjernberg and Ursing found three additional genomic species, genomospecies TU13, TU14 and TU15 in 1989 (99). At the same time, Bouvet and Jeanjean reported five genomospecies, BJ13 to BJ17, to the scheme of Bouvet and Grimont. DNA group 13 sensu Bouvet and Jeanjean (BJ13) corresponds to genomic species 14 sensu Tjernberg and Ursing (TU14). In addition, "Close to TU13" and "Between 1 and 3" were demonsatrated by Gerner-Smidt *et al.* in 1993 (96). To date, at least of 32 genomic species were identified and 17 of them have been assigned species name as described in Table 1 (58).

DNA-DNA hybridization is the standard method for genotypic identification but this technique is complex, time-consuming and cannot be performed in most clinical laboratories. So, many techniques were developed, including amplified ribosomal DNA restriction analysis (ARDRA) (100), the analysis of restriction fragment length polymorphisms (RFLPs) (101), ribotyping and restriction analysis of the 16S-23S ribosomal RNA Intergenic Spacer Sequences (102).



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Table 1. Classification of the genus *Acinetobacter* (58)

Species	Source
Species that have valid names	
<i>A. calcoaceticus</i> (Genomospecies 1)	Soil and humans (including clinical specimens)
<i>A. baumannii</i> (Genomospecies 2)	Humans (including clinical specimens), soil, meat and vegetables
<i>A. haemolyticus</i> (Genomospecies 4)	Humans (including clinical specimens)
<i>A. junii</i> (Genomospecies 5)	Humans (including clinical specimens)
<i>A. johnsonii</i> (Genomospecies 7)	Humans (including clinical specimens) and animals
<i>A. lwoffii</i> (Genomospecies 8/9)	Humans (including clinical specimens) and animals
<i>A. radioresistens</i> (Genomospecies 12)	Humans (including clinical specimens), soil and cotton
<i>A. ursingii</i>	Humans (including clinical specimens)
<i>A. schindleri</i>	Humans (including clinical specimens)
<i>A. parvus</i>	Humans (including clinical specimens) and animals
<i>A. baylyi</i>	Activated sludge and soil
<i>A. bouvetii</i>	Activated sludge
<i>A. townneri</i>	Activated sludge
<i>A. tandoii</i>	Activated sludge
<i>A. grimontii</i>	Activated sludge
<i>A. tjernbergiae</i>	Activated sludge
<i>A. gerneri</i>	Activated sludge
Species that have provisional designations	
<i>A. venetianus</i>	Sea water
Genomospecies 3	Humans (including clinical specimens), soil and vegetables
Genomospecies 6	Humans (including clinical specimens)
Genomospecies 10	Humans (including clinical specimens), soil and vegetables
Genomospecies 11	Humans (including clinical specimens) and animals
Genomospecies 13BJ or 14TU	Humans (including clinical specimens)
Genomospecies 14BJ	Humans (including clinical specimens)
Genomospecies 15BJ	Humans (including clinical specimens)
Genomospecies 16	Humans (including clinical specimens) and vegetables
Genomospecies 17	Humans (including clinical specimens) and soil
Genomospecies 13TU	Humans (including clinical specimens)
Genomospecies 15TU	Humans (including clinical specimens)
Genomospecies between 1 and 3	Humans (clinical specimens)
Genomospecies close to 13TU	Humans (clinical specimens)

5. TREATMENT OF *A. BAUMANNII* INFECTION

Broad-spectrum cephalosporins, β -lactam- β -lactamase inhibitor combinations such as ampicillin combined with sulbactam, carbapenems that used alone or combination with an aminoglycoside and other combinations of a β -lactam with a fluoroquinolone or rifampin have been used for treatment of *A. baumannii* infections (103). Carbapenems are a class of β -lactam antibiotics with a broad spectrum of antibacterial activity, and have a structure which renders them highly resistant to β -lactamases. Carbapenems that usually use for treatment of *A. baumannii* infection are imipenem and meropenem.

For infections caused by multidrug-resistant isolates, the most active agents are the polymyxins, polymyxin B and polymyxin E (colistin). These agents caused disruption of the integrity of bacterial cell membrane, leading to leakage of intracellular contents and cell death (104). They were abandoned in 1960s and 1970s but they have brought back into use again during the past few years for treatment of multidrug-resistant gram negative bacilli including *Acinetobacter*. Bronchoconstriction is the main side effect of inhaled colistin when used for treatment of ventilator-associated pneumonia (105). Garancho-Montero *et al.* suggested that intravenous polymyxins could be used successfully for the treatment of ventilator-associated *A. baumannii* pneumonia, with less nephrotoxicity (106). The cure rates for colistin were 57-77% among severely ill patients with multidrug-resistant *Acinetobacter* infections, including pneumonia, bacteremia, sepsis, intra-abdominal infection and central nervous system infection (107-110). Motaouakkil *et al.* demonstrated the successfully treatment of ventilator-associated pneumonia and bloodstream infections by combination of colistin and rifampin (111). Yoon *et al.* also demonstrated the synergy activities of polymyxin B combined with imipenem and rifampin against multidrug-resistant *A. baumannii* (112). It might be because of rapid permeable through the outer membrane of polymyxin B, allowing enhanced penetration and activity of both imipenem and rifampin. However, Saballs *et al.* found a high failure rate and emergence of rifampin resistance in 70% of carbapenem-resistant *Acinetobacter* infected patients treated

with rifampin plus imipenem (113). Bernabeu-Witlel *et al.* also demonstrated the activities of imipenem combined amikacin were worse than imipenem alone for treatment of imipenem-resistant pneumonia in a guinea pig model (114).

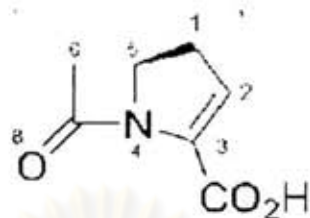
New glycolcycline antibiotic, tigecycline, has been reported to be active against some multidrug-resistant *A. baumannii* (115, 116). However, tigecycline-resistant *A. baumannii* isolated were reported recently (117-123). Peleg *et al.* and Ruzin *et al.* demonstrated that tigecycline resistance was associated with upregulation of chromosomally mediated efflux pumps (124). Cefoperazone combined with sulbactam, sulperazone, was also used to treat multidrug-resistant *Acinetobacter* spp. Lim *et al.* found 62% of cefoperazone-resistant *Acinetobacter* spp. were susceptible to cefoperazone-sulbactam (125).

6. CARBAPENEMS

Carbapenems are β -lactam antibiotics that contain a β -lactam ring in their structures. They differ from other β -lactams by having a hydroxyethyl side chain in trans-configuration at position 6 and a sulfur atom at position 1 of the structure has been replaced with a carbon atom, and hence the name of the group, the carbapenems (Figure 3.). The unique stereochemistry of the hydroxyethyl side chain confers stability against β -lactamases (126, 127).

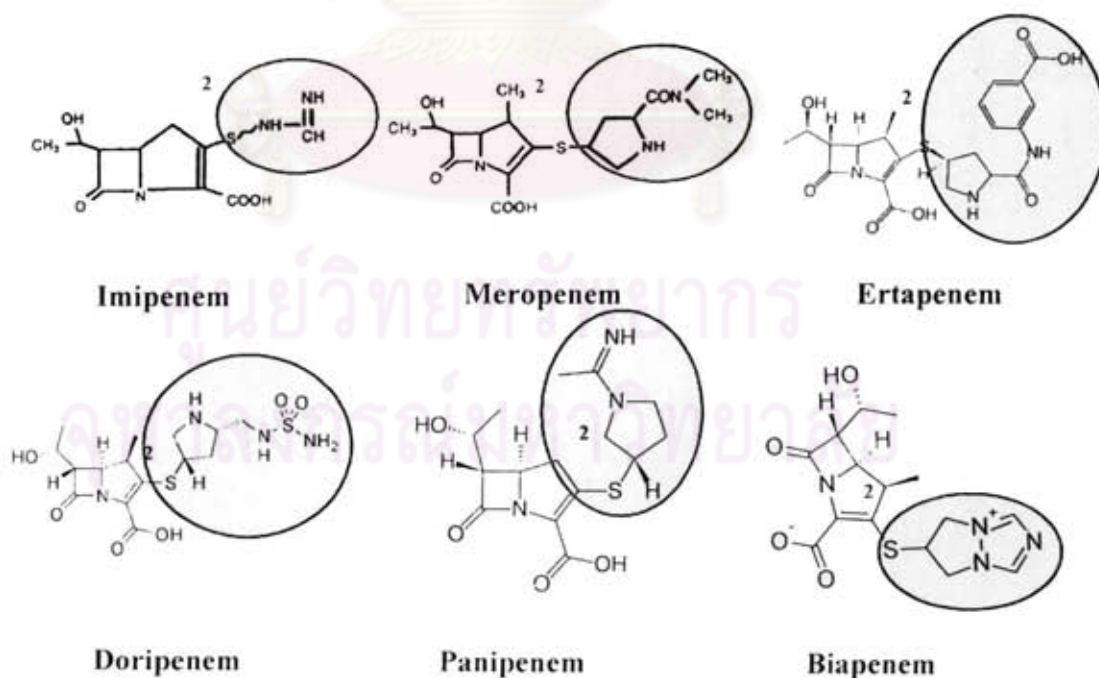
All β -lactam antibiotics are bactericidal, and act by inactivating cell wall enzymes such as transpeptidases which are members of the family of penicillin binding proteins (PBPs). These enzymes catalyze the cross-linking of the peptidoglycan polymers in the bacterial cell wall (128). β -Lactam antibiotics are similar to the D-alanyl-D-alanine of the pentapeptide which attached to N-acetylmuramic acid (NAM) unit in the nascent peptidoglycan layer. PBPs mistakenly use penicillin as a substrate for cell wall synthesis and transpeptidase is acylated. The acylated PBPs inhibit cell wall synthesis, while autolysis by cell wall autolytic continues. These events lead to permeability of water, rapidly take up fluid and eventually lyse of bacterial cells (129).

Figure 3. Structure of carbapenem backbone



Carbapenem agents currently available are imipenem (N-formimidoyl thienamycin), semisynthetic derivative of thienamycin, meropenem, ertapenem, doripenem, panipenem and biapenem. Imipenem and meropenem are the most clinical use. Structures of these carbapenems are shown in Figure 4., which differed in side chain at position 2.

Figure 4. Structures of carbapenems



Imipenem is an intravenous β -lactam antibiotic developed in 1985. It is derivatives of thienamycin, which is produced by the *Streptomyces cattleya*. Nomenclature by International Union of Pure and Applied Chemistry (IUPAC) is (5R,6S)-3-[2-(aminomethylideneamino)ethylsulfanyl]-6-(1-hydroxyethyl)-7-oxo-1-azabicyclo[3.2.0]hept-2-ene-2-carboxylic acid. Imipenem has a broad spectrum of activity against aerobic and anaerobic gram positive as well as gram negative bacteria. This agent remains very stable in the presence of β -lactamase (both penicillinase and cephalosporinase) produced by some bacteria, and is a strong inhibitor of β -lactamases from some gram negative bacteria that are resistant to most β -lactam antibiotics. Imipenem can be hydrolysed in the mammalian kidney by a dehydropeptidase enzyme. Cilastatin is a competitive, reversible and specific inhibitor of dehydropeptidase-I enzyme. So, imipenem is given with a dehydropeptidase inhibitor, cilastatin, to prevent the breakdown of antibiotic in the kidney (126, 130).

Meropenem is an ultra-broad-spectrum injectable antibiotic used to treat a wide variety of infection. This agent was developed by Sumitomo Pharmaceuticals, Japan and was approved by FDA in July, 1996. Systematic (IUPAC) name is 3-[5-(dimethylcarbamoyl) pyrrolidin-2-yl] sulfanyl-6-(1-hydroxyethyl)-4-methyl-7-oxo-1-azabicyclo[3.2.0] hept-2-ene-2-carboxylic acid. It is bactericidal except against *Listeria monocytogenes* where it is bacteriostatic. This agent is also highly resistant to degradation by β -lactamases or cephalosporinases. The overall spectrum is similar to imipenem although it is more active against Enterobacteriaceae and less active against gram positive bacteria. It is also resistant to ESBL but more susceptible to metallo- β -lactamases (126).

Other carbapenems include ertapenem, doripenem, panipenem and biapenem. All carbapenems except imipenem have 1- β -methyl group in their structures, confer β -lactamase stability and resistance to inactivation by renal dehydropeptidases (131). Ertapenem is effective against gram negative bacteria and anaerobic bacteria, but not active against MRSA, ampicillin-resistant enterococci, *Ps. aeruginosa* and *Acinetobacter* spp (126, 132, 133). Doripenem was approved by the United States

Food and Drug Administration on October 12, 2007. This agent has a spectrum and potency against gram positive cocci similar to imipenem and ertapenem and gram negative activity similar to meropenem (two or four folds superior to imipenem) (126, 134). Panipenem is a parenteral carbapenem antibacterial agent which was launched in 1993. This agent has a broad spectrum of gram negative and gram positive aerobic and anaerobic bacteria, including *Streptococcus pneumoniae* and β -lactamase producing organisms. A panipenem is coadministered with betamipron to inhibit panipenem uptake into the renal tubule and prevent nephrotoxicity (126, 135, 136). Biapenem is a parenteral carbapenem that possessed antibacterial activities against a wide range of gram positive, gram negative and anaerobic bacteria (126, 135).

7. MECHANISMS OF CARBAPENEM RESISTANCE IN *A. BAUMANNII*

The emergences of multidrug resistance including aminoglycosides, quinolones and broad-spectrum beta-lactams in *A. baumannii* have been reported (137-140). Carbapenems have become the preferred treatment for serious *Acinetobacter* infections in many countries because of their stability against β -lactamases. However, resistance to carbapenems has been increasingly reported worldwide (141-144). A major contributing factor in the emergence of antibiotic-resistant *A. baumannii* is the acquisition and transferability of antibiotic resistance genes on plasmids, transposons and integrons. The presence of integrons related to epidemic strains in *Acinetobacter* spp (39, 46, 145-147). Three main classes of integrons have been described, class I, class II and class III differed by amino acid sequences of gene encoding integrase enzymes. Class I integrons have found predominantly in *A. baumannii* (146, 148, 149). Class II integrons hybrid with class I integron was reported in one *A. baumannii* isolate (150). The epidemic potential of *A. baumannii* may be linked to the presence of class I integrons that contain antibiotic resistance genes.

The most common mechanism found in carbapenem-resistant *A. baumannii* is production of carbapenemases, either chromosomally-encoded or plasmid

mediated. Other mechanisms include alteration of PBPs structure, decreased outer membrane permeability for taking up antibiotics and active efflux pumps for excreting antibiotics (151). Combination of these resistance mechanisms can occur. Mechanisms of carbapenem resistance in *A. baumannii* are described below.

1. Production of carbapenemase enzymes

The β -lactamases can be classified into four different molecular groups, A, B, C and D, according to amino acid sequence identities (152-154). β -Lactamase class A, C (AmpC) and D use a catalytically active serine residue for inactivation of the β -lactam drug (155), while class B β -lactamases are metallo-enzymes requiring zinc for their catalytic activity (156, 157). Classification scheme for β -lactamases is shown in Table 2. Carbapenemases belong to class A, B and D β -lactamases. Carbapenemases mostly found in carbapenem-resistant *A. baumannii* are OXA-type carbapenemases which belong to class D β -lactamase. Some of metallo- β -lactamases which belong to class B β -lactamase and have carbapenemase activity were reported.

1.1 OXA-type carbapenemase enzymes

OXA-type carbapenemase enzymes are major carbapenemases produced by *A. baumannii*. Walther-Rasmussen demonstrated that these enzymes were classified in class D β -lactamase which was attributed to the presence of three highly conserved active site elements (158, 159). The first element was the tetrad, Ser⁷⁰-X-X-Lys, where X represents a variable residue, containing the active site serine [Ser⁷⁰ according to the DBL (class D β -lactamase) numbering]. The second element was Ser¹¹⁸-X-Val/Ile. The third element was Lys²¹⁶-Thr/Ser-Gly element. Other conserved motifs in class D β -lactamases were the triad Tyr/Phe¹⁴⁴-Gly-Asn and the Trp²³²-X-X-Gly. Mature OXA-type carbapenemases contain between 243 and 260 amino acid residues with molecular masses ranged from 23 to 35.5 kDa. The isoelectric points (pIs) of OXA-type carbapenemase enzymes that found in *A. baumannii* varied between 6.3 and 9.0 (11, 12, 14, 16, 22-26, 33, 160). These enzymes were referred to as oxacillinases because they hydrolyzed the isoxazoyl

penicillin oxacillin more efficiently than benzylpenicillin and usually hydrolyzed amoxicillin, methicillin, cephaloridine and some cephalothin. These enzymes hydrolyzed imipenem and meropenem weakly and did not hydrolyze extended spectrum cephalosporins and aztreonam. Their activities were inhibited more efficiently by clavulanic acid. In addition, most OXA-type carbapenemases were inhibited by NaCl. This was attributed to the presence of a Tyr¹⁴⁴-Gly-Asn motif. OXA-type carbapenemases containing a Phe-Gly-Asn element instead (OXA-23, -25, -26, -27, -40, -49, -72) were not or weakly inhibited by NaCl. By their nucleotide sequences identities, these enzymes could be subclassified into eight distinct subgroups but only four subgroups have been identified in *A. baumannii* (11, 12, 14, 16, 22-26, 33, 160). These enzymes were grouped and termed carbapenem-hydrolyzing oxacillinases (CHDLs). The identities between subgroups ranged from 40 to 70% whereas the amino acid sequences of the members in the same group were more than 92.5% or differed by 1-5 amino acids as shown in Appendix G (159).

The first subgroup of OXA-type carbapenemases is formed by OXA-23, together with OXA-27 and OXA-49. Donald *et al.* and Afzal-Shah *et al.* demonstrated that these enzymes contained an open reading frame of 822 bp which translates into a protein of 273 amino acids and differed by 2-5 amino acids (14, 23). OXA-23, also named ARI-1 (an acronym of *Acinetobacter* resistant to imipenem), was the first OXA-type carbapenemase enzyme that were found in imipenem-resistant *A. baumannii* isolated from patient in Edinburgh, United Kingdom, in 1995. OXA-27 and OXA-49 were isolated from patients in Singapore and China, respectively. These enzymes contained the S-T-F-K tetrad at amino acid position 81 to 84 and S-X-V triplet at position 126-128, which was typical of class D β -lactamases. However, the Y-G-N motif at position 154-156 was replaced by F-G-N, resulting in weak inhibition by NaCl. OXA-23 was more active than OXA-27 against cephaloridine, whereas imipenem hydrolyzing activity was relatively weaker. Moreover, OXA-23 hydrolyzed oxacillin and ampicillin rapidly whereas OXA-27 had weak activity against both these compounds. The amino acid alignment of this subgroup is shown in Appendix G.

Table 2. Classification schemes for bacterial β -lactamases (161)

Functional group	Molecular class	Produced enzymes	Inhibited by		Representative enzymes
			CA ^A	EDTA ^B	
1	C	Cephalosporins	-	-	AmpC enzymes from Gram negative bacteria ; MIR-1
2a	A	Penicillins	+	-	Penicillinases from Gram positive bacteria
2b	A	Penicillins, cephalosporins	+	-	TEM-1, TEM-2, SHV-1
2be	A	Penicillins, narrow-spectrum and extended-spectrum cephalosporins, monobactam	+	-	TEM-3 to 26, SHV-2 to 6, <i>Klebsiella oxytoca</i> K1
2br	A	Penicillins	\pm^E	-	TEM-30 to 36, TRC-1
2c	A	Penicillins, carbenicillin	+	-	PSE-1, -3, -4
2d	D	Penicillins, cloxacillin	\pm	-	OXA-1 to -11, PSE-2 (OXA-10)
2e	A	Cephalosporins	+	-	Inducible cephalosporinase from <i>P. vulgaris</i>
2f	A	Penicillins, cephalosporins, carbapenems	+	-	NMC-A from <i>E. cloacae</i> , Sme-1 from <i>S. marcescens</i>
3	B	Most β -lactams, including carbapenems	-	+	L1 from <i>Xanthomonas maltophilia</i> , CcrA from <i>B. fragilis</i>
4	ND ^F	Penicillins	-	ND	Penicillinases from <i>Pseudomonas cepacia</i>

^ACA = clavulanic acid, ^BEDTA = ethylenediaminetetraacetic acid,

^E \pm = low binding to CA, ^FND = nondetermined.

The second subgroup consists of OXA-40/24, 25, 26, 33 and OXA-72. Walther-Rasmussen demonstrated that these enzymes shared 60% amino acid identity to OXA-23. The members of this cluster vary from 1-5 amino acids (159). The alignment of amino acid sequences of this subgroup are shown in Appendix G. Bou *et al.*, Heritier *et al.* and Afzal-Shah *et al.* demonstrated that these enzymes contained 825 bp open reading frame encoding a 274 amino acid protein (22-24). Conserved motif, serine-threonine-phenylalanine-lysine tetrad (S-T-F-K), indicated

serine β -lactamases. The typical motifs of the OXA-24 enzyme, tyrosine-glycine-asparagine (Y-G-N) and lysine-threonine-arginine (K-T-G) were replaced by F-G-N and K-S-G, respectively. OXA-24 differed from other oxacillinase by lacking hydrolytic activity against oxacillin, cloxacillin and methicillin but showed moderate hydrolysis of imipenem and meropenem. Although OXA-24 had FGN motif but the enzymatic activity was inhibited by chloride ions. In addition, it was also inhibited by sulbactam, tazobactam and clavulanic acid. OXA-24, -25, -26 and -40 had pIs (isoelectric points) of 9.0, 7.9, 8.0 and 8.6, respectively. The pIs of OXA-25 and OXA-26 were low because of the presence of additional glutamate residues in their structures. OXA-40 had a narrow-spectrum hydrolytic profile including most penicillins. Hydrolysis of imipenem was low, whereas hydrolysis of meropenem was not detected. Both OXA-24 and OXA-25 were identified in carbapenem-resistant *A. baumannii* isolated from Spain (22, 23). OXA-26 and OXA-40 were identified in carbapenem-resistant *A. baumannii* isolated from Belgium and France, respectively (22, 24). OXA-33 and OXA-72 were identified in carbapenem-resistant *A. baumannii* isolated from Portugal and Thailand, which were unpublished.

The third subgroup is OXA-51 family enzymes including OXA-51, OXA-64 to -71, OXA-75 to -80, OXA-82 to -84, OXA-86 to -95, OXA-99, OXA-100, OXA-104, OXA-106 to -113, OXA-115 to -117, OXA-128, OXA-130 to -132. The members of this family diverged by 1-15 amino acids (159). OXA-51 shares 56%, 63% and 59% with OXA-23, OXA-24 and OXA-58, respectively. The alignment of amino acid sequences of this subgroup is shown in Appendix G. Many studies demonstrated that *bla*_{OXA-51-like} genes were naturally harboured by *A. baumannii* (27, 28, 30). Brown *et al.* demonstrated that the amino acid sequences contained the conserved serine active site motif S-T-F-K (DBL numbering 70-73) (26). These enzymes had a Thr \rightarrow Ser change in the K-T-G motif (DBL numbering 216-218). This K-S-G motif was found as in OXA-40/24, 25, 26, 33, 72, 58, 96 and 97. A unique Val \rightarrow Ile change was in the S-X-V motif, which was not present in the other class D carbapenemases. Moreover, these enzymes also retained the Y-G-N motif (DBL numbering 144-146). OXA-51 could hydrolyze both oxacillin and cloxacillin, and hydrolyzed ampicillin effectively. It was not hydrolyzed cephalosporins except cephaloridine. Slow hydrolysis of imipenem was detected.

OXA-51 activity was inhibited by sulbactam and chloride ions and weakly inhibited by clavulanate. The pI of this enzyme was 7.0 (26, 159).

The fourth subgroup consists of OXA-58, together with OXA-96 and OXA-97. These enzymes shared 47% amino acid identities with OXA-23 and OXA-24 and 59% amino acid identities with OXA-51 group (159). The alignment of amino acid sequences of this subgroup is shown in Appendix G. Poirel *et al.* demonstrated that these enzymes contained a 843-bp open reading frame which encoded a 280 amino-acid protein (33). A serine-threonine-phenylalanine-lysine tetrad (S-T-F-K) was at position 70, K-S-G element is at position 216-218. The Y-G-N element at position 144-146 was not replaced by F-G-N motif. OXA-58 had a narrow-spectrum hydrolysis profile, including penicillins and oxacillin. Hydrolysis of imipenem was low, while hydrolysis of meropenem was not detected but this enzyme hydrolyzed imipenem twice as much as OXA-40. In addition, OXA-58 had some hydrolytic activity against ceftazidime, whereas hydrolytic activity against ceftaxime, cefotaxime and cefepime was not detected. Their activity was weakly inhibited by clavulanic acid, tazobactam and sulbactam, and well inhibited by NaCl. OXA-58 was identified in carbapenem-resistant *A. baumannii* isolated from France and Greece (143, 144). OXA-96 and OXA-97 were identified in carbapenem-resistant *A. baumannii* isolated from Singapore and Tunisia, respectively (18, 34). Alignments of nucleotide sequences and amino-acid sequences of the four main groups of OXA-type carbapenemase enzymes identified in *A. baumannii* are shown in Appendix F and G., respectively.

Turton *et al.* demonstrated that the activity of OXA-type carbapenemases also depended on insertion sequence (IS) element that found upstream of *bla*_{OXA} gene. It might play a role in *bla*_{OXA} expression by providing promoter sequences (162). There were many reports indicated that IS*Aba1* element was found upstream of *bla*_{OXA51} and *bla*_{OXA23}, showed high-level resistance to carbapenems (162, 163). In addition, Poirel *et al.* demonstrated that IS*Aba2*, IS*Aba3* and IS*18* were shown to provide promoter sequences enhancing *bla*_{OXA58} expression (164).

1.2 Metallo- β -lactamase enzymes

Metallo- β -lactamase enzymes (MBL, class B β -lactamase) such as IMP (Imipenem-hydrolyzing β -lactamase), VIM (Verona integron-encoded metallo- β -lactamase) and SIM-1 enzymes (Seoul imipenemase) were identified rarely in *A. baumannii* (18, 35-42, 45, 46, 165-167). These MBL-encoding genes are embedded in class-I integron structures and form part of the gene cassettes together with other antibiotic resistance genes especially aminoglycoside-modifying enzymes. IMP-1 enzyme was first isolated from nosocomial isolates of *Serratia marcescens*, *Klebsiella pneumoniae* and *Pseudomonas aeruginosa* from Japan (168). The amino acid sequences of IMP-2 enzyme was 85% identity to IMP-1 (39). Both, *bla*_{IMP} and *bla*_{VIM} genes were also found on conjugative plasmids (32, 168-170). VIM-1 enzyme was first isolated in a carbapenem-resistant *Pseudomonas aeruginosa* clinical isolate (VR-143/97) from an Italian patient at the Verona University Hospital (Northern Italy) (171). Lauretti *et al.* demonstrated that *bla*_{VIM} encoded a 266-amino acid protein. The G+C content of the *bla*_{VIM} was 56%, being higher than that of the *bla*_{IMP} cassette (40%) (171). The IMP-like and VIM-like conferred a high level of carbapenemase resistance in *A. baumannii* isolates (18, 39, 172). The hydrolytic efficiency of these MBL against carbapenems was much higher (100 to 1,000-fold) than that of the OXA-type carbapenemases (151). These enzymes hydrolyzed many β -lactam substrates including penicillins, narrow- to expanded-spectrum cephalosporins including cephamycins and carbapenems. Hydrolysis of aztreonam was not detected. The activities of these enzymes were not inhibited by β -lactam inhibitor such as clavulanate and tazobactam were inhibited by EDTA. It is helpful for identification of MBL production such as using Etest strips containing imipenem with or without EDTA and EDTA-disk synergy test (173). Lee *et al.* demonstrated that SIM-1 enzyme was also encoded by a class I integron-borne gene cassette and was more closely related to IMP-type enzymes than other MBLs by exhibiting 64 to 69% amino acid identities to IMP-type MBLs. The theoretical molecular weight and pI of the mature SIM-1 protein were 25,439 kDa and 7.28, respectively. Both IMP-1 and SIM-1 also hydrolyzed broad array of β -lactams, including penicillins, narrow- to expanded-spectrum cephalosporins and carbapenems (46).

2. Alteration of the target site

Target sites of β -lactam antibiotics are PBPs. Changing in structure of PBP structure confers reduced affinity for binding between bacteria and these antibiotics (174). Fernandez-Cuenca *et al.* found that production of oxacillinase and the absence of PBP2 were associated with carbapenem resistance (175). Similarly, Gehrlein *et al.* reported that PBP alterations were responsible for imipenem resistance in *A. baumannii* isolates (176).

3. Reduction in permeability of outer membrane proteins.

Resistance to carbapenems may also be explained by other mechanisms such as porin loss. Porins are proteins able to form channels allowing the transport of molecules across lipid bilayer membranes. Variation in their structures and regulation of porin expression in the presence of antibiotics are survival strategies that have been developed by many bacteria including *A. baumannii*. The small number and size of porins or outer membrane proteins (OMP) could explain the decrease in permeability to antimicrobial agents (177).

Gribun *et al.* demonstrated the major OMP of *A. baumannii* was the heat-modifiable protein, HMP-AB (178). This protein consisted of 346 amino acids with a molecular mass of 35,636 Da and belongs to the OmpA family. Mussi *et al.* and Siroy *et al.* demonstrated that a heat-modifiable 29 kDa outer-membrane protein, CarO, was involved in taking up carbapenem antibiotics in *A. baumannii* (179, 180). The CarO gene encoded a 247-amino acids protein which had a typical N-terminal signal sequence and a predicted trans-membrane β -barrel topology. Resistance to carbapenem in multidrug-resistant *A. baumannii* isolates was associated with loss of this outer-membrane protein. Fernandez-Guenca *et al.* also found that resistance to carbapenems was related to the absence of an OMP of 22.5 kDa (175). Tomas *et al.* demonstrated that losing of a 33- to 36- kDa outer membrane protein was associated with carbapenem resistance in *A. baumannii* isolated from Spain (181). This protein had amino acid sequence similar to typical of gram-negative bacterial porins. Dupont *et al.* also demonstrated that a 43 kDa protein was associated with imipenem

resistance in *A. baumannii* (182). Mechanism of carbapenem resistance in *A. baumannii* may cause by combine mechanisms such as carbapenemase production and decreased permeability of drugs.

4. Efflux system

Efflux pump activity is to export multiple structurally-distinct classes of antimicrobial agents out of bacteria. Efflux transporters are expressed in all living cells, protecting them from toxic effects of organic chemicals. Multidrug resistance in bacteria has often been associated with overexpression of these transporters. Magnet *et al.* demonstrated AdeABC efflux system in *A. baumannii*. It belongs to the resistance-nodulation-division (RND) family (183). This efflux system played a role in aminoglycoside resistance and was also responsible for decreased susceptibility to chloramphenicol, fluoroquinolones, cefotaxime and trimethoprim. Heritier *et al.* demonstrated a synergic effect when AdeABC system was combined with production of carbapenem-hydrolyzing oxacillinase enzymes. This resulted in increasing of resistance level of carbapenems in *A. baumannii* (10).

8. EPIDEMIOLOGY OF CARBAPENEM RESISTANCE IN *A. BAUMANNII*

Carbapenems have been used for treatment of serious nosocomial infection caused by *Acinetobacter* spp. in many countries, resulting in better activity than other antimicrobial agents. However, many reports on carbapenem resistance are increasing around the world, including Europe, America and Asia (141-144). In Spain, there were many studies to investigate the prevalence of imipenem resistance *A. baumannii*. Martin-Lozano *et al.* showed imipenem resistance in *A. baumannii* was 34% in 2002 (4). At the same time, Betriu *et al.* demonstrated the 28.1% of *A. baumannii* isolated from 12 Spanish medical centers were resistant to imipenem (184). Between 1991 and 2001, Cisneros *et al.* demonstrated carbapenem-resistant *A. baumannii* isolates was increasing from 0% to 50% in Seville (185). In Greece, imipenem resistance in *A. baumannii* isolated from ICUs, medical wards

and surgical wards rose from 0% to 91%, 8% to 71% and 5% to 71%, respectively, between 1996 and 2006 (139). At the same country, Souli *et al.* also demonstrated the 84% of bacteraemic *A. baumannii* isolated from ICUs were resistant to imipenem in 2005 (186). Data from Meropenem Yearly Susceptibility Test Information Collections program (MYSTIC) in 1997-2000, showed that 490 *A. baumannii* isolates were resistant to meropenem 30%, 34% and 23% in Italy, Turkey and UK, respectively, whereas isolates were resistant to imipenem 22%, 38% and 22% respectively (9). By the Ministry of Health National Antimicrobial Resistance Surveillance Net (Mohnarin) in 2008, imipenem and panipenem resistance in *A. baumannii* were 10.4% and 14.5%, respectively in China (187). In 2008, Nemeč *et al.* found carbapenem resistance in 23 out of 108 isolates of *A. baumannii* in Czech Republic (188).

In USA, carbapenem resistance in *A. baumannii* isolates were 53% in 1999 (3). Qi *et al.* found imipenem-resistant *A. baumannii* isolates increased from 52% to 96% in 2005 to 2007 in Chicago (189). In Shanghai and Hong Kong, both imipenem and meropenem-resistant rates of *A. baumannii* collected from Shanghai were 6.3% while those from Hong Kong were 2.7% and 10.8%, respectively (138). In China, national resistance surveillance data in 1996-2002 from intensive care units (ICUs) of 19 hospitals showed that imipenem resistance rate in *Acinetobacter* spp. was 5% in 1996 to 2002 (190). At the same country, another surveillance program showed carbapenem resistance rate increased from 4.5% in 2003 to 18.2% in 2004 (191).

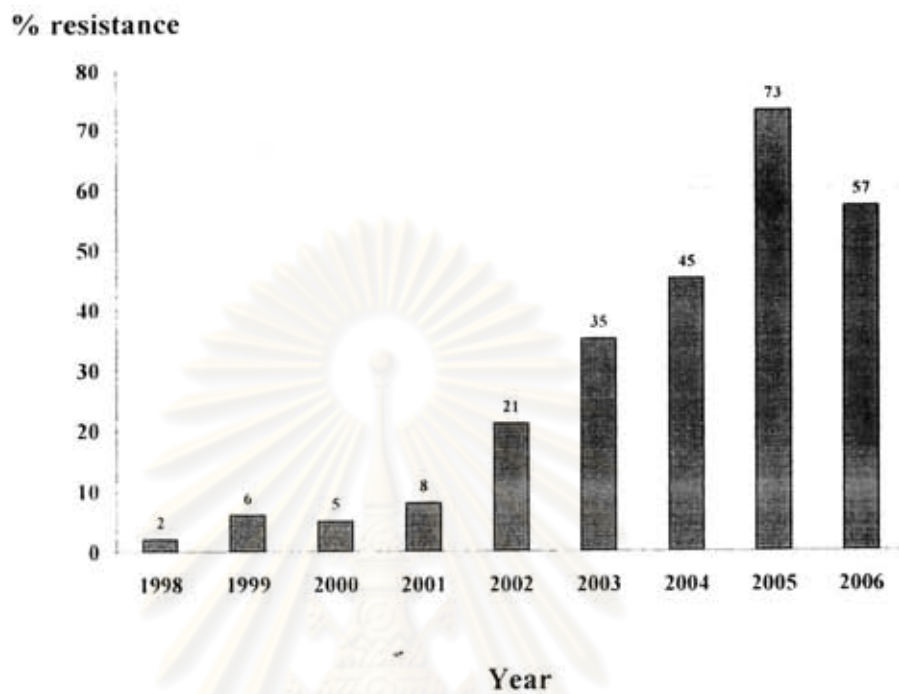
Most of carbapenemase enzymes found in *A. baumannii* were OXA-type carbapenemases (oxacillinases). IMP-type and VIM-type were rarely reported (35-46). ARI-1 was the first enzyme that reported in *A. baumannii* in 1995 (14). This enzyme was renamed OXA23 following its genetics and biochemical characterization. After that, there have been many reports about OXA-type carbapenemases in *Acinetobacter* spp. worldwide. OXA-type carbapenemases found in *A. baumannii* were classified into 4 subgroups depending on their amino acid sequences (159). The first subgroup, OXA23 group enzymes were identified in *A. baumannii* isolated from Brazil, Spain, Korea, China, Singapore, Scotland and Tahiti (15-17, 23). Second subgroup, OXA24 group enzymes, were identified in

Spain (22, 23), Belgium (23) and France (24). The third subgroup, OXA-51 family enzymes, were found in Argentina (25-27), Spain, Hong Kong, Singapore, South Africa (25), France (28), Poland (29), United Kingdom (30), Greece (31, 32) and Turkey. The fourth subgroup, OXA-58, were reported in *A. baumannii* isolated from South Europe (13), France (33), Singapore (18) and Tunisia (34).

Besides OXA-type carbapenemases, metallo- β -lactamases, IMP-type and VIM-type, were identified in *A. baumannii* isolates. IMP-1 was reported in Japan (35), Korea (36, 37) and Italy (38). IMP-2, IMP-4, IMP-5, IMP-6 and IMP-11 were reported in Italy (39), Hong Kong (40), Portugal (41), Brazil (42) and Japan (43), respectively. VIM-type, VIM-2 were found in *A. baumannii* in Korea (36, 44). VIM-1 and VIM-2 were reported in *Acinetobacter* spp. in Italy (41) and Korea (36, 45), respectively whereas SIM-1 was reported in South Korea (46).

In Thailand, there was no evidence of carbapenem resistance *Acinetobacter* spp. from the study at Siriraj Hospital in 1998 (47). In 1999, 21% of *Acinetobacter* spp. isolates were resistant to imipenem at Vajira Hospital (48). In 2003, the imipenem resistance rate of *A. baumannii* was 61% at Police General Hospital (51). Sixty-eight percents of *A. baumannii* isolated from Siriraj Hospital in 2006 were resistant to carbapenems and 57% were resistant to all antimicrobials currently available in Thailand (52). In 2007, imipenem resistance rate of *A. baumannii* collected from Chiang Mai University Hospital were 35.5% (49). At the same period, the imipenem resistance rate of 2,130 *A. baumannii* isolated from clinical specimens at Songklanagarind Hospital was 34.7%. The 61.9% of these imipenem-resistant *A. baumannii* isolates were from respiratory tract, and 49.9% from ICU. Moreover, 14.8% of all imipenem-resistant *A. baumannii* isolates were resistant to all routine tested antibiotics, including gentamicin, amikacin, ampicillin, cephalothin, cefoxitin, ceftazidime, ceftriaxone, meropenem, sulperazone, ciprofloxacin and cotrimoxazole (50). Moreover, the data from the National Antimicrobial Resistance Surveillance Center Thailand (NARST) showed that imipenem resistance in *Acinetobacter calcoaceticus-baumannii* complex increased from 2% in 1998 to 57% in 2006 as shown in Figure 5 (53).

Figure 5. Imipenem resistance rates of *Acinetobacter calcoaceticus-baumannii* complex during 1998-2006 (NARST) (53)



ศูนย์วิทยทรัพยากร
จุฬาลงกรณ์มหาวิทยาลัย

CHAPTER IV

MATERIALS AND METHODS

The chemical agents used in this study were molecular biology grade. Name list of all media, chemical reagents materials, instruments and reagents are shown in Appendix I.

PART I : BACTERIAL STRAINS

1. *Acinetobacter baumannii* isolates

Five hundred and one isolates of *A. baumannii* were collected from Department of Microbiology, King Chulalongkorn Memorial Hospital, Bangkok during January 2004 to August 2007. Each was from a different patient. They were identified as *A. baumannii* according to the Manual of Clinical Microbiology and Koneman's Color Atlas and Textbook of Diagnostic Microbiology (54, 131).

2. Quality control strain for bacterial identification

A. baumannii ATCC 19606

3. Quality control strains for MIC determination

Escherichia coli ATCC 25922, *Pseudomonas aeruginosa* ATCC 27853, *Staphylococcus aureus* ATCC 29213 and *Enterococcus faecalis* ATCC 29212

CULTURE PRESERVATION

All culture isolates were grown entirely on tryptic soy agar (BBL, Becton Dickinson and Company, Cockeysville, MD) at 37°C. The overnight cultures were

transferred to microcentrifuge tubes of 1 ml trypticase soy broth containing 10% glycerol and mix-well suspensions were kept at -70°C until required.

PART II BACTERIAL IDENTIFICATION

A. baumannii isolates were identified by conventional method including colonial morphology, gram stain and biochemical tests.

1. Colonial Morphology

A. baumannii is a lactose non-fermenter. Colonies are between 0.5-2 mm in diameter, smooth, opaque, colorless or slightly pink on MacConkey agar.

2. Gram stain

A. baumannii is a gram-negative coccobacillus. Individual cell is 1 to 1.5 µm by 1.5 to 2.5 µm in size and frequently arranged in pairs.

3. Biochemical test

A single colony was picked and inoculated to testing media. The biochemical test lists and interpretation criteria for *A. baumannii* are described below and summarized in Table 3 (54). *A. baumannii* ATCC 19606 was used as a reference control for bacterial identification.

3.1 Triple Sugar Iron medium test (TSI)

Triple sugar iron medium is the nutrient agar containing glucose, lactose and sucrose (1:10:10). There are thiosulfate and iron salt for the detection of hydrogen sulfide production. Phenol red is the indicator used to determine acidity or alkalinity in the medium. For TSI testing, tested strains were stabbed by needle into butt and streaked on the surface of slant, and then incubated at 37°C for 24 h.

Interpretation

- The organisms that can ferment only glucose but not lactose and sucrose, are recorded as K/A (alkaline (purple) slant / acid (yellow) butt). This may be with gas production.
- The organisms that can ferment glucose, lactose and/or sucrose, are recorded as A/A (acid (yellow) butt / acid (yellow) slant). This may be with gas production.
- The organisms that cannot ferment any sugars, are recorded as K/N (alkaline (purple) slant / neutral (no change) butt).
- A black precipitation in the butt indicates the production of H₂S.
A. baumannii shows K/N (alkaline slant / neutral butt) on TSI medium.

3.2 Oxidase test

The oxidase test detects the presence of cytochrome oxidase. This enzyme can oxidize the substrate N,N,N,N-tetramethyl-*p*-phenylenediamine dihydrochloride (Sigma, U.S.A) to indophenol and produce a purple color. To test for oxidase, tested strains were transferred with a loop onto filter paper soaked with oxidase reagent. A dark purple color will appear within 5-10 seconds if the microorganism has cytochrome oxidase. *A. baumannii* does not produce cytochrome oxidase, and shows a negative result for oxidase test.

3.3 Urease test

The purpose of the urease test is to detect whether a microorganism possesses the enzyme urease which hydrolyzes urea. The urea agar contains phenol red indicator, which turns pink at an alkaline pH. When urea is hydrolyzed, it releases ammonia, which causes an alkaline reaction and a vivid pink color develops. Urease activity was detected by inoculating a loopfull of the organism onto slope of the urea agar slant, and then incubated at 37°C for 24 h. *A. baumannii* cannot produce urease enzyme, and shows a negative result for urease test.

3.4 Growth at 37°C, 42°C and 44°C

To determine the ability to grow at 37°C, 42°C and 44°C, the organism was inoculated on 2 plates of tryptic soy agar and in a tube of tryptic soy broth. The plates were incubated at 37°C and 42°C in the incubators. A tube of tryptic soy broth was incubated at 44°C in the waterbath. Growth was observed after 24 h of incubation. *A. baumannii* can grow at 37°C, 42°C and 44°C.

3.5 Hemolysis on sheep blood agar

The organism was inoculated on sheep blood agar plate. The plate was incubated at 37°C for 24 h. Hydrolysis of red blood on sheep blood agar was interpreted as positive result. *A. baumannii* shows no hemolysis on sheep blood agar and gives a negative result.

3.6 Oxidation / Fermentation of dextrose

Fermentation is an anaerobic process, while oxidation is aerobic process. The main difference between fermentative and oxidative metabolism of carbohydrate is the requirement for atmospheric oxygen and initial phosphorylation. Fermentation requires initial phosphorylation of glucose prior to degradation to relatively strong mixed acids, whereas oxidation is a strict aerobic process involving direct oxidation of a nonphosphorylated glucose molecule. Fermentation produces higher acidity than oxidation. Medium used to determine the oxidative or fermentative metabolism was OF basal medium (BBL). The tested organism was inoculated in a pair of OF tubes by stabbing into the medium to approximately ¼ inch from bottom. One tube was overlaid with approximately 1.0-2.0 mL of sterile melted petrolatum. The tubes were incubated at 35°C for 48 h. The medium contains bromthymol blue which will turn to yellow because of acid production from metabolic pathway of the organism while blue or green means that carbohydrate cannot be used. Oxidation will occur in an opened tube, while fermentation will occur in tube covered with sterile melted petrolatum. *A. baumannii* can use dextrose by oxidation. Acid production changes the color of the medium from green to yellow in the opened tube.

3.7 Arginine decarboxylase

To measure the enzymatic ability of an organism to decarboxylate arginine to form an amine. Tested strains were inoculated into arginine decarboxylase medium and were covered with sterile melted petrolatum. The tubes were incubated at 37°C for 24 h. If the organism can use arginine for their metabolism, colour of the medium will turn to violet by alkalinity while the organism that cannot use arginine, the medium will change to yellow by acidity. *A. baumannii* can decarboxylate arginine and shows a positive result in arginine decarboxylase medium.

3.8 Malonate utilization

Malonate broth was used to determine an organism's ability to use sodium malonate as the sole source of carbon. Bromthymol blue is an indicator. The color of the medium changes from light blue to deep Prussian blue color by alkalinity when the organism uses malonate as a carbon source, interpreted as positive result. No color change or yellow is interpreted as negative result. Tested strains were inoculated into the medium by a loop, and then incubated at 37°C for 24 h. *A. baumannii* can use malonate as a carbon source and gives a positive result for malonate utilization.

3.9 Nitrate reduction

To determine the ability of an organism to reduce nitrate to nitrite or nitrogen gas, tested organism was heavily inoculated into nitrate broth and incubated at 35°C for 24 h. Nitrate reagents, reagent A (α -Naphthylamine) and reagent B (sulfanilic acid), were added before attempting an interpretation. If the tested medium turns to pink to a deep red color within 1-2 min, it means that nitrate was reduced to nitrite by the organism. No color development means that nitrite is not present and zinc dust will be added. Pink to deep red occurred within 5-10 min confirms negative result. This means that nitrate is not reduced by the organism. No color development means that the organism can reduce nitrate to nitrite and then further reduce nitrite to nitrogen gas (N₂). Ammonia is tested by adding a few drops of Nessler's reagent.

Positive result shows a deep orange color. *A. baumannii* cannot reduce nitrate to nitrite or nitrogen gas and shows a negative result for nitrate reduction test.



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Table 3. Biochemical schemes of genus *Acinetobacter* (54)

ORGANISM	GENOMO-SPECIES	UREASE	NITRATE REDUCTION	GROWTH AT			HEMOLYSIS OF SHEEP BLOOD	OXIDIZES DEXTROSE	ARGININE DECARBOXY-LASE	MALONATE UTILIZATION
				37°C	42°C	44°C				
<i>Acinetobacter johnsonii</i>	7	-	-	-	-	-	-	-	V (35)	V (13)
<i>Acinetobacter baumannii</i>	2	-	-	+	+	+ ^a	-	+	+	+
<i>Acinetobacter haemolyticus</i>	4	-	-	+	-	-	+	V (52)	+	-
<i>Acinetobacter</i> spp.	6	-	-	+	-	-	+	V (66)	+	-
<i>Acinetobacter</i> spp.	10	-	-	+	-	-	-	+	-	-
<i>Acinetobacter calcoaceticus</i>	1	-	-	+	-	-	-	+	+	+
<i>Acinetobacter</i> spp.	3	-	-	+	+	-	-	+	+	V (87)
<i>Acinetobacter</i> spp.	12	-	-	+	-	-	-	V (33)	+	+
<i>Acinetobacter junii</i>	5	-	-	+	+	-	-	-	+	-
<i>Acinetobacter hwoffii</i>	8/9	-	-	+	-	-	-	-	-	-
<i>Acinetobacter</i> spp.	11	-	-	+	-	-	-	-	-	-

Compiled from

^a Must also be OF dextrose positive

+, 90% or more strains positive; -, 90% or more strains negative; V, 11-89% of strains positive; Numbers in parentheses are percentages of strains giving positive reactions.

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PART III : ANTIMICROBIAL SUSCEPTIBILITY TEST

All 501 *A. baumannii* isolates were tested for antimicrobial susceptibility against imipenem and meropenem. The minimal inhibitory concentrations (MICs) of carbapenems were examined by agar dilution technique on Muller-Hinton agar as recommended by CLSI (192). The MIC is the lowest concentration of antimicrobial agents required to inhibit the growth of a microorganism *in vitro*.

MIC determination by agar dilution

Escherichia coli ATCC 25922, *Pseudomonas aeruginosa* ATCC 27853, *Staphylococcus aureus* ATCC 29213 and *Enterococcus faecalis* ATCC 29212 were used as reference controls for MIC determination. Standardization of inoculum was prepared from a pure overnight culture in tryptic soy broth. The turbidity of cell suspension was adjusted to 0.5 McFarland (approximately 1.5×10^8 CFU/mL) in 0.85% NaCl. After adjusting the turbidity of inoculum, the suspension was diluted 10-fold to yield the final inoculum suspension. The inoculum suspension was used for inoculation within 15 minutes. After that, the 500 μ L of inoculum suspension was transferred to the multi-point inoculator wells. The inoculum suspension was inoculated on plate with two-fold serial dilution of each imipenem (Merck & Co., U.S.A.) and meropenem (AstraZeneca UK Limited, United Kingdom) starting at 0.015- \geq 256 mg/L. (The concentration of antimicrobial for use in agar dilution are shown in Table 4). Before inoculation on the plate containing the lowest concentration of antibiotic, the growth control was inoculated on the plate without antibiotic. The inoculum-spots were allowed to dry and inverted the plates before incubated at 37°C for 18-24 h. The final inoculum on the agar was approximately 10^4 CFU/spot. After 24 hours of incubation, the MIC was read as the lowest concentration of antimicrobial agent without visible growth as shown in Figure 6. A faint haze, pinpoint colonies or growth of a single colony were ignored. The MIC breakpoint criteria recommended by CLSI are shown in the Table 5. Acceptable MIC limits for quality control strains are listed in Table 6.

Table 4. Scheme for preparing dilutions of antimicrobial agents to be used in agar dilution susceptibility tests (192).

Step	Concentration (mg/L)	Source	Volume (mL)	Diluent (mL)	Intermediate concentration (mg/L)	Final concentration at 1:10 dilution in agar (mg/L)	Log ₂
	5,120	Stock	-	-	5,120	512	9
1	5,120	Stock	2	2	2,560	256	8
2	5,120	Stock	1	3	1,280	128	7
3	5,120	Stock	1	7	640	64	6
4	640	Step 3	2	2	320	32	5
5	640	Step 3	1	3	160	16	4
6	640	Step 3	1	7	80	8	3
7	80	Step 6	2	2	40	4	2
8	80	Step 6	1	3	20	2	1
9	80	Step 6	1	7	10	1	0
10	10	Step 9	2	2	5	0.5	-1
11	10	Step 9	1	3	2.5	0.25	-2
12	10	Step 9	1	7	1.25	0.125	-3

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Figure 6. Inoculum plate of agar dilution method

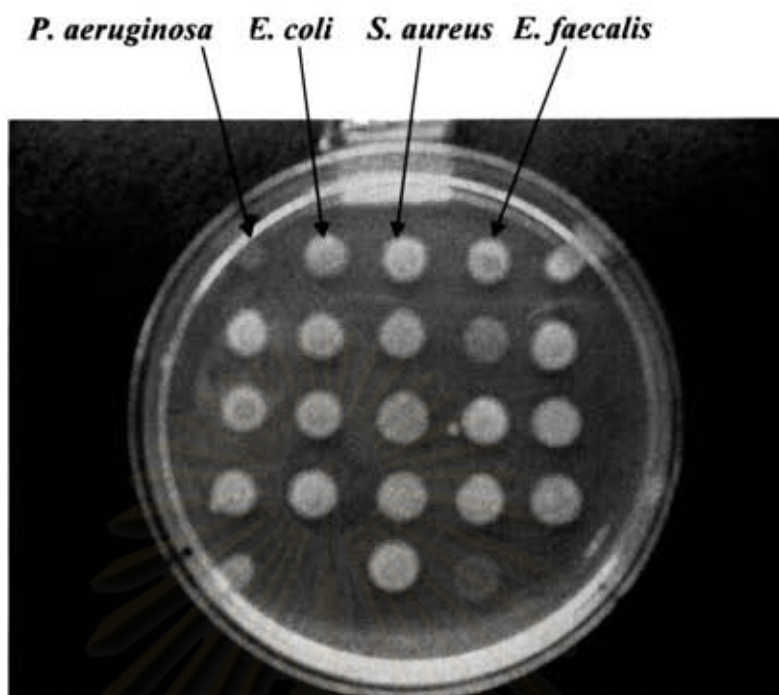


Table 5. MIC Interpretive Standards for *Acinetobacter* spp. (192)

Antimicrobial agents	MIC (mg/L)		
	Interpretive Standard		
	Susceptible	Intermediate	Resistant
Imipenem	≤ 4	8	≥ 16
Meropenem	≤ 4	8	≥ 16

Table 6. Acceptable limits of MIC (mg/L) for quality control strains (192).

Antimicrobial agents	<i>Escherichia coli</i> ATCC 25922	<i>Pseudomonas aeruginosa</i> ATCC 27853	<i>Staphylococcus aureus</i> ATCC 29213	<i>Enterococcus faecalis</i> ATCC 29212
Imipenem	0.06-0.25	1-4	0.015-0.06	0.5-2
Meropenem	0.008-0.06	0.25-1	0.03-0.12	2-8

PART IV : DETERMINATION OF CARBAPENEMASE

Modified Hodge test is the method for screening carbapenemase-producing strains (173). The surface of a Mueller-Hinton agar plate was inoculated evenly by using a cotton swab with an overnight culture suspension of *Escherichia coli* ATCC 25922, which was adjusted to one-tenth turbidity of 0.5 McFarland. After brief drying, a 10- μ g imipenem disk was placed at the center of the plate, and imipenem-resistant isolates from the overnight culture plates were streaked heavily from the edge of the disk to the periphery of the plate. The Mueller-Hinton agar plate was incubated at 35°C for 24 h. The presence of a distorted inhibition zone after overnight incubation was interpreted as modified Hodge test positive (Figure 7.).

PART V : DETERMINATION OF METALLO- β -LACTAMASE

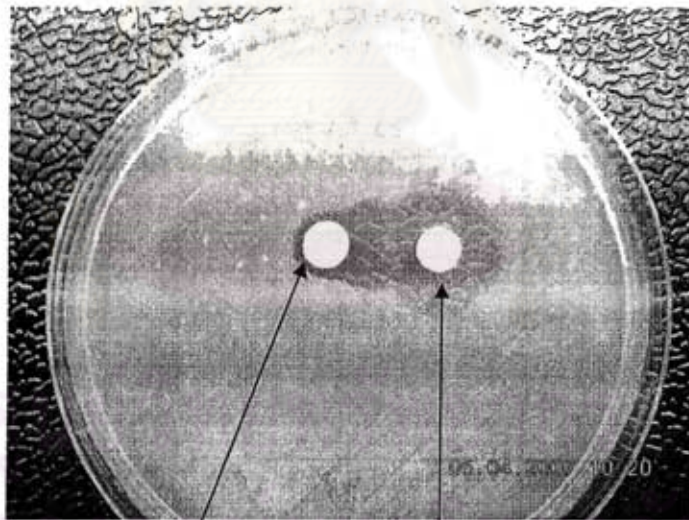
EDTA-disk synergy test was used to screen metallo- β -lactamase-producing isolates (173). An overnight culture of the tested strain was suspended to the turbidity of 0.5 McFarland and inoculated onto a Mueller-Hinton agar plate by using a cotton swab. After drying, a 10- μ g imipenem disk and a blank filter paper disk were placed 10 mm apart from edge to edge. Ten microlitres of 0.5 M EDTA solution was then applied to the blank disk, which resulted in approximately 1.5 mg/disk. After overnight incubation at 35°C, the presence of an enlarged zone of inhibition was interpreted as EDTA-synergy test positive (Figure 8.).

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Figure 7. Distorted inhibition zone of *E. coli* by Modified Hodge test



Figure 8. Enlarged inhibition zone of tested isolate by EDTA-disk synergy test



10-µg imipenem disk

Filter paper with EDTA

PART VI : SCREENING OF GENES ENCODING OXA- , IMP- AND VIM-TYPE CARBAPENEMASES BY PCR AND DNA SEQUENCING OF ENTIRE *BLA*-OXA GENE

1. Preparation of genomic DNA

1.1 Boiling method

Bacterial DNA was prepared by suspending 4-5 colonies of pure culture in 100 μ L of sterile deionized distilled water and boiled at 100°C for 15 min. The suspension was centrifuged at 13,000 rpm at room temperature for 5 min. Supernatant was stored at -20°C.

1.2 QIAamp DNA Mini kit

The extraction and purification of *A. baumannii* DNA for amplifying entire *bla*_{OXA51-like} genes was performed by QIAamp[®] DNA Mini kit (QIAGEN, Germany), according to the manufacturer's directions. *A. baumannii* colonies were scraped from the culture plate with inoculation loop and suspended with 180 μ L of ALT. Twenty microliters of proteinase K were added, mixed by vortexing, and incubated at 56°C until bacterial cells were completely lysed. The samples were then added by 200 μ L of buffer AL. After well mixing, the suspensions were heated at 70°C for 10 min, and briefly centrifuged to remove drops from inside the lid. The samples were added by 200 μ L of ethanol and mixed by pulse-vortexing for 15 sec. The supernatants were then transferred into spin columns and centrifuged at 8,000 rpm for 1 min. The QIAamp spin columns were placed in clean 2 mL collection tubes and the tubes containing the filtrate were discarded. QIAamp spin columns were carefully opened and 500 μ L of buffer AW1 were added and centrifuged at 8,000 rpm for 1 min. The filtrates were then discarded. QIAamp spin columns were washed with 500 μ L of AW2 and centrifuged at 14,000 rpm for 3 minutes. QIAamp spin columns were placed in clean 1.5 mL microcentrifuge tube and added with 200 μ L of buffer AE. The samples were incubated at room temperature for 1 minute and

centrifuged at 8,000 rpm for 1 minute. Extracted DNA samples were stored at -20°C .

2. Preparation of plasmid DNA

The extraction of *A. baumannii* plasmid DNA for amplifying entire *bla*_{OXA23-like}, *bla*_{OXA24-like}, *bla*_{OXA58-like} genes was performed by Aurum™ Plasmid Mini Kit (BIO-RAD, USA). The DNA was purified according to the manufacturer's directions. *A. baumannii* were cultured in Luria-Bertani broth (Pronadisa, Spain) and measure the density of bacterial cells up to 12 OD.mL (OD600). Bacterial cells were transferred to a 1.5 mL capped microcentrifuge tube and centrifuged at 12,000 g for 1 min. The supernatant was removed. The 250 μL of resuspension solution were added and mixed by vortexing. The 250 μL of lysis solution were added to the sample and mixed by inverting the capped tube briskly 6-8 times. After that, the 350 μL of neutralizing solution were added to the sample and mixed by inverting the capped tube briskly 6-8 times. Then the sample was centrifuged for 5 min. A compact white debris pellet was formed at the bottom of the tube, while supernatant or cleared lysate contained the plasmid DNA. The cleared lysate was transferred into a plasmid mini column which was inserted in a 2 mL capless wash tube and the column was centrifuged for 1 min. The filtrate was removed from the tube. The column was replaced into the same wash tube. Then, 750 μL of wash solution were added to the column and centrifuged for 1 min. The wash solution was discarded from the tube and the column was replaced into the same wash tube and centrifuged for 1 additional minute to remove residual wash solution. Finally, the plasmid mini column was transferred to a 1.5 mL capped microcentrifuge tube and 50 μL of elution solution was added onto the membrane stack at the base of the column and allowed for 1 min. for saturating of solution to the membrane. Then, the column was centrifuged for 1 min. to elute the plasmid. The eluted plasmid DNA samples were stored at 4°C .

3. Screening for the presence of *bla*_{OXA-like}, *bla*_{IMP-like} and *bla*_{VIM-like}

The presence of carbapenemase genes including *bla*_{OXA-like}, *bla*_{IMP-like} and *bla*_{VIM-like} was screened by PCR. The PCR primers of *bla*_{OXA-like}, *bla*_{IMP-like} and *bla*_{VIM-like} genes are demonstrated in Table 7.

Table 7. Primers used for amplification of *bla*_{OXA-like}, *bla*_{IMP-like} and *bla*_{VIM-like} and size of expected PCR products.

Specific for	Primer	Primer sequence	Location	Product size (bp)	Reference	
<i>bla</i> _{OXA23-like}	OXA23-F	5'-GATCGGATTGGAGAACCAGA-3'	261-761	501	(193)	
	OXA23-R	5'-ATTTCTGACCGCATTTCAT-3'				
<i>bla</i> _{OXA24-like}	OXA24-F	5'-GGTTAGTTGGCCCCCTTAAA-3'	500-748	249		
	OXA24-R	5'-AGTTGAGCGAAAAGGGGATT-3'				
<i>bla</i> _{OXA51-like}	OXA51-F	5'-TAATGCTTTGATCGGCCTTG-3'	255-607	353		
	OXA51-R	5'-TGGATTGCACTTCATCTTGG-3'				
<i>bla</i> _{OXA58-like}	OXA58-F	5'-AAGTATTGGGGCTTGTGCTG-3'	39-637	599		
	OXA58-R	5'-CCCCTCTGCGCTCTACATAC-3'				
<i>bla</i> _{IMP-like}	IMP-F	5'-CTACCGCAGCAGAGTCTTTG-3'	47-633	587		(194)
	IMP-R	5'-AACCAGTTTTGCCTTACCAT-3'				
<i>bla</i> _{VIM-like}	VIM-F	5'-TTTGGTCGCATATCGCAACG-3'	158-657	500	(195)	
	VIM-R	5'-CCATTCAGCCAGATCGGCAT-3'				

3.1 Amplification of the *bla*_{OXA-like} by multiplex PCR

The presence of *bla*_{OXA23-like}, *bla*_{OXA24-like}, *bla*_{OXA51-like} and *bla*_{OXA58-like} was screened using OXA23-F, OXA23-R, OXA24-F, OXA24-R, OXA51-F, OXA51-R, OXA58-F and OXA58-R primers. In a 25 μ L PCR reaction mixture, the amplification reaction was as follows: 1X PCR buffer, 1.5 mM MgCl₂, 200 μ M dNTP (Fermentas, USA), 1.25 pmol of each primer except 0.625 pmol of OXA58-F and OXA58-R, and 0.625 U *Taq* polymerase (Fermentas, USA) and 1 μ L of DNA template from boiling method. The amplification conditions were, initial denaturation at 94°C for 5 minutes, 30 cycles of 94°C for 25 seconds, 52°C for 40 seconds and 72°C for 50 seconds, and a final elongation at 72°C for 6 minutes

(193). The PCR products of *bla*_{OXA-23-like}, *bla*_{OXA-24-like}, *bla*_{OXA-51-like} and *bla*_{OXA-58-like}, were 501 bp, 249 bp, 353 bp and 599 bp, respectively.

3.2 Amplification of the *bla*_{IMP-like}

The presence of *bla*_{IMP-like} was screened using IMP-F and IMP-R primers. In a 25 μ L PCR reaction mixture, the amplification reaction was as follows : 1X PCR buffer , 1.5 mM MgCl₂, 200 μ M dNTP (Fermentas, USA), 1.25 pmol of each primer, and 0.625 U *Taq* polymerase (Fermentas, USA) and 1 μ L of DNA template from boiling method. The amplification conditions were, initial denaturation at 94°C for 2 minutes, 30 cycles of 94°C for 1 minute, 55°C for 1 minute and 72°C for 1.5 minutes, and a final elongation at 72°C for 10 minutes (194). The PCR product of *bla*_{IMP-like} was 587 bp.

3.3 Amplification of the *bla*_{VIM-like}

The presence of *bla*_{VIM-like} was screened using VIM-F and VIM-R primers. In a 25 μ L PCR reaction mixture, the amplification reaction was as follows : 1X PCR buffer , 1.5 mM MgCl₂, 200 μ M dNTP (Fermentas, USA), 1.25 pmol of each primer, and 0.625 U *Taq* polymerase (Fermentas, USA) and 1 μ L of DNA template from boiling method. The amplification conditions were, initial denaturation at 95°C for 5 minutes, 30 cycles of 95°C for 30 seconds, 66°C for 1 minute and 72°C for 1 minute, and a final elongation at 72°C for 10 minutes (195). The PCR product of *bla*_{VIM-like} was 502 bp.

4. Amplification and DNA sequencing of entire *bla*_{OXA-like} genes

4.1 Amplification of entire *bla*_{OXA-like} genes

Primers for amplification of entire *bla*_{OXA23-like} , *bla*_{OXA24-like} , *bla*_{OXA51-like} , *bla*_{OXA58-like} are demonstrated in Table 8. Ten *A. baumannii* isolates which carried either of these genes and had different levels of MIC to imipenem were selected for amplification of *bla*_{OXA23-like} , *bla*_{OXA24-like} , *bla*_{OXA51-like} and *bla*_{OXA58-like}.

4.1.1 Amplification of entire *bla*_{OXA-23-like} and *bla*_{OXA-58-like} genes

OXA23-F and OXA23-R primers were used for amplification of the entire *bla*_{OXA23-like} gene whereas OXA58-F and OXA58-R primers were for entire *bla*_{OXA58-like} gene amplification. Amplification of entire *bla*_{OXA-23-like} and *bla*_{OXA-58-like} used the same conditions. The 50 μ L PCR mixture contained ; 1X *Pfu* buffer , 2.0 mM MgSO₄, 200 μ M dNTP (Fermentas, USA), 5 pmol of each primer, 4 U *Pfu* DNA polymerase (Fermentas, USA), and 3 μ L of plasmid DNA template. The amplification conditions were, initial denaturation at 94°C for 5 minutes and 30 cycles of 94°C for 25 seconds, 52°C for 40 seconds, 72°C for 50 seconds and final elongation at 72 °C for 6 minutes. The PCR products of entire *bla*_{OXA-23-like} and *bla*_{OXA-58-like} were 1,062 bp and 933 bp, respectively.

4.1.2 Amplification of entire *bla*_{OXA-51-like} genes

OXA51-F and OXA51-R primers were used for amplification of entire *bla*_{OXA51-like} gene. The 50 μ L PCR mixture contained ; 1X *Pfu* buffer , 2.0 mM MgSO₄, 200 μ M dNTP (Fermentas, USA) , 5 pmol of each primer, 4 U *Pfu* DNA polymerase (Fermentas, USA), and 3 μ L of extracted DNA template. The amplification conditions were, initial denaturation at 95°C for 5 minutes and 35 cycles of 95°C for 30 seconds, 52°C for 1 minute, 72°C for 90 seconds and final elongation at 72 °C for 10 minutes. The PCR product of entire *bla*_{OXA-51-like} was 825 bp.

4.1.3 Amplification of entire *bla*_{OXA-24-like} genes

OXA24-F and OXA24-R primers were used for amplification of the entire *bla*_{OXA24-like} gene. The 50 μ L PCR mixture contained ; 1X PCR buffer , 1.5 mM MgCl₂, 200 μ M dNTP (Fermentas, USA) , 2.5 pmol of each primer, 1.25 U *Taq* polymerase (Fermentas, USA), and 1 μ L of plasmid DNA template. The amplification conditions were, initial denaturation at 94°C for 4 minutes and 30 cycles of 94°C for 1 minute, 52°C for 1 minute, 72°C for 2 minutes and final

elongation at 72 °C for 10 minutes. The PCR product of entire *bla*_{OXA-24-like} was 1,021 bp.



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Table 8. Sequences of the oligonucleotides used as primers for amplifications of entire *bla*_{OXA-like} gene and DNA sequencing.

Primer	Primer sequence	Product size (bp)	Reference	
PCR primers				
entire <i>bla</i> _{OXA23-like}				
OXA23-likeF	5'-GATGTGTCATAGTATTCGTCG-3'	1,065	} (23)	
OXA23-likeR	5'-TCACAACAACAAAAGCACTG-3'			
entire <i>bla</i> _{OXA24-like}				
OXA24-likeF	5'-GTACTAATCAAAGTTGTGAA-3'	1,021		
OXA24-likeR	5'-TTCCCCTAACATGAATTTGT-3'			
entire <i>bla</i> _{OXA51-like}				
OXA51-likeF	5'-TACGCCAATCCATACAGCAA-3'	1,416	(GenBank accession no. CU468230)	
OXA51-likeR	5'-GCTTGACGCTGCTTTTTACC-3'			
entire <i>bla</i> _{OXA58-like}				
OXA58-likeF	5'-TTATCAAAATCCAATCGGC-3'	933	(143)	
OXA58-likeR	5'-TAACCTCAAACCTCTAATTC-3'			
Sequencing primers				
For entire <i>bla</i> _{OXA23-like}				
OXA23-likeF	5'-GATGTGTCATAGTATTCGTCG-3'	} (23)	} (23)	
OXA23-likeR	5'-TCACAACAACAAAAGCACTG-3'			
For entire <i>bla</i> _{OXA24-like}				
OXA24-likeF	5'-GTACTAATCAAAGTTGTGAA-3'			
OXA24-likeR	5'-TTCCCCTAACATGAATTTGT-3'			
OXA21-likeR1	5'-AGTTGAGCGAAAAGGGGATT-3'			
For entire <i>bla</i> _{OXA51-like}				
OXA51-likeF	5'-TACGCCAATCCATACAGCAA-3'	} (193)	(GenBank accession no. CU468230)	
OXA51-likeFM	5'-TAATGCTTTGATCGGCCTTG-3'			
OXA51-likeFM1	5'-ATGAACATTAAGCACTC-3'			
OXA51-likeR1	5'-CTATAAAATACCTAATTGTTC-3'			
For entire <i>bla</i> _{OXA58-like}				
OXA58-likeF	5'-TTATCAAAATCCAATCGGC-3'	} (143)	(143)	
OXA58-likeR	5'-TAACCTCAAACCTCTAATTC-3'			
OXA58-likeFM	5'-AAGTATTGGGGCTTGTGCTG-3'			
			(193)	

5. Analysis of PCR Product

The PCR products were analyzed on 1.2 % agarose gels (Pronadisa, Spain) containing 0.5 $\mu\text{g}/\text{mL}$ ethidium bromide (Sigma, USA) in TBE buffer. PCR products were mixed with 6X of gel loading buffer (20% ficoll, 0.05% bromophenol blue). The electrophoresis was carried out at 100 volts for 60 minutes. The amplified products were visualized on a UV light transilluminator. A 100 base pair DNA ladder (Fermentas, USA) and a 100 base pair plus DNA ladder (Fermentas, USA) were used as DNA size markers.

6. Purification of PCR product

The PCR products were purified by QIAquick PCR purification kit as described by the manufacturer (QIAGEN, GmbH, Germany). The QIAquick system is combination of spin-column technology with the selective binding properties of a uniquely- designed silica-gel membrane. DNA is absorbed to the silica- membrane in the presence of high salt while contaminants pass through the column. Five volumes of buffer PB (Contains guanidine hydrochloride and isopropanol) were added to 1 volume of PCR product sample. After well mixing, the suspension was transferred into QIAquick spin column in a provided 2 mL collection tube and centrifuged at 13,000 rpm for 60 sec. The flow-through was discarded and 750 μL of buffer PE (washing buffer) were added to the column. The column was centrifuged at 13,000 rpm for 60 sec. The flow-through was discarded from the tube and column was replaced into the same tube and centrifuged for 1 additional minute to remove residual wash solution. QIAquick spin columns were placed in a clean 1.5 mL microcentrifuge tube and added with 50 μL of buffer EB (elution buffer). The samples were incubated at room temperature for 1 minute and centrifuged at 13,000 rpm for 60 sec. The purified PCR product was stored at $-20\text{ }^{\circ}\text{C}$. The concentration of DNA was determined by spectrophotometer (BIORAD, U.S.A).

7. Preparation of sequencing reactions

Purified PCR products were sequenced under BigDye terminator cycling conditions using 3730xl DNA analyzer (Applied Biosystems, USA) by Macrogen Inc., Korea. Sequencing oligonucleotide primers are shown in Table 4.

8. Sequencing analysis

The nucleotide sequences and the deduced protein sequences were analyzed with the software available over the Internet at the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/BLAST>), Multalin (www.toulouse.inra.fr/multalin.html) and ExPASy (www.expasy.org).



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CHAPTER V

RESULTS

PART I : BACTERIAL STRAINS

A total of 501 isolates of *A. baumannii* were used in the present study. The clinical isolates collected in 2004, 2005, 2006 and 2007 were 194, 177, 16 and 114 isolates, respectively. Two hundred and eighty-four (56.7%) isolates and 217 (43.3%) isolates were isolated from male and female, respectively. Two hundred and fifty-nine (51.7%) specimens and 242 (48.3%) specimens were collected from patients in ICUs and other hospital wards (non-ICUs), respectively. The clinical isolates were recovered from blood 69 (13.8%) isolates, body fluid 20 (4%) isolates, cerebrospinal fluid 1 (0.2%) isolate, sputum 238 (47.5%) isolates, respiratory aspirate 73 (14.6%) isolates, pus 17 (3.4%) isolates, tissue 14 (2.8%) isolates, urine 52 (10.4%) isolates and other specimen 17 (3.4%) isolates.

PART II : BACTERIAL IDENTIFICATION

Biochemical patterns of 501 *A. baumannii* isolates are shown in Table 9. A total of 501 isolates were identified as *A. baumannii* based on colonial morphology, cell morphology and biochemical characteristics. *A. baumannii* isolates were gram-negative coccobacilli usually diploid form. Colonies on MacConkey agar were lactose non-fermenting, 0.5-2 mm in diameter, smooth, opaque, colorless or slightly pink. Biochemical characteristics included alkaline slant / neutral butt on triple sugar iron agar, no hemolysis on sheep blood agar, oxidase negative, urease negative, non motile and negative for nitrate reduction. It grew at 37°, 42° and 44°C and oxidized dextrose. There were six biochemical patterns in 501 isolates differed by citrate, malonate and arginine utilization as shown in Table 9. Of the 501 isolates, 287 (57.3%) were belonged to biochemical pattern B and 178 (35.5%) were belonged to biochemical pattern D. Twenty-two

(4.4%) , 11 (2.2%) , 2 (0.4%) and 1 (0.2%) were belonged to biochemical pattern C, A, E and F, respectively. The results suggested that most of *A. baumannii* isolates were belonged to biochemical pattern B and D.



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Table 9. Biochemical patterns of 501 *A. baumannii* isolates

Biochemical pattern	Triple sugar iron	Oxidase test	Motility	Urease	Nitrate reduction	Growth at			Hemolysis of sheep blood	Oxidize dextrose	Arginine decarboxylase	Malonate utilization	Citrate utilization	% of isolates (n)
						37°C	42°C	44°C						
A	K/N ^a	-	-	-	-	+	+	+	-	+	+	+	+	2.2 (11)
B	K/N	-	-	-	-	+	+	+	-	+	-	-	+	57.3 (287)
C	K/N	-	-	-	-	+	+	+	-	+	+	-	+	4.4 (22)
D	K/N	-	-	-	-	+	+	+	-	+	-	+	+	35.5 (178)
E	K/N	-	-	-	-	+	+	+	-	+	-	-	-	0.4 (2)
F	K/N	-	-	-	-	+	+	+	-	+	-	+	-	0.2 (1)

^a Alkaline slant / neutral butt

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PART III : ANTIMICROBIAL SUSCEPTIBILITY TEST

The minimal inhibitory concentrations (MICs) of carbapenems in the 501 *A. baumannii* isolates were examined by agar-dilution technique on Muller-Hinton agar. The MIC results of these *A. baumannii* isolates are shown in Appendix D. MIC breakpoints of imipenem and meropenem were ≥ 16 mg/L. Susceptibility and resistance rates of the 501 *A. baumannii* isolates to carbapenems are shown in Table 10. Prevalence of imipenem and meropenem resistance was 82.4% (413 isolates) and 81.8% (410 isolates), respectively. MICs required to inhibit 50% (MIC₅₀) of isolates for imipenem and meropenem were 64 and 32 mg/L, respectively. MICs required to inhibit 90% (MIC₉₀) of isolates for imipenem and meropenem were 256 and 64 mg/L, respectively. Distributions of the MICs for imipenem and meropenem are shown in Figure 9, and 10. It was demonstrated that MICs of imipenem-susceptible in *A. baumannii* isolates ranged from 0.12 to 4 mg/L. Most of imipenem-susceptible isolates (96.6%) had imipenem MICs of ≥ 0.5 mg/L. The majority of imipenem-resistant isolates (82.8%) had imipenem MICs of ≥ 64 mg/L. Meropenem-susceptible isolates had meropenem MIC range of 0.12 to 4 mg/L. The majority of meropenem-susceptible isolates had meropenem MIC of ≥ 0.25 mg/L. Three isolates were intermediately resistant. Most of meropenem-resistant isolates (77.4%) had meropenem MIC range of 16 to 64 mg/L. Peaks of imipenem and meropenem MIC were at 64 mg/L and 32 mg/L, respectively.

Carbapenem resistance rates of *A. baumannii* isolated from patients in ICUs and non-ICUs are shown in Figure 11. Imipenem resistance of ICU and non-ICU isolates was 90.3% (234/259 isolates) and 74.0% (179/242 isolates), respectively, whereas meropenem resistance was 89.6% (232/259 isolates) and 73.5% (178/242 isolates), respectively. MIC₅₀ and MIC₉₀ values of imipenem for both ICU and non-ICU isolates were 64 and 256 mg/L, respectively. MIC₅₀ values of meropenem for ICU and non-ICU isolates were 32 and 16 mg/L, respectively. MIC₉₀ values of meropenem for both ICU and non-ICU isolates were 64 mg/L. Distributions of the MICs for imipenem and meropenem of ICU and non-ICU isolates are shown in Figure 12, and 13. It was demonstrated that peaks of imipenem MIC of ICUs and non-ICUs isolates were at 64 mg/L and 128 mg/L, respectively. Peaks of

meropenem MIC of ICUs and non-ICUs isolates were at 16 mg/L and 32 mg/L, respectively. The MICs of imipenem-susceptible in ICU isolates ranged from 0.12 to 4 mg/L. Most of imipenem-susceptible in ICU isolates (88%) had imipenem MICs of 0.5-2 mg/L. The majority of imipenem-resistant in ICU isolates (89.2%) had imipenem MICs of ≥ 32 mg/L. Meropenem-susceptible isolates had meropenem MIC range of 0.12 to 4 mg/L. The majority of meropenem-susceptible isolates (96%) had meropenem MIC of 0.25 to 2 mg/L. The majority of meropenem-resistant isolates (83.8%) had imipenem MICs of 16 to 64 mg/L.

The MICs of imipenem-susceptible in non-ICU isolates ranged from 0.12 to 4 mg/L. Most of imipenem-susceptible in non-ICU isolates (93.6%) had imipenem MICs of 0.5 to 2 mg/L. The majority of imipenem-resistant non-ICU isolates (95.5%) had imipenem MICs of ≥ 32 to 256 mg/L. Meropenem-susceptible in non-ICU isolates had meropenem MIC range of 0.12 to 4 mg/L. The majority of meropenem-susceptible in non-ICU isolates (90.5%) had meropenem MIC of 0.25 to 2 mg/L. The majority of meropenem-resistant in non-ICU isolates (96.1%) had imipenem MICs of 16 to 64 mg/L. By statistical analysis using Chi-square test, imipenem and meropenem resistance rates of *A. baumannii* isolated from patients in ICUs were significantly higher than those from non-ICUs ($P < 0.01$).

By comparison between isolates from sterile sites and non sterile sites, prevalence of imipenem resistance was 83.5% (81/97 isolates) and 82.2% (332/404 isolates), respectively, whereas prevalence of meropenem resistance was 82.5% (80/97 isolates) and 81.7% (330/404 isolates), respectively. MIC₅₀ and MIC₉₀ values of imipenem for isolates from both sterile sites and non sterile sites were 64 and 256 mg/L, respectively. MIC₅₀ and MIC₉₀ values of meropenem for isolates from both sterile sites and non sterile sites were 32 and 64 mg/L, respectively. Distributions of the MICs for imipenem and meropenem of isolates from sterile sites and non sterile sites are shown in Figure 14, and 15. Peaks of imipenem MIC of isolates from both sterile sites and non sterile sites were at 64 mg/L. Peaks of meropenem MIC of isolates from sterile sites and non sterile sites were at 16 mg/L and 32 mg/L, respectively. Most of imipenem-resistant in isolates from sterile site (82.2%) had imipenem MICs of >32 mg/L. The majority of meropenem-resistant in

isolates from sterile site (74.4%) had meropenem MICs of 16 to 64 mg/L. Most of imipenem-resistant in isolates from non-sterile site (67.7%) had imipenem MICs of >64 mg/L. The majority of meropenem-resistant in isolates from non-sterile site (78.1%) had meropenem MICs of 16 to 64 mg/L. By statistical analysis using Chi-square test, there was no significant difference in imipenem and meropenem resistance rates in *A. baumannii* isolated from sterile and non sterile clinical specimens ($P = 0.758$).

Table 10. Carbapenem MICs and prevalence of carbapenem resistance in 501 *A. baumannii* isolates.

Antimicrobial agents	MICs (mg/L)			Resistance (%)
	Range	MIC ₅₀	MIC ₉₀	
Imipenem	0.12->256	64	256	413 (82.4)
Meropenem	0.12->256	32	64	410 (81.8)

Figure 9. Distribution of imipenem MICs

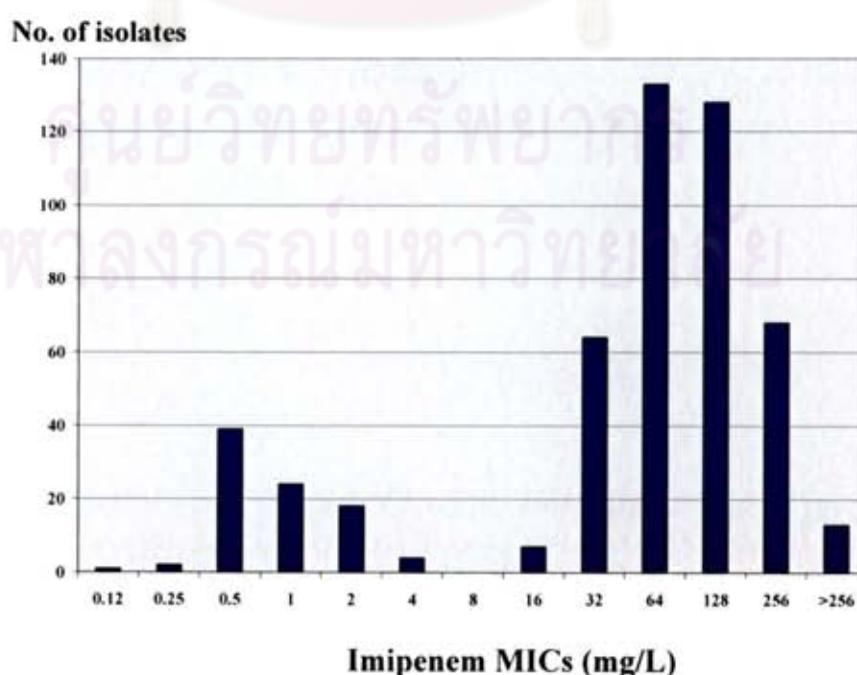


Figure 10. Distribution of meropenem MICs.

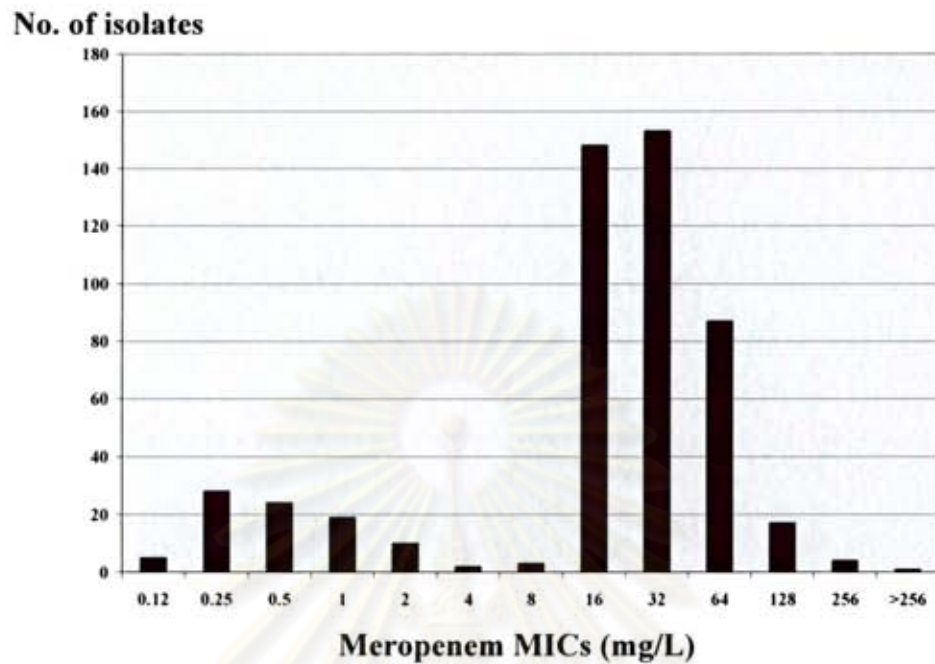


Figure 11. Prevalence of carbapenem resistance in ICU and non-ICU *A. baumannii* isolates

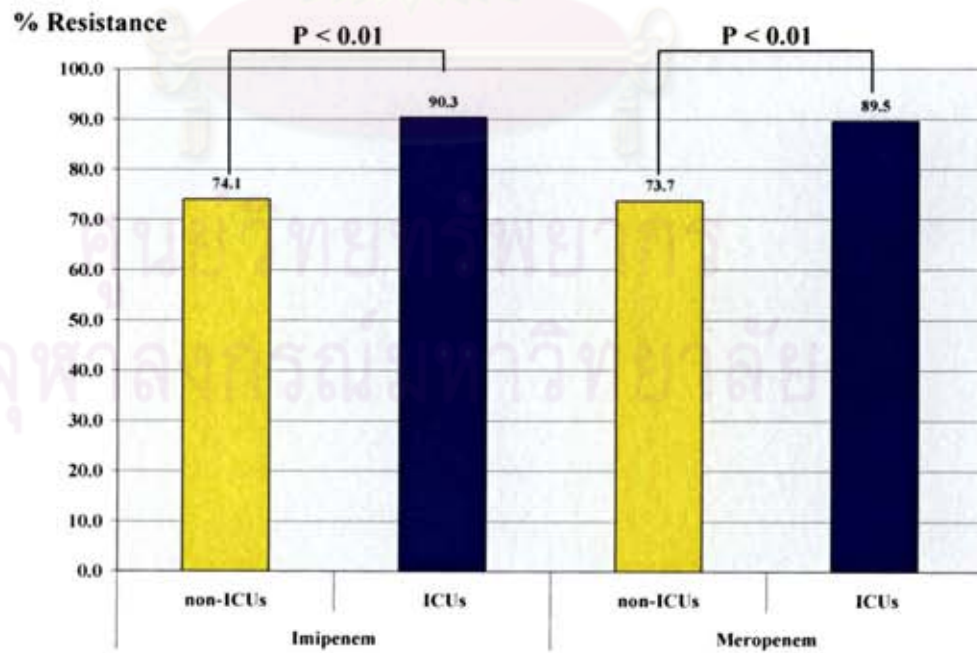


Figure 12. Distributions of imipenem MICs of ICU and non-ICU isolates

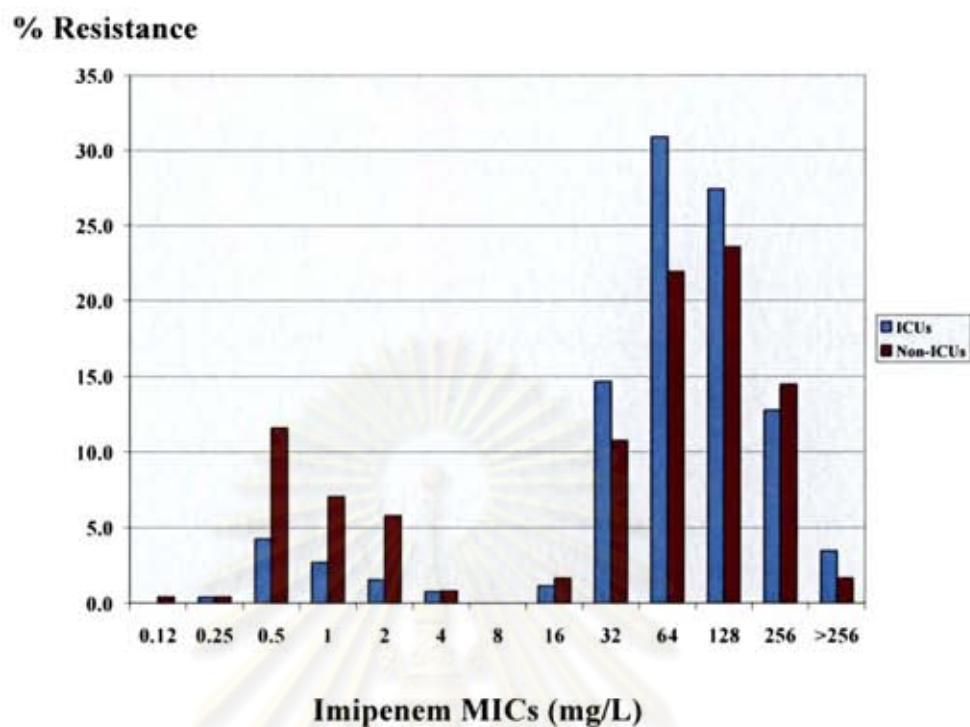


Figure 13. Distributions of the meropenem MICs of ICU and non-ICU isolates

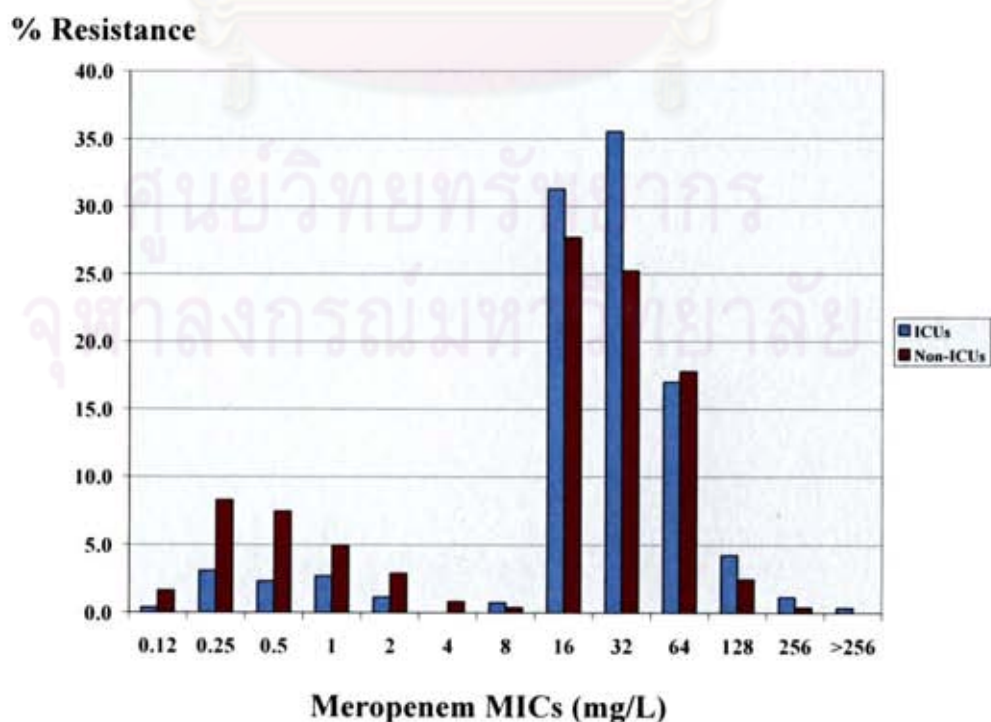


Figure 14. Distributions of imipenem MICs of isolates from sterile sites and non sterile sites

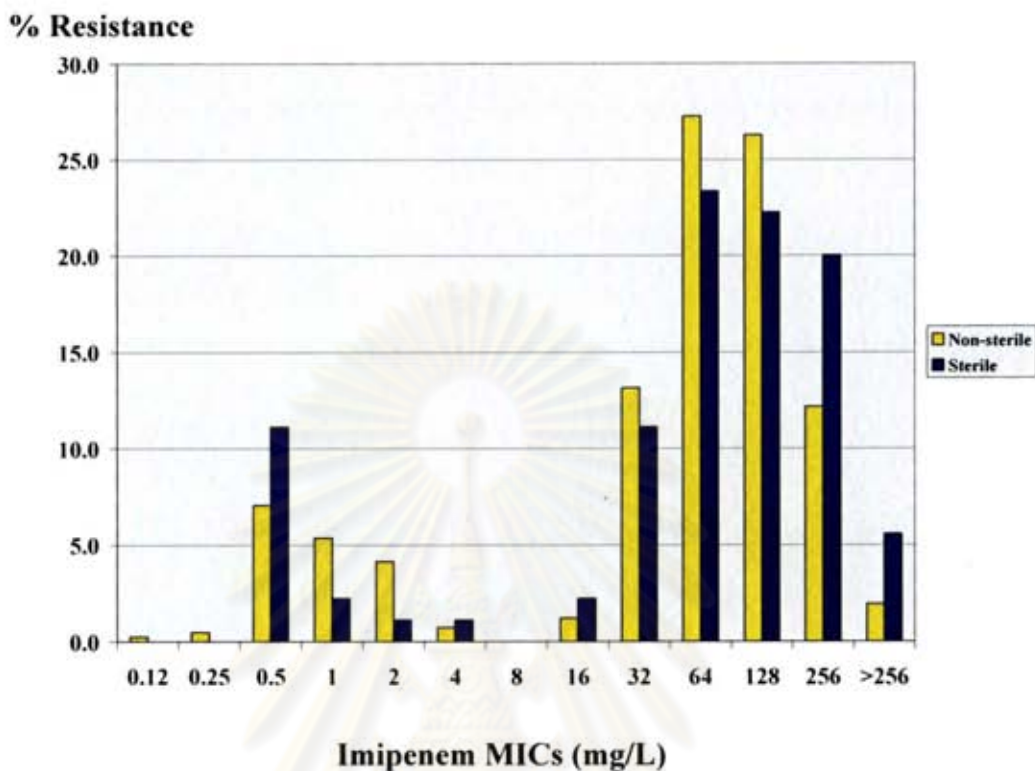
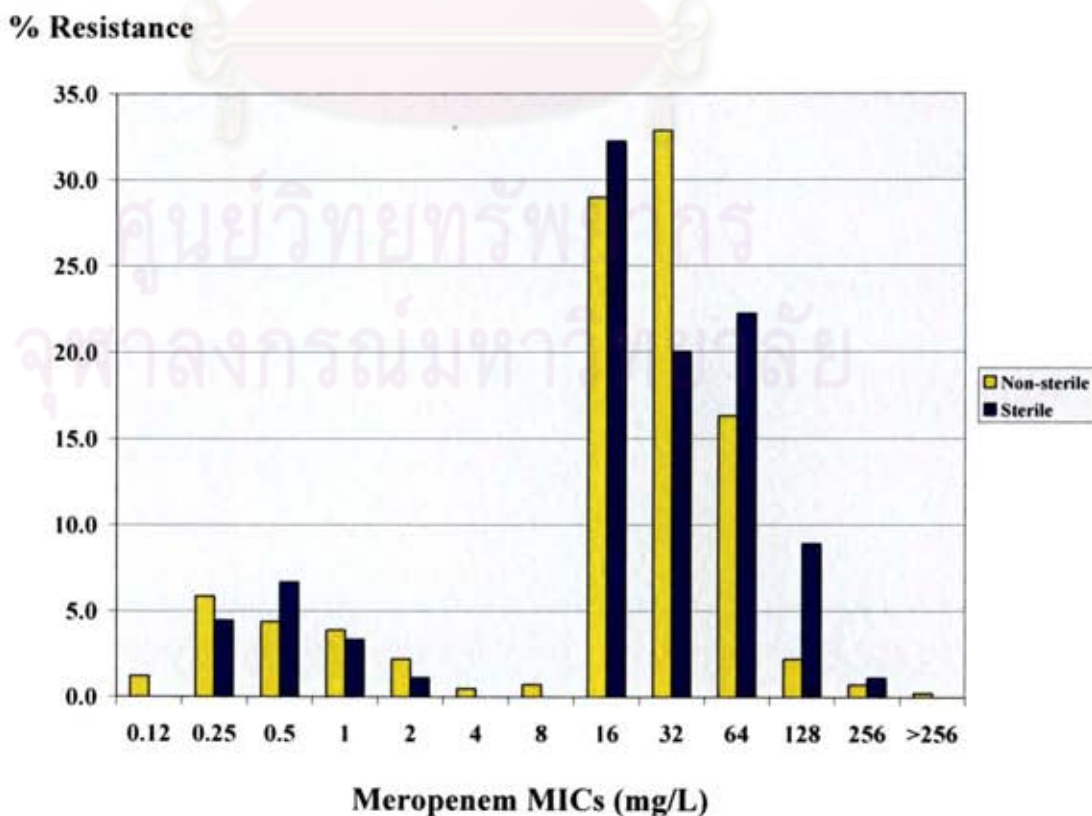


Figure 15. Distributions of meropenem MICs of isolates from sterile sites and non sterile sites



PART IV : DETERMINATION OF CARBAPENEMASE ACTIVITY

Detection of carbapenemase activity was determined by modified Hodge test. The carbapenemase activities of the 501 *A. baumannii* isolates are shown in Appendix D. Four hundred and thirteen (82.4 %) isolates had carbapenemase activity. Comparisons between MICs of carbapenems in *A. baumannii* isolates and the presence of carbapenemase activity are shown in Figures 16 and 17. The MIC ranges of imipenem and meropenem of isolates with carbapenemase activity were 16->256 mg/L and 8->256 mg/L, respectively, whereas the MIC ranges of imipenem and meropenem of isolates with no carbapenemase activity were 0.12-4 mg/L. All 413 isolates showing carbapenemase activity, were resistant to imipenem (MIC \geq 16 mg/L) but 410 (99.3%) isolates were resistant to meropenem (MIC \geq 16 mg/L) and 3 (0.7%) isolates were intermediately resistant to meropenem (MIC = 8 mg/L).

Figure 16. Comparison between the presence of carbapenemase activity and imipenem MIC.

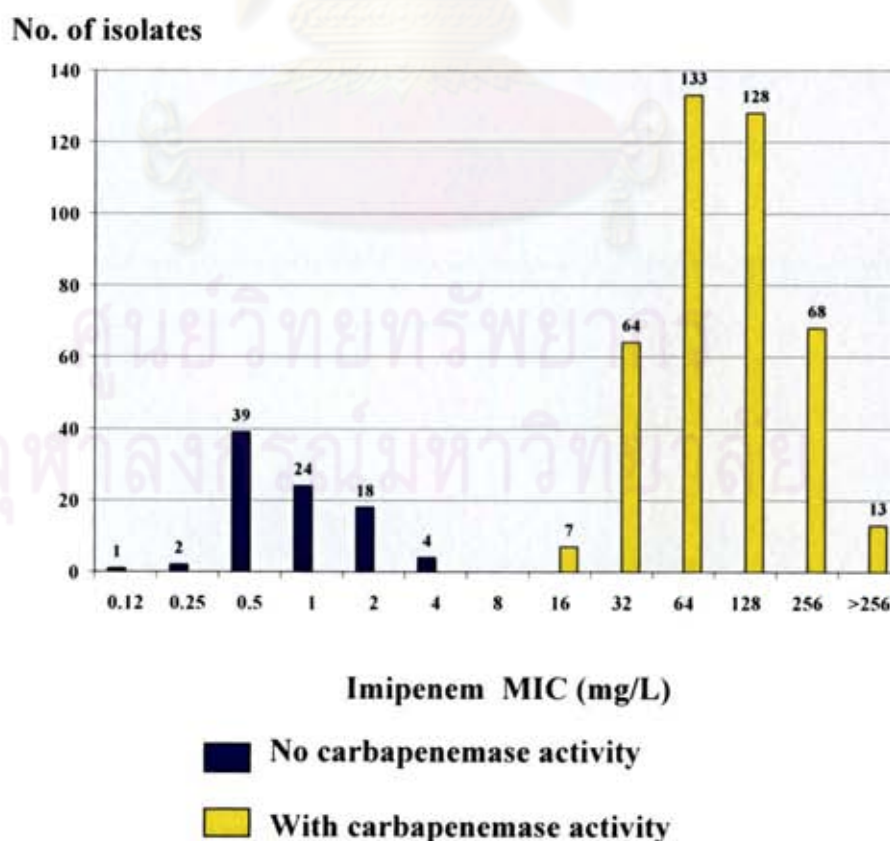
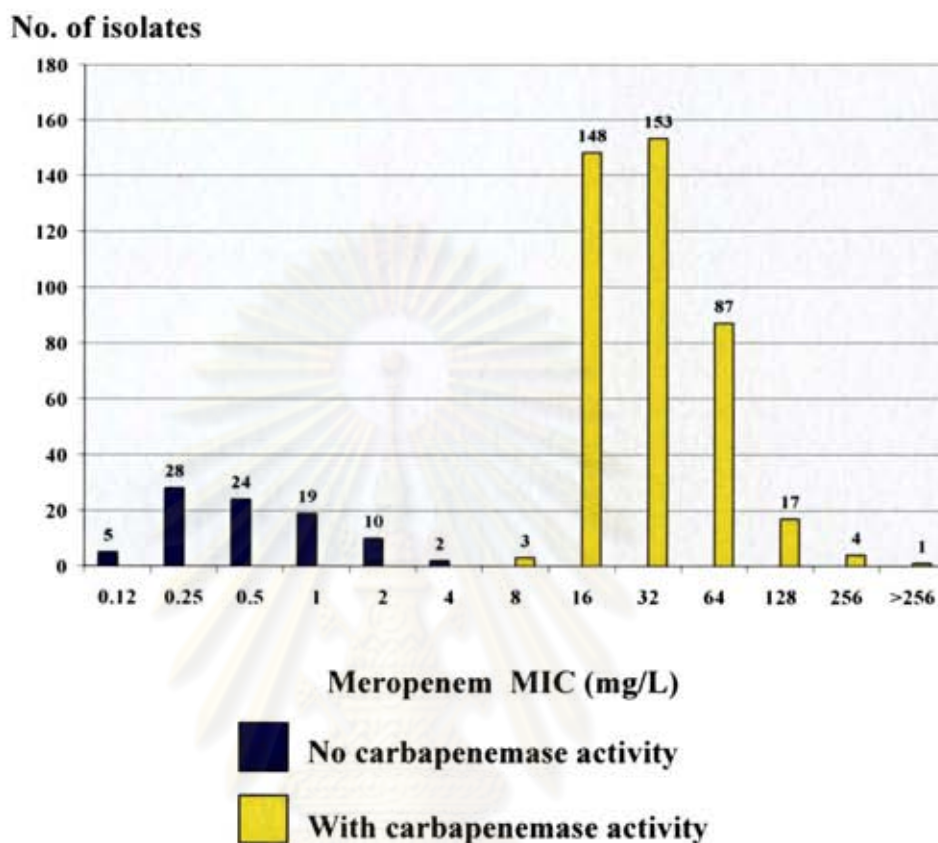


Figure 17. Comparison between the presence of carbapenemase activity and meropenem MIC.



PART V : DETERMINATION OF METALLO- β -LACTAMASES

Determination of metallo- β -lactamase was performed by EDTA-disk synergy test by using imipenem and EDTA disks. Metallo- β -lactamase activity of the 501 *A. baumannii* isolates are shown in Appendix D. No metallo- β -lactamase was detected in any isolates.

PART VI : SCREENING OF GENES ENCODING OXA- , IMP- AND VIM-TYPE CARBAPENEMASES BY PCR AND DNA SEQUENCING OF ENTIRE *BLA*-OXA GENE

Screening for the presence of *bla*_{OXA-like} , *bla*_{IMP-like} and *bla*_{VIM-like}

All *A. baumannii* isolates were screened for the presence of carbapenemase genes, *bla*_{OXA-like} , *bla*_{IMP-like} and *bla*_{VIM-like} , with primers specific for each type by multiplex PCR. The expected PCR products of *bla*_{OXA-23-like} , *bla*_{OXA-24-like}, *bla*_{OXA-51-like}, *bla*_{OXA-58-like}, *bla*_{IMP-like} and *bla*_{VIM-like} were 501 bp, 249 bp, 353 bp, 599 bp, 587 bp and 500 bp, respectively (Figure 18.). The presence of *bla*_{OXA-like}, *bla*_{IMP-like} and *bla*_{VIM-like} in the 501 *A. baumannii* isolates are shown in Appendix D. The *bla*_{OXA-51-like} was detected in all isolates. Eighty-eight (17.6%) isolates had only *bla*_{OXA-51-like}. Three hundred and fifty-six (71.1%) isolates had both *bla*_{OXA-23-like} and *bla*_{OXA-51-like}. Four (0.4%) isolates carried both *bla*_{OXA-24-like} and *bla*_{OXA-51-like}. Six (1.2%) isolates had *bla*_{OXA-51-like} , *bla*_{OXA-23-like} and *bla*_{OXA-24-like}. Seven (1.4%) isolates harbored *bla*_{OXA-51-like} , *bla*_{OXA-23-like} and *bla*_{OXA-58-like}. Twenty-four (4.8%) isolates carried *bla*_{OXA-51-like} , *bla*_{OXA-24-like} and *bla*_{OXA-58-like}. Sixteen (3.2%) isolates had all *bla*_{OXA-like} types, *bla*_{OXA-51-like}, *bla*_{OXA-23-like}, *bla*_{OXA-24-like} and *bla*_{OXA-58-like}. The results are summarized in Table 14.

Of the 413 imipenem-resistant *A. baumannii* isolates, 385 (93.2%) isolates had *bla*_{OXA23-like}. Fifty (12.1%) isolates carried *bla*_{OXA24-like}. Forty-seven (11.4%) isolates had *bla*_{OXA-58-like}. The results are summarized in Table 15.

The distribution of carbapenemase genes and imipenem and meropenem MICs in 501 *A. baumannii* isolates are shown in Figures 19 and 20 and Table 14. The isolates carrying only *bla*_{OXA51-like} showed low-level MICs to imipenem and meropenem (MIC range of 0.12 to 4 mg/L). MIC₅₀ of these isolates for imipenem and meropenem were 1 and 0.5 mg/L, respectively, whereas MIC₉₀ for both imipenem and meropenem were 2 mg/L. Isolates harboring *bla*_{OXA51-like} and *bla*_{OXA23-like} had imipenem and meropenem MIC range of 16 to >256 mg/L and 8 to 256 mg/L, respectively. MIC₅₀ of these isolates for imipenem and meropenem were

64 and 32 mg/L, respectively, whereas MIC₉₀ were 256 and 64 mg/L, respectively. Isolates carrying *bla*_{OXA51-like} and *bla*_{OXA24-like} had imipenem and meropenem MIC of ≥ 256 mg/L and 64 to 256 mg/L, respectively. MIC₅₀ of these isolates for imipenem and meropenem were 256 and 128 mg/L, respectively, whereas MIC₉₀ were >256 and 256 mg/L, respectively.

Isolates carrying *bla*_{OXA51-like}, *bla*_{OXA23-like} and *bla*_{OXA24-like} had imipenem MIC range of 128 to ≥ 256 mg/L, and meropenem MIC range of 64 to 128 mg/L. Isolates carrying *bla*_{OXA51-like}, *bla*_{OXA23-like} and *bla*_{OXA58-like} had imipenem MIC range of 32 to 128 mg/L and meropenem MIC range of 16 to 32 mg/L. Isolates harboring *bla*_{OXA51-like}, *bla*_{OXA24-like} and *bla*_{OXA58-like} had imipenem MIC range of 128 to 256 mg/L and meropenem MIC range of 32 to ≥ 256 mg/L. Isolates carrying *bla*_{OXA51-like}, *bla*_{OXA23-like}, *bla*_{OXA24-like} and *bla*_{OXA58-like} had imipenem MIC range of 128 to >256 mg/L and meropenem MIC range of 32 to 128 mg/L. It was demonstrated that most isolates carrying *bla*_{OXA-24-like} had high level of carbapenem resistance (MIC range of 128 to >256 mg/L).

Carbapenemase activity was found in isolates carrying *bla*_{OXA-51-like} together with other *bla*_{OXA-like} genes including *bla*_{OXA-23-like}, *bla*_{OXA-24-like} and *bla*_{OXA-58-like} whereas no carbapenemase activity was detected in those carrying only *bla*_{OXA-51-like}.

Comparison between type of clinical specimen, carbapenem MIC and carbapenemase genes are shown in Table 11. Isolates from sterile site, including body fluid, CSF and blood had imipenem and meropenem MIC range of 0.5- >256 mg/L and 0.25-256 mg/L, respectively. Isolates from non-sterile site, including sputum, urine, respiration aspirate, pus, tissue had both imipenem and meropenem MIC range of 0.12- >256 mg/L. Most isolates from sterile and non-sterile site carried *bla*_{OXA-51-like} together with *bla*_{OXA-23-like}. The results suggested that *bla*_{OXA-23-like} disseminated in both invasive and non-invasive clinical isolates.

Comparison between ICU isolates, non-ICU isolates and carbapenemase genes are shown in Table 12. Of the 259 isolates from ICU, 203 (78.4%) carried

*bla*_{OXA-51-like} together with *bla*_{OXA-23-like}. One (0.4%) carried *bla*_{OXA-51-like} together with *bla*_{OXA-24-like}. Six (2.3%) had *bla*_{OXA-51-like} together with *bla*_{OXA-23-like} and *bla*_{OXA-24-like}. Six (2.3%) carried *bla*_{OXA-51-like} together with *bla*_{OXA-23-like} and *bla*_{OXA-58-like}. Eight (3.1%) had *bla*_{OXA-51-like} together with *bla*_{OXA-24-like} and *bla*_{OXA-58-like}. Ten (3.7%) carried *bla*_{OXA-51-like} together with *bla*_{OXA-23-like}, *bla*_{OXA-24-like} and *bla*_{OXA-58-like}. Twenty-five (9.7%) had only *bla*_{OXA-51-like}. Of the 242 isolates from non-ICU, 153 (63.2%) carried *bla*_{OXA-51-like} together with *bla*_{OXA-23-like}. Three (1.2%) carried *bla*_{OXA-51-like} together with *bla*_{OXA-24-like}. One (0.4%) had *bla*_{OXA-51-like} together with *bla*_{OXA-23-like} and *bla*_{OXA-58-like}. Sixteen (6.6%) carried *bla*_{OXA-51-like} together with *bla*_{OXA-24-like} and *bla*_{OXA-58-like}. Six (2.5%) had *bla*_{OXA-51-like} together with *bla*_{OXA-23-like}, *bla*_{OXA-24-like} and *bla*_{OXA-58-like}. Sixty-three (26%) carried only *bla*_{OXA-51-like}. The results suggested that *bla*_{OXA-51-like} and *bla*_{OXA-23-like} was the major carbapenemase genes found in ICU and non-ICU *A. baumannii* isolates.

Correlation between biochemical patterns of *A. baumannii* isolates and OXA-type carbapenemase genes in 413 carbapenem-resistant *A. baumannii* isolates are shown in Table 13. Of the 8 isolates with biochemical pattern A, 6 (75%) carried *bla*_{OXA-51-like} together with *bla*_{OXA-23-like}, whereas one (12.5%) carried *bla*_{OXA-51-like} together with *bla*_{OXA-24-like} and one (12.5%) had *bla*_{OXA-51-like} together with *bla*_{OXA-23-like} and *bla*_{OXA-24-like}. Of the 242 isolates with biochemical pattern B, 199 (82.2%) had *bla*_{OXA-51-like} together with *bla*_{OXA-23-like}, whereas 3 (1.2%) isolates had *bla*_{OXA-51-like} together with *bla*_{OXA-24-like} and 3 (1.2%) had *bla*_{OXA-51-like} together with *bla*_{OXA-23-like} and *bla*_{OXA-24-like}. Seven (2.9%) had *bla*_{OXA-51-like} together with *bla*_{OXA-23-like} and *bla*_{OXA-58-like}, 20 (8.3%) had *bla*_{OXA-51-like} together with *bla*_{OXA-24-like} and *bla*_{OXA-58-like} and 10 (4.1%) had *bla*_{OXA-51-like} together with *bla*_{OXA-23-like} and *bla*_{OXA-24-like} and *bla*_{OXA-58-like}. All isolates with biochemical pattern C (15 isolates), E (1 isolate) and F (1 isolate) carried *bla*_{OXA-51-like} together with *bla*_{OXA-23-like}. Of the 146 isolates with biochemical pattern D, 134 (91.8%) had *bla*_{OXA-51-like} together with *bla*_{OXA-23-like}, whereas 2 (1.4%) had *bla*_{OXA-51-like} together with *bla*_{OXA-23-like} and *bla*_{OXA-24-like}. Four (2.7%) had *bla*_{OXA-51-like} together with *bla*_{OXA-24-like} and *bla*_{OXA-58-like} and 6 (4.1%) had *bla*_{OXA-51-like} together with *bla*_{OXA-23-like} and *bla*_{OXA-24-like} and *bla*_{OXA-58-like}. The results suggested *bla*_{OXA-51-like}

together with *bla*_{OXA-23-like} was the most prevalent carbapenemase genes found in all biochemical patterns.



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Table 11. Carbapenem MICs and OXA-type carbapenemase genes of 501 *A. baumannii* isolates by type of clinical specimens

Type of specimen	No. of isolates	MICs (mg/L)						Presence of <i>bla</i> _{OXA-like}						
		Imipenem			Meropenem			OXA-51-like.	OXA-51-like, OXA-23-like	OXA-51-like, OXA-24-like	OXA-51-like, OXA-23-like, OXA-24-like	OXA-51-like, OXA-23-like, OXA-58-like	OXA-51-like, OXA-24-like, OXA-58-like	OXA-51-like, OXA-23-like, OXA-24-like, OXA-58-like
		Range	MIC ₅₀	MIC ₉₀	Range	MIC ₅₀	MIC ₉₀							
Blood	69	0.5->256	128	256	0.25-256	32	128	13	47		1		6	2
Body fluid	20	0.5->256	64	128	0.25-64	16	64	3	17					
CSF	1	64			16				1					
Sputum	238	0.12->256	64	256	0.12->256	32	64	36	169	2	4	7	10	10
respiratory aspirate*	73	0.25->256	64	256	0.25-128	32	64	14	55	1			1	2
Pus	17	0.5->256	64	256	0.25-128	32	64	5	11	1				
Urine	52	0.5-256	64	256	0.25-64	16	64	11	31		1		7	2
Tissue	14	0.25-128	32	128	0.25-32	16	32	3	11					
Other	17	0.5-256	64	256	0.5-64	16	64	3	14					

* Bronchial lavage, endotracheal secretion included

Table 12. Carbapenem MICs and OXA-type carbapenemase genes of 501 *A. baumannii* isolates by wards

Type of ward	No. of isolates	MICs (mg/L)						No. of isolates carried <i>bla</i> _{OXA-like} (%)						
		Imipenem			Meropenem			OXA-51-like.	OXA-51-like. OXA-23-like	OXA-51-like. OXA-24-like	OXA-51-like. OXA-23-like. OXA-24-like	OXA-51-like. OXA-23-like. OXA-58-like	OXA-51-like. OXA-24-like. OXA-58-like	OXA-51-like. OXA-23-like. OXA-24-like. OXA-58-like
		Range	MIC ₅₀	MIC ₉₀	Range	MIC ₅₀	MIC ₉₀							
ICU	259	0.25->256	64	256	0.12->256	32	64	25 (9.7)	203 (78.4)	1 (0.4)	6 (2.3)	6 (2.3)	8 (3.1)	10 (3.7)
Non-ICU	242	0.12->256	64	256	0.12-256	16	64	63 (26)	153 (63.2)	3 (1.2)		1 (0.4)	16 (6.6)	6 (2.5)

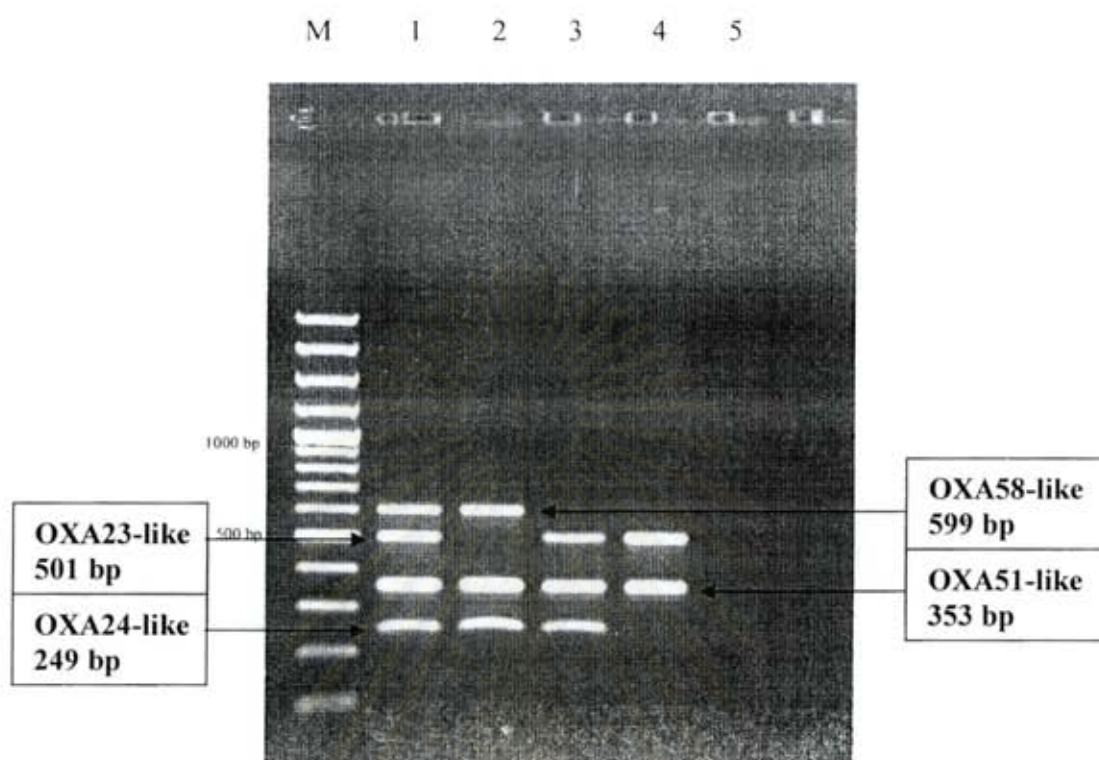
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Table 13. Correlation of biochemical patterns and OXA-type carbapenemase genes in 413 carbapenem-resistant *A. baumannii* isolates

OXA-type carbapenemase gene	% of isolates in biochemical patterns (n)					
	A (8)	B (242)	C (15)	D (146)	E (1)	F (1)
OXA-51-like, OXA-23-like	75 (6)	82.2 (199)	100 (15)	91.8 (134)	100 (1)	100 (1)
OXA-51-like, OXA-24-like	12.5 (1)	1.2 (3)				
OXA-51-like, OXA-23-like, OXA-24-like	12.5 (1)	1.2 (3)		1.4 (2)		
OXA-51-like, OXA-23-like, OXA-58-like		2.9 (7)				
OXA-51-like, OXA-24-like, OXA-58-like		8.3 (20)		2.7 (4)		
OXA-51-like, OXA-23-like, OXA-24-like, OXA-58-like		4.1 (10)		4.1 (6)		

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Figure 18. PCR products of OXA-type carbapenemase genes by multiplex PCR.



Lane M	Marker
Lane 1	<i>bla</i> _{OXA58-like} , <i>bla</i> _{OXA23-like} , <i>bla</i> _{OXA51-like} , <i>bla</i> _{OXA24-like}
Lane 2	<i>bla</i> _{OXA58-like} , <i>bla</i> _{OXA51-like} , <i>bla</i> _{OXA24-like}
Lane 3	<i>bla</i> _{OXA23-like} , <i>bla</i> _{OXA51-like} , <i>bla</i> _{OXA24-like}
Lane 4	<i>bla</i> _{OXA23-like} , <i>bla</i> _{OXA51-like}

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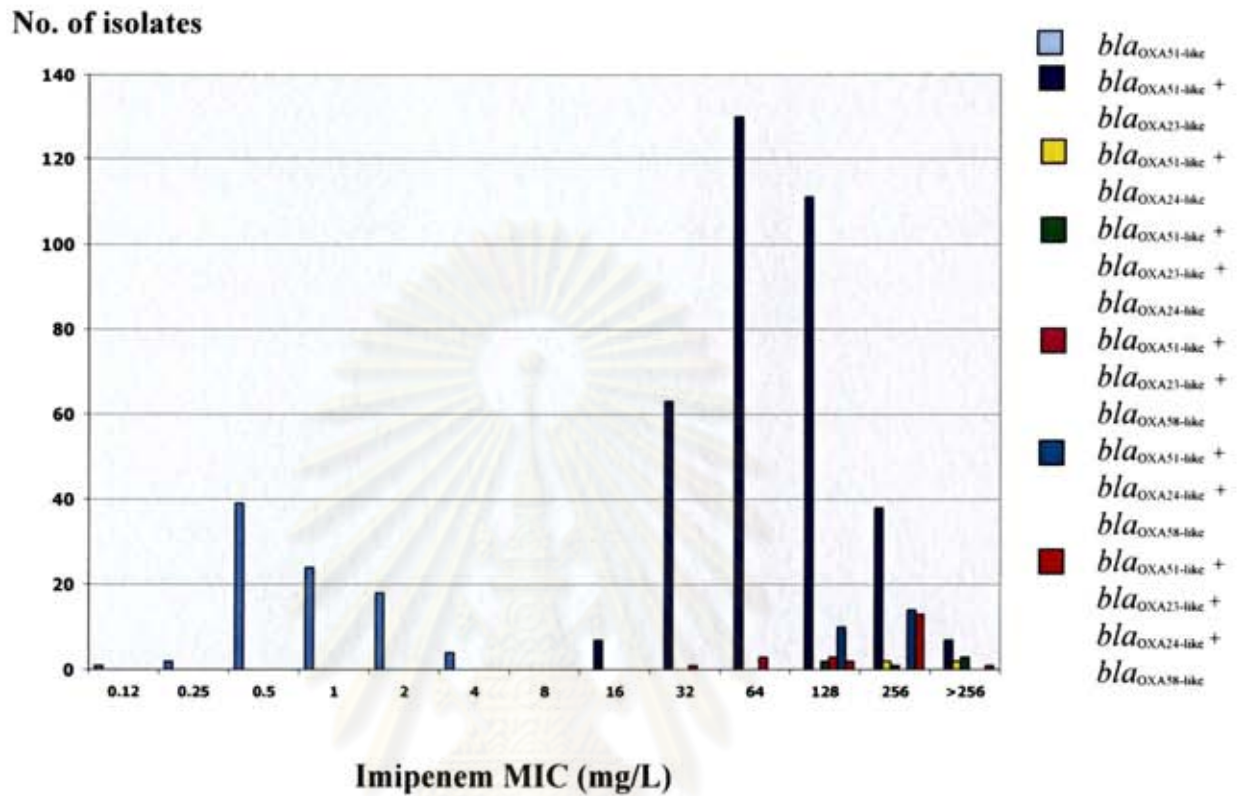
Table 14. OXA-type carbapenemase genes in the 501 *A. baumannii* isolates.

Carbapenemase activity	<i>bla</i> _{OXA-like}	No. of isolates (%)	Imipenem MIC (mg/L)			Meropenem MIC (mg/L)		
			Range	MIC ₅₀	MIC ₉₀	Range	MIC ₅₀	MIC ₉₀
Negative	<i>bla</i> _{OXA51-like}	88 (17.6)	0.12-4	1	2	0.12-4	0.5	2
Positive	<i>bla</i> _{OXA51-like} <i>bla</i> _{OXA23-like}	356 (71.1)	16->256	64	256	8-256	32	64
Positive	<i>bla</i> _{OXA51-like} <i>bla</i> _{OXA24-like}	4 (0.8)	≥256	256	>256	64-256	128	256
Positive	<i>bla</i> _{OXA51-like} <i>bla</i> _{OXA23-like} <i>bla</i> _{OXA24-like}	6 (1.2)	128->256	256	>256	64->256	64	>256
Positive	<i>bla</i> _{OXA51-like} <i>bla</i> _{OXA23-like} <i>bla</i> _{OXA58-like}	7 (1.4)	32-128	64	128	16-32	32	32
Positive	<i>bla</i> _{OXA51-like} <i>bla</i> _{OXA24-like} <i>bla</i> _{OXA58-like}	24 (4.8)	128-256	256	256	32-256	64	128
Positive	<i>bla</i> _{OXA51-like} <i>bla</i> _{OXA23-like} <i>bla</i> _{OXA24-like} <i>bla</i> _{OXA58-like}	16 (3.2)	128->256	256	256	32-128	64	128

Table 15. OXA-type carbapenemase genes associated with carbapenem resistance in the 413 imipenem-resistant *A. baumannii* isolates.

<i>bla</i> _{OXA-like}	No. of isolates (%)
<i>bla</i> _{OXA23-like}	385 (93.2)
<i>bla</i> _{OXA24-like}	50 (12.1)
<i>bla</i> _{OXA58-like}	47 (11.4)

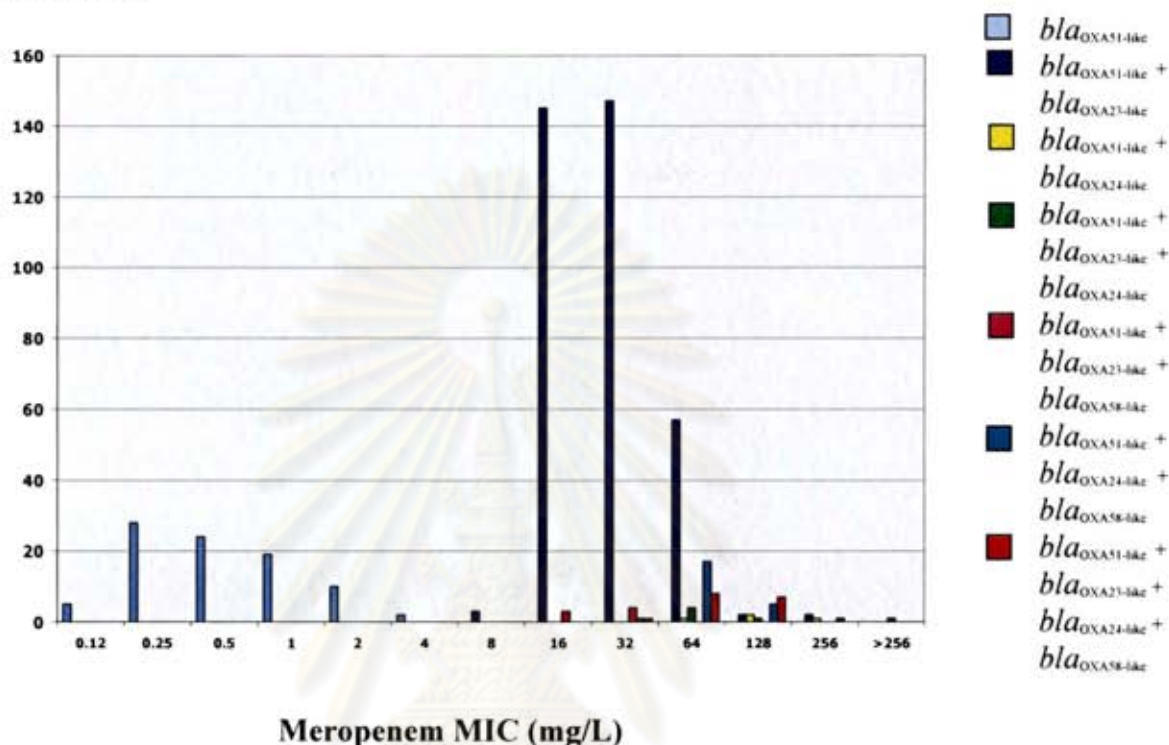
Figure 19. Distribution of genes encoding OXA-type carbapenemases and imipenem MICs.



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Figure 20. Distribution of genes encoding OXA-type carbapenemases and meropenem MICs.

No. of isolates



DNA sequencing of entire *bla*_{OXA} genes

Entire *bla*_{OXA23-like}, *bla*_{OXA24-like}, *bla*_{OXA51-like} and *bla*_{OXA58-like} genes were amplified by PCR and sequenced in ten *A. baumannii* isolates carrying different *bla*_{OXA-like} genes. Each *bla*_{OXA-like} gene was amplified by PCR and then sequenced. DNA sequences were analysed by the software available over the Internet at the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/BLAST>), Multalin (www.toulouse.inra.fr/multalin.html), and ExPASy (www.expasy.org). The results are summarized in Table 16. Similar to studies by Walther *et al.*, Donald *et al.*, Afzal *et al.*, Bou *et al.*, Heritier *et al.*, Brown *et al.* and Poirel *et al.*, the nucleotide sequences of all *bla*_{OXA-like} genes were belonged to class D β -lactamases which were attributed to the presence of three highly conserved active site elements (14, 22-24, 26, 33, 159). The first element contained the conserved serine active site motif S-T-F-K (DBL numbering 70-73).

The second element was the S-X-V triad (DBL numbering 118-120), which valine (V) was replaced by an isoleucine (I) in OXA-51-like enzymes. The third element was the K-T-G triad (DBL numbering 216-218) in OXA-23-like enzymes whereas it was replaced by K-S-G triad in OXA-24-like, OXA-51-like and OXA-58-like enzymes. The other conserved motif, Y-G-N motif (DBL numbering 144-146) was retained in OXA-51-like and OXA-58-like whereas it was replaced by F-G-N in OXA-23-like and OXA-24-like enzymes. (Figure 21.)

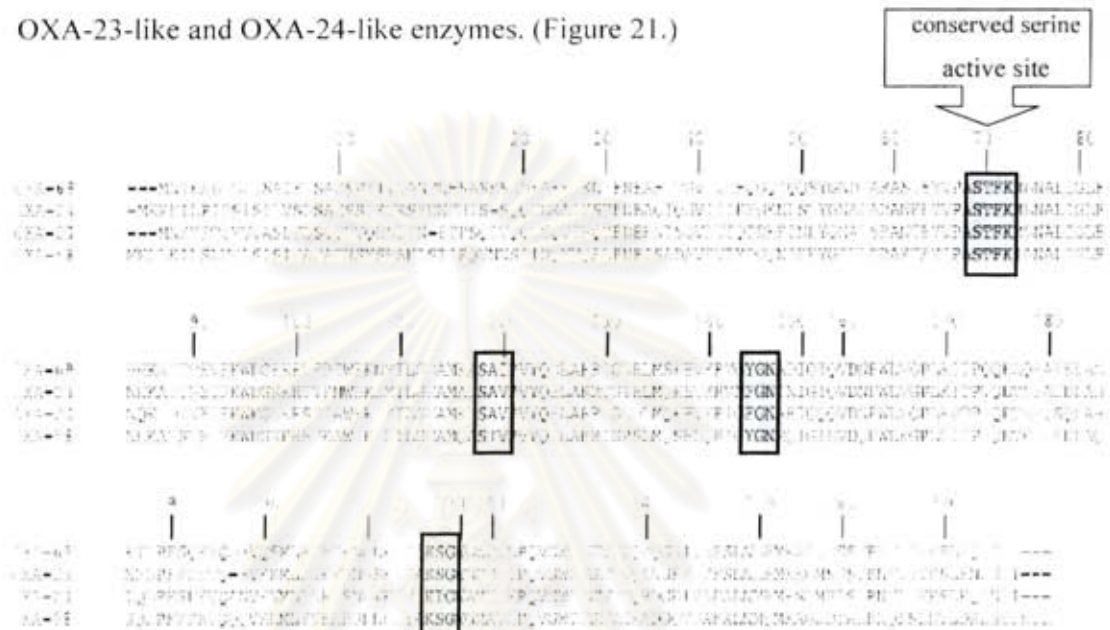


Figure 21. Alignment of amino acid sequences of four main groups of carbapenem-hydrolyzing class D β -lactamases (CHDLs) identified in *A. baumannii*, including OXA-23, OXA-24 and OXA-58 as representatives of the three groups of acquired CHDLs, and OXA-51 as a representative of the naturally occurring CHDLs. The conserved residues for oxacillinases are shaded and conserved residues for class D β -lactamases are blocked. Numbering of β -lactamases is according to Ambler class D β -lactamase numbering DBL (151).

All 10 representative *A. baumannii* isolates that were selected for *bla*_{OXA-23-like} sequencing, A66, A67, 72, A266, A74, A150, A472, A446, A433 and A519, had imipenem MIC range of 16->256 mg/L. These isolates carried various

combinations of *bla*_{OXA-like} genes (Table 16.1). DNA sequence analysis of the 1,065-bp fragments revealed an open reading frame of 822 bp, encoding a 271-amino-acid protein, which showed 100% nucleotide and amino acid sequences identity to *bla*_{OXA-23} and OXA-23 enzyme, respectively (GenBank accession no. AJ132105 and CAB69042, respectively). OXA-23 enzyme shared 99% amino acid sequence identity to OXA-27 and OXA-49. Alignments of nucleotide sequences of OXA-23 and those from ten representative *A. baumannii* isolates are shown in Appendix E.

All 10 representative *A. baumannii* isolates that were selected for *bla*_{OXA-24-like} sequencing, A150, A180, A471, A472, A242, A146, A519, A177, A288 and A446, had imipenem MIC range of 128->256 mg/L. These isolates carried various combinations of *bla*_{OXA-like} genes (Table 16.2.). DNA sequence analysis of the 1,021-bp fragments revealed an open reading frame of 825 bp, encoding a 274-amino-acid protein, which showed 100% nucleotide and amino acid sequence identity to *bla*_{OXA-72} and OXA-72 enzyme, respectively (GenBank accession no. AY739646 and AAU86900, respectively). OXA-72 enzyme shared 99% amino acid sequence identity to OXA-26, OXA-33 and OXA-40 (OXA24) whereas shared 98% amino acid sequence identity to OXA-25. Alignments of nucleotide sequences of OXA-24 and those from ten representative *A. baumannii* isolates are shown in Appendix E.

All 10 representative *A. baumannii* isolates that were selected for *bla*_{OXA-58-like} sequencing, A266, A188, A262, A292, A180, A150, A471, A472, A242 and A446, had imipenem MIC range of 32-256 mg/L. These isolates carried various combinations of *bla*_{OXA-like} genes (Table 16.4). DNA sequence analysis of the 933-bp fragments revealed an open reading frame of 841 bp, encoding a 280-amino-acid protein, which showed 100% nucleotide and amino acid sequence identity to *bla*_{OXA-58} and OXA-58, respectively (GenBank accession no. AY570763 and AAT95987, respectively). This enzyme shared 99% amino acid sequence identity to OXA-96 and OXA-97. Alignments of nucleotide sequences of OXA-58 and those from ten representative *A. baumannii* isolates are shown in Appendix E.

All 10 representative *A. baumannii* isolates that were selected for *bla*_{OXA-51-like} sequencing, A80, A405, A433, A74, A66, A266, A150, A471, A472 and A242, had imipenem MIC range of 0.5->256 mg/L. These isolates carried various combinations of *bla*_{OXA-like} genes (Table 16.3.). DNA sequence analysis of the 1,416-bp amplicons revealed an open reading frame of 825 bp, encoding a 274-amino-acid protein, which showed 100% nucleotide and amino acid sequence identity to *bla*_{OXA-68} and OXA-68 (5 isolates), *bla*_{OXA-66} and OXA-66 (2 isolates), *bla*_{OXA-64} and OXA-64 (1 isolate), *bla*_{OXA-67} and OXA-67 (1 isolate) and showed 99% nucleotide sequence identity to *bla*_{OXA-51} and OXA-51 (1 isolate).

The *bla*_{OXA-68} was found in 5 *A. baumannii* isolates, A266, A150, A471, A472 and A242. A266 carrying *bla*_{OXA-51-like} together with *bla*_{OXA-23-like} and *bla*_{OXA-58-like} had imipenem MIC of 32 mg/L. A150, A471, A472 and A242 carrying *bla*_{OXA-51-like} together with *bla*_{OXA-23-like}, *bla*_{OXA-24-like} and *bla*_{OXA-58-like} had imipenem MIC of 256 mg/L. OXA-68 shared 99% amino acid sequence identity to OXA-77, OXA-91, OXA-117 and OXA-128. Alignments of nucleotide sequences of *bla*_{OXA-68} (GenBank accession no.AY750910) and those from five representative *A. baumannii* isolates are shown in Appendix F.

The *bla*_{OXA-66} was presented in 2 *A. baumannii* isolates, A405 and A433. A405 carrying only *bla*_{OXA-51-like}, had imipenem MIC of 4 mg/L whereas A433 carrying *bla*_{OXA-51-like} together with *bla*_{OXA-23-like} had imipenem MIC of >256 mg/L. OXA-66 shared 99% amino acid sequence identity to OXA-65, OXA-76, OXA-79, OXA-80, OXA-82, OXA-83, OXA-84, OXA-88, OXA-90, OXA-109 and OXA-115. Alignments of nucleotide sequences of *bla*_{OXA-66} (GenBank accession no.AY750909) and those from two representative *A. baumannii* isolates are shown in Appendix E.

The *bla*_{OXA-64} was identified in one *A. baumannii* isolate, A74. This isolate carried *bla*_{OXA-51-like} together with *bla*_{OXA-23-like} and had imipenem MIC of 64 mg/L. OXA-64 shared 99% amino acid sequence identity to OXA-71 and 98% amino acid sequence identity to OXA-51, OXA-65, OXA-66, OXA-67, OXA-88, OXA-90, OXA-91, OXA-95, OXA-99, OXA-100, OXA-104, OXA-106, OXA-111 and

OXA-113. Alignments of nucleotide sequences of *bla*_{OXA-64} (GenBank accession no.AY750907) and those from A74 are shown in Appendix E.

The *bla*_{OXA-67} was found in one *A. baumannii* isolate, A66. This isolate carried *bla*_{OXA-51-like} together with *bla*_{OXA-23-like} and had imipenem MIC of 16 mg/L. OXA-67 shared 99% amino acid sequence identity to OXA-51, OXA-64, OXA-86, OXA-87, OXA-89 and OXA-100. Alignments of nucleotide sequences of *bla*_{OXA-67} (GenBank accession no.DQ491200) and those from A66 are shown in Appendix E.

Novel *bla*_{OXA-51-like} was found in isolate A80 with imipenem MIC of 0.5 mg/L. Nucleotide and amino acid sequences showed 99% identity to *bla*_{OXA-51} and OXA-51 enzyme. The nucleotide sequences differed from *bla*_{OXA-51} (GenBank accession no.AJ309734) by two nucleotides. Cytosine (C) was replaced by adenosine (A) at position 152 and cytosine (C) was replaced by guanine (G) at position 388. This enzyme differed from OXA-51 (GenBank accession no.ABD47672) by two amino acids. The threonine (T) was replaced by lysine (K) at position 51 and the proline (P) was replaced by alanine (A) at position 130. All amino-acid changes were located outside the class D carbapenemase motifs. It shared 99% amino acid sequence identity to OXA-132, OXA-99, OXA-111, OXA-64 and OXA-95. The alignment of amino acid sequences of the novel OXA-51-like and these enzymes are shown in Figure 22. This novel enzyme shared 98% amino acid sequence identity to OXA-67, OXA-70, OXA-71, OXA-86, OXA-87, OXA-88, OXA-89, OXA-90, OXA-91, OXA-93, OXA-100, OXA-106, OXA-113, OXA-117 and OXA-130. Alignments of amino acid and nucleotide sequences of OXA-51 subgroup and those from A80 isolate are shown in Figure 23 and Appendix E, respectively.

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Table 16. Sequencing analysis of entire *bla*_{OXA-like} genes.Table 16.1. Sequencing analysis of *bla*_{OXA-23-like} genes from 10 representative isolates.

Isolates	Imipenem MIC (mg/L)	Presence of <i>bla</i> _{OXA-like} by multiplex PCR				<i>bla</i> _{OXA-23-type} gene
		<i>bla</i> _{OXA-51-like}	<i>bla</i> _{OXA-23-like}	<i>bla</i> _{OXA-24-like}	<i>bla</i> _{OXA-58-like}	
A66	16	+	+	-	-	<i>bla</i> _{OXA-23}
A67	32	+	+	-	-	<i>bla</i> _{OXA-23}
A72	32	+	+	-	-	<i>bla</i> _{OXA-23}
A266	32	+	+	-	+	<i>bla</i> _{OXA-23}
A74	64	+	+	-	-	<i>bla</i> _{OXA-23}
A150	256	+	+	+	+	<i>bla</i> _{OXA-23}
A472	256	+	+	+	+	<i>bla</i> _{OXA-23}
A446	256	+	+	+	+	<i>bla</i> _{OXA-23}
A433	>256	+	+	-	-	<i>bla</i> _{OXA-23}
A519	>256	+	+	+	-	<i>bla</i> _{OXA-23}

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Table 16.2. Sequencing analysis of *bla*_{OXA-24-like} genes from 10 representative isolates.

Isolates	Imipenem MIC (mg/L)	Presence of <i>bla</i> _{OXA-like} by multiplex PCR				<i>bla</i> _{OXA-24-type} gene
		<i>bla</i> _{OXA-51-like}	<i>bla</i> _{OXA-24-like}	<i>bla</i> _{OXA-23-like}	<i>bla</i> _{OXA-58-like}	
A180	128	+	+	-	+	<i>bla</i> _{OXA-72}
A288	128	+	+	-	+	<i>bla</i> _{OXA-72}
A177	256	+	+	-	-	<i>bla</i> _{OXA-72}
A146	256	+	+	-	-	<i>bla</i> _{OXA-72}
A150	256	+	+	+	+	<i>bla</i> _{OXA-72}
A471	256	+	+	+	+	<i>bla</i> _{OXA-72}
A472	256	+	+	+	+	<i>bla</i> _{OXA-72}
A242	256	+	+	+	+	<i>bla</i> _{OXA-72}
A446	256	+	+	+	+	<i>bla</i> _{OXA-72}
A519	>256	+	+	+	-	<i>bla</i> _{OXA-72}

Table 16.3. Sequencing analysis of *bla*_{OXA-51-like} genes from 10 representative isolates.

Isolates	Imipenem MIC (mg/L)	Presence of <i>bla</i> _{OXA-like} by multiplex PCR				<i>bla</i> _{OXA-51-type} gene
		<i>bla</i> _{OXA-51-like}	<i>bla</i> _{OXA-23-like}	<i>bla</i> _{OXA-24-like}	<i>bla</i> _{OXA-58-like}	
A80	0.5	+	-	-	-	novel <i>bla</i> _{OXA-51-like}
A405	4	+	-	-	-	<i>bla</i> _{OXA-66}
A66	16	+	+	-	-	<i>bla</i> _{OXA-67}
A266	32	+	+	-	+	<i>bla</i> _{OXA-68}
A74	64	+	+	-	-	<i>bla</i> _{OXA-64}
A150	256	+	+	+	+	<i>bla</i> _{OXA-68}
A471	256	+	+	+	+	<i>bla</i> _{OXA-68}
A472	256	+	+	+	+	<i>bla</i> _{OXA-68}
A242	256	+	+	+	+	<i>bla</i> _{OXA-68}
A433	>256	+	+	-	-	<i>bla</i> _{OXA-66}

Table 16.4. Sequencing analysis of *bla*_{OXA-58-like} genes from 10 representative isolates.

Isolates	Imipenem MIC (mg/L)	Presence of <i>bla</i> _{OXA-like} by multiplex PCR				<i>bla</i> _{OXA-58-type} gene
		<i>bla</i> _{OXA-51-like}	<i>bla</i> _{OXA-58-like}	<i>bla</i> _{OXA-23-like}	<i>bla</i> _{OXA-24-like}	
A266	32	+	+	+	-	<i>bla</i> _{OXA-58}
A188	64	+	+	+	-	<i>bla</i> _{OXA-58}
A262	64	+	+	+	-	<i>bla</i> _{OXA-58}
A292	64	+	+	+	-	<i>bla</i> _{OXA-58}
A180	128	+	+	-	+	<i>bla</i> _{OXA-58}
A150	256	+	+	+	+	<i>bla</i> _{OXA-58}
A471	256	+	+	+	+	<i>bla</i> _{OXA-58}
A472	256	+	+	+	+	<i>bla</i> _{OXA-58}
A242	256	+	+	+	+	<i>bla</i> _{OXA-58}
A446	256	+	+	+	+	<i>bla</i> _{OXA-58}

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Figure 23. Alignments of amino acid sequences of OXA-51 subgroup and that from A80 isolate.

	1						70
OXA-51	MNINIKLLLLIT	SAIFISACSP	YIVTANPNHS	ASKSDEKAEK	IKNLFNEVHT	TGVLVIQQGQ	TQQSYGNDLA
OXA-132
OXA-99	R.....
OXA-111	S.....	A.....
OXA-64	..A.....	G.....	A.....
OXA-71	..A.....	A.....
OXA-113	..A.....	A.....
A80	K.....
OXA-67	..A.....	T.....	T.....	A.....
OXA-100	..A.....	T.....	T.....	A.....
OXA-86	T.....	T.....	A.....
OXA-87	T.....	T.....	A.....
OXA-65	..A.....	A.....
OXA-88	..A.....	A.....
OXA-66	..A.....	K.....	A.....
OXA-83	..A.....	V.....	A.....
OXA-82	..A.....	V.....	A.....
OXA-76	..A.....	V.....	A.....
OXA-131	..A.....	V.....	A.....
OXA-80	..A.....	V.....	A.....
OXA-115	..A.....	V.....	A.....
OXA-109	..A.....	V.....	A.....
OXA-84	..A.....	V.....	A.....
OXA-79	..A.....	V.....	A.....
OXA-90	..A.....	A.....
OXA-95	..A.F.....	A.....
OXA-108	..A.....	T.....	A.....
OXA-130	..A.....	T.....	A.....
OXA-94	..QA.....	S.....	A.....
OXA-69	..A.....	D.....	A.....	H.....
OXA-110	..A.....	D.....	A.....	H.....
OXA-107	..A.....	D.....	A.....	H.....
OXA-112	..A.....	D.....	A.....	H.....
OXA-92	..A.....	D.....	A.....	H.....
OXA-68	..A.....	S.....	A.....
OXA-77	..A.....	S.....	A.....
OXA-91	..A.....	S.....	A.....
OXA-104	..A.....	A.....
OXA-128	..A.....	S.....	A.....	V.....
OXA-78	..A.....	S.....	A.....
OXA-89	..A.....	H.....	S.....	A.....
OXA-93	..A.....	T.....	A.....
OXA-70	..A.....	K.....	A.....
OXA-106	..A.....	K.....	A.....
OXA-75	..QA.....	A.....
OXA-116	S.....	D.....	A.....
OXA-117	S.....	A.....
Consensus	mnikal.....	t.....	e.....	A.....

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	71						140
OXA-51	RASTEYVPAS	TFKMLNALIG	LEHHKATTE	VFKWDGQRL	FPEWEKMTL	GDAMKSAIP	VYQDLARRIG
OXA-132
OXA-99
OXA-111
OXA-64
OXA-71	T
OXA-113	T
A80
OXA-67	I
OXA-100	I
OXA-86	..I.....	I
OXA-87	..I.....	I
OXA-65	K
OXA-88	K
OXA-66	K
OXA-83	K	L
OXA-82	K
OXA-76	K
OXA-131	K	V
OXA-80	K	L
OXA-115	K	L
OXA-109	K	Q
OXA-84	K	S
OXA-79	K
OXA-90	K
OXA-95	K
OXA-108	K
OXA-130	K
OXA-94	K
OXA-69	E	N
OXA-110	E	N
OXA-107	E	N
OXA-112	E	N
OXA-92	E	N
OXA-68	N
OXA-77	N
OXA-91	N
OXA-104	N
OXA-128	N
OXA-78	A	N
OXA-89	N
OXA-93	S	N
OXA-70	N
OXA-106	N
OXA-75	N
OXA-116	N
OXA-117	N
Consensus

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	141						210
OXA-51	LELMSKEVKR	VGYGNADIGT	QVDNFWLVGP	LKITPQQEAQ	FAYKLANRTL	PFSPKVQDEV	QSMLFIEEKN
OXA-132
OXA-99	M.
OXA-111	M.
OXA-64
OXA-71
OXA-113	V.....
A80
OXA-67	L.....
OXA-100	Q.....
OXA-86	L.....
OXA-87	L.A.....
OXA-65	Q.....
OXA-88	Q.....
OXA-66	Q.....
OXA-83	Q.....
OXA-82	V.....	Q.....
OXA-76	Q.....
OXA-131	Q.....
OXA-80	Q.....
OXA-115	V.....	Q.....
OXA-109	Q.....
OXA-84	A.....	Q.....
OXA-79	Q.....
OXA-90	Q.....
OXA-95	Q.....
OXA-108	T.....	V.....	Q.....
OXA-130	T.....	Q.....
OXA-94	Q.....
OXA-69	Q.....
OXA-110	Q.....
OXA-107	V.....	Q.....
OXA-112	Q.....
OXA-92	Q.....
OXA-68	N.....	QE.....
OXA-77	N.....	Q.....
OXA-91	N.....	Q.....
OXA-104	N.....	Q.....
OXA-128	N.....	QE.....
OXA-78	N.....	Q.....
OXA-89	N.....	T.....	Q.....
OXA-93	N.....	Q.....
OXA-70	N.....	Q...H..
OXA-106	N.....	Q.....
OXA-75	N...I..	Q.....
OXA-116	N.....	Q.....
OXA-117	N.....	Q.....
Consensus	k.....	q.....

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	211					274
OXA-51	GNKIYAKSGW	GWDVDPOVGW	LTGWVVQPQG	NIVAFSLNLE	MKKGIPSSVR	KEITYKSLEQ LGIL
OXA-132M.....
OXA-99
OXA-111
OXA-64
OXA-71
OXA-113
A80
OXA-67
OXA-100
OXA-86
OXA-87
OXA-65N.....
OXA-88N.....
OXA-66N.....
OXA-83N.....
OXA-82N.....
OXA-76N.....K.....
OXA-131NQ.....
OXA-80N.....
OXA-115N.....
OXA-109N.....
OXA-84N.....
OXA-79G.N.....
OXA-90
OXA-95
OXA-108
OXA-130
OXA-94N.....H.....
OXA-69N.....
OXA-110N.....
OXA-107N.....
OXA-112N.....P.....
OXA-92N.....	..S.....
OXA-68N.....
OXA-77N.....
OXA-91
OXA-104
OXA-128N.....
OXA-78N.....T.....
OXA-89N.....
OXA-93N.....
OXA-70
OXA-106
OXA-75N.....S.....RG.....
OXA-116
OXA-117N.....	..E.....
Consensus#.....	..g.....eq lgil

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CHAPTER VI

DISCUSSION

Antibiotic-resistant *A. baumannii* is a major problem worldwide because it has become resistant to almost all currently available antimicrobial agents. Carbapenems are a class of β -lactam antibiotics with a broad spectrum of antibacterial activity, and have a structure which renders them highly resistant to β -lactamase. In 2007, imipenem resistance rate of *A. baumannii* collected from Chiang Mai University Hospital and Songklanagarind Hospital were 35.5% and 34.7%, respectively (49, 50). Among imipenem-resistant *A. baumannii* isolated from Songklanagarind Hospital, 61.9% were from respiratory tract, 49.9% from ICU and 14.8% were resistant to all routine tested antibiotics. In 2003, the imipenem resistance rate of *A. baumannii* was 61% at Police General Hospital, whereas those was 68% at Siriraj Hospital in 2006 (51, 52). Among carbapenem-resistant isolates, 57% were resistant to all antimicrobials currently available in Thailand. The data from the National Antimicrobial Resistance Surveillance Center Thailand (NARST) showed that imipenem resistance in *Acinetobacter calcoaceticus-baumannii* complex increased from 2% in 1998 to 57% in 2006 (53). In this study, prevalence of carbapenem resistance in *A. baumannii* isolated from patients at King Chulalongkorn Memorial Hospital, Bangkok during January 2004 to August 2007 was 82.4% for imipenem and 81.8% for meropenem, which were higher than those reported by other studies in Thailand. This may be because King Chulalongkorn Memorial Hospital is a referral hospital. Transferring of severe patients from other hospitals may be resulting in increasing in the prevalence of carbapenem resistance in *A. baumannii*.

The carbapenem resistance rates from this study were also higher than other countries. In 2005, both imipenem and meropenem resistance rates of *A. baumannii* collected from Shanghai were 6.3% while those from Hong Kong were 2.7% and 10.8%, respectively (138). Another surveillance program showed carbapenem-resistant rate increased from 4.5% in 2003 to 18.2% in 2004 (191). The carbapenem-resistant rates in 3,601 isolates of *A. baumannii* from more than 311

U.S. hospitals surveyed by the NCCLS, increased from 9% in 1995 to 40% in 2004 (196). In 2008, carbapenem-resistant rate in *A. baumannii* isolated from Greece was 70.1% (197). High prevalence of carbapenem resistance on this study may be because of high consumption of carbapenem for treatment of *A. baumannii* and other bacteria.

For infections caused by carbapenem-resistant *A. baumannii* isolates, antibiotic choices may be quite limited because this organism always resist to multiple antibiotics. Antimicrobial combination therapy appears to be a reasonable alternative for treatment of carbapenem-resistant *A. baumannii* isolates. Combination of imipenem and amikacin, colistin and rifampin, imipenem combined with rifampin and colistin are suggested (111, 112). Tigecycline was used for treatment of this organism, but high level of tigecycline resistance were recently reported (117, 119, 123). In addition, sulperazone may be used to treat carbapenem-resistant *A. baumannii* isolates (125).

The imipenem resistance rates of *A. baumannii* isolates in ICUs and non ICUs were 90.3% and 74.1%, whereas meropenem resistance rates of those were 89.5% and 73.7%, respectively. The carbapenem resistance rate in *A. baumannii* isolates from ICUs was significantly higher than that in non ICUs ($P < 0.01$). High carbapenem resistance rate in ICUs is similar to study by Bogaerts *et al.* and Souli *et al.* that found the carbapenem resistance rate of *A. baumannii* in ICUs were 70.6% and 84%, respectively (186, 198). In contrast to this study, Sinha *et al.* found that meropenem resistance rate of *Acinetobacter* spp. in ICUs and other wards were 42.8% and 57.2%, respectively (199). In this study, the carbapenem resistance in ICUs was higher than non-ICUs, which similar to study by Falagas *et al.* that found imipenem resistance rate of *A. baumannii* in ICUs medical wards was 91% whereas those in medical wards and surgical wards were 71% (139). Higher carbapenem resistance rate of *A. baumannii* isolates from ICUs may be because carbapenem-resistant isolates are selected by increased use of carbapenems in severe patients. *A. baumannii* can colonize in the environment in ICU such as contaminated equipment including ventilator, bed rail, pillow and bed. Transmission of microorganism also occurred via hand of staff. In addition, transferring of severed

and trauma patients from other hospitals also associated to the high prevalence of carbapenem resistance in ICUs.

Identification and elimination of common source of *A. baumannii* reservoir are most important for infection control of *A. baumannii* in the hospital. Outbreak managements required an active infection-control programme for patients and medical personnel, including contact isolation to prevent transmission as well as active surveillance cultures to identify *A. baumannii*-colonized patients. Improved hand hygiene, cleaning and disinfection of the environment, including equipment decontamination, cohort nursing, the isolation of patients in single room, the restriction of access to the ICU, control of antibiotic usage, improving staffing ratio and closing a ward for cleaning and disinfection, can be used to control the spread of *A. baumannii* in hospital.

In our study, *bla*_{OXA-51-like} was detected in all carbapenem-susceptible and -resistant *A. baumannii* isolates. This is similar to the studies of Turton *et al.*, Merquier *et al.*, Heritier *et al.* and Wang *et al.* which reported that *bla*_{OXA-51-like} were found in all carbapenem-susceptible and resistant *A. baumannii* isolates (27, 28, 30, 200). The results suggested that OXA-51-like enzymes were very poor carbapenemases and may be natural and chromosomally encoded in all *A. baumannii* isolates. However, Tsakris *et al.* and Koh *et al.* found *bla*_{OXA-51-like} in 90.9% and 77.3% of *A. baumannii* isolates, respectively (18, 31).

The OXA-51 was first described in imipenem-resistant *A. baumannii* clones from Argentina and was the largest and most diverse collection of class D carbapenemases in *A. baumannii* (26). To date, forty-six enzymes of this group have been reported. In the present study, the variations were found in *bla*_{OXA-51-like} group with 50% of *bla*_{OXA-68}, 20% of *bla*_{OXA-66}, 10% each for *bla*_{OXA-64}, *bla*_{OXA-67} and a novel *bla*_{OXA-51-like}. OXA-64, OXA-67 and OXA-68 were reported in *A. baumannii* isolated from South Africa, Argentina and Spain, respectively (25), whereas OXA-66 was reported in Spain, Greece and China (25, 197, 200). The sequences of entire *bla*_{OXA-51-like} in the isolate A80 was 99% similar to *bla*_{OXA-51} and differed by two nucleotides, resulting in two amino acid changes at positions 51 and

130. This novel enzyme has conserved sequences of class D β -lactamases. However, biochemical properties and susceptibility patterns of this enzyme have to be further investigated.

The presence of *bla*_{OXA-23-like} were detected in the majority of our carbapenem-resistant *A. baumannii* isolates (93.2%). The results suggested that *bla*_{OXA-23-like} plays an important role in carbapenem resistance in this study. Similar to many studies, *bla*_{OXA-23-like} was predominant in carbapenem-resistant *A. baumannii* isolates (11, 18, 37, 193, 201). Wang *et al.* found *bla*_{OXA-23-like} in 97.7% of imipenem-resistant *A. baumannii* isolates, and both Zong *et al.* and Stoeva *et al.* found in 100% of imipenem-resistant *A. baumannii* isolates (200-202). Imipenem MICs of these isolates varied from 16 to >256 mg/L. This may be due to the involvement of other resistance mechanisms such as impermeability of outer membrane proteins or loss of porin and efflux system. Heritier *et al.* found that overexpression of AdeABC efflux pump associated with expression of these oxacillinases induced a higher level of carbapenem resistance (10).

In this study, *bla*_{OXA-23} in carbapenem-resistant *A. baumannii* was amplified and sequenced from plasmid DNA. There were many reports demonstrated that *bla*_{OXA-23} is plasmid-encoded (14, 163). Villegas reported that *bla*_{OXA-23} was chromosomal encoded in three of four clones of carbapenem-resistant *A. baumannii* isolates and plasmid encoded in one clone (19). In addition, Wang *et al.*, Meric *et al.* and Stoeva *et al.* also found that *bla*_{OXA-23} was chromosomally encoded (200, 201, 203). Therefore, the gene location of this gene has to be further investigated.

OXA-23 group consists of OXA-23, OXA-27 and OXA-49. In the present study, *bla*_{OXA-23} was detected in all ten representative *A. baumannii* isolates by sequencing of entire *bla*_{OXA-23-like}. OXA-23 enzyme was first described in an imipenem-resistant *A. baumannii* isolated from Scotland in 1985 (14). From late 2003 to the end of 2005, the dissemination of two carbapenem-resistant clones with OXA-23 carbapenemase at multiple hospitals in London and Southeast England were reported (20). OXA-23-producing in carbapenem-resistant *A. baumannii* isolates have also been reported in Brazil (100%) and French Polynesia (100%),

China (100%) and Korea (69%) (11, 15, 16, 202). Wang *et al.* also found OXA-23-producing in 97.7% of imipenem-resistant *A. baumannii* (200). In addition, this enzyme was also reported in Singapore (18), South America (19) and Australia (21). OXA-27 was reported in one isolate of carbapenem-resistant *A. baumannii* isolated from Singapore (23).

The MIC level to imipenem in strains carrying *bla*_{OXA-51-like} together with *bla*_{OXA-24-like} were to ≥ 256 mg/L. The MIC range for isolates carrying *bla*_{OXA-24-like} together other *bla*_{OXA} were 128->256 mg/L for imipenem, 32->256 mg/L for meropenem. These suggested that *bla*_{OXA-24-like} conferred a high level of MICs to carbapenems and played an importance role in carbapenem resistance in these isolates. Afzal-Shah *et al.* demonstrated that the hydrolytic activity to imipenem of OXA-25 and OXA-26 were higher than those of OXA-27, so leading to higher imipenem MIC than others (23).

The OXA-24 cluster consists of OXA-24, OXA-25, OXA-26, OXA-33, OXA-40 and OXA-72. The OXA-24 enzyme was first described in carbapenem-resistant *A. baumannii* isolated from Spain (22). The nucleotide sequences of this enzyme were corrected in 2006 by the same researchers, resulting in amino acid sequences identical to OXA-40 described in 2003 (204). In the present study, OXA-72 was detected in all ten representative *A. baumannii* isolates. OXA-72 was also detected in one isolate of imipenem-resistant *Acinetobacter* genomospecies 3 and *Acinetobacter* spp. isolated from China (200).

There were many reports previously demonstrated that *bla*_{OXA-24} is chromosomally encoded (22, 24). However, Lolans *et al.* investigated the *bla*_{OXA-40} gene location and found that it was on both chromosome and plasmid in imipenem-resistant *A. baumannii* isolates (117). In this study, *bla*_{OXA-24} in carbapenem-resistant *A. baumannii* was amplified and sequenced from plasmid DNA. It could not be amplified from chromosomal DNA. So, the gene location of this gene has to confirm by other techniques such as Southern blot analysis.

In this study, there were isolate carrying *bla*_{OXA-58-like} together with *bla*_{OXA-51-like} and other *bla*_{OXA}. So, the activity of OXA-58 could not be discussed. Tsakris *et al.* found that *A. baumannii* isolates carrying *bla*_{OXA-58} showed low level of imipenem MIC (31). This is similar to the study by Poirel *et al.* that OXA-58 showed low hydrolysis to imipenem (33). In addition, Heritier *et al.* demonstrated that OXA-58 exhibited weak carbapenemase activity and played a role in carbapenem resistance in *A. baumannii* when *bla*_{OXA-58} was highly expressed (10). Bertini *et al.* also found that the increase in carbapenem resistance level was associated with an increased production of OXA-58 by multiple copies of the *bla*_{OXA-58} gene (205).

The OXA-58 group consists of OXA-58, OXA-96 and OXA-97. In the present study, OXA-58 was detected in all ten representative *A. baumannii* isolates. This enzyme was first described in carbapenem-resistant *A. baumannii* isolated from France in 2005 (33). At the same time, it was detected in seven out of eight carbapenem-resistant *A. baumannii* by Heritier *et al.* (143). Marque *et al.* found *A. baumannii* carrying *bla*_{OXA-58} gene in 22 out of 42 carbapenem-resistant *A. baumannii* isolated from France, Spain, Turkey and Romania (13). Both *bla*_{OXA-58} and *bla*_{OXA-51} were detected in many *A. baumannii* isolated from ICU in Greece (31, 144). Coelho *et al.* also found *Acinetobacter* spp. carrying *bla*_{OXA-58} and *bla*_{OXA-51} isolated from Argentina, Kuwait and United Kingdom over a 10 year period in 2006 (206). The *bla*_{OXA-58} also was detected in 7 imipenem-resistant *A. baumannii* isolated from China (200). Between October 2003 and June 2004, *bla*_{OXA-58} was detected in 44 of 45 *A. baumannii* isolated from Italy (140). In addition, between April 2005 and March 2007, this gene also was detected in 26 of 31 *A. baumannii* isolated from ICU patients in Greece (207). The *bla*_{OXA-96} was detected in one imipenem-resistant *A. baumannii* isolated from Singapore (18). Poirel *et al.* found *bla*_{OXA-97} in 19 of 39 carbapenem-resistant *A. baumannii* isolated from Tunisia (34).

Among carbapenem-resistant *A. baumannii* isolates, 4 isolates carried *bla*_{OXA-23-like} together with *bla*_{OXA-58-like}, 4 isolates carried *bla*_{OXA-24-like} together with *bla*_{OXA-58-like} and 4 isolates carried *bla*_{OXA-23-like} together with *bla*_{OXA-24-like} and

*bla*_{OXA-58-like} were isolated from patients at the same period of time and the same ward. The results suggested that clonal spread of carbapenem-resistant *A. baumannii* may involve and should be further investigated by genotyping such as pulse field gel electrophoresis (PFGE), amplified fragment length polymorphism (AFLP) and random amplified polymorphic DNA (RAPD).

Unlike OXA-type carbapenemase, metallo β -lactamases-producing *A. baumannii* is less than OXA-type-producing isolates. In this study, the metallo- β -lactamase was not detected in all 501 *A. baumannii* isolates by EDTA-disk synergy test and by PCR amplification of *bla*_{IMP-like} and *bla*_{VIM-like}. This was in contrast to the study by Sung *et al.* that found high prevalence of metallo- β -lactamase-producing *A. baumannii* isolates (208). Among carbapenemase-producing *A. baumannii*, 69.6% was metallo- β -lactamase whereas 30.4% was OXA-type carbapenemase. IMP-1 and VIM-2 were found in 93.7% and 6.3% of metallo β -lactamase-producing isolates whereas OXA-23 was detected in all carbapenemase-producing isolates. In contrast, Koh *et al.* reported that OXA-type carbapenemase-producing *A. baumannii* was found higher than metallo- β -lactamase-producing isolates. OXA-51-like was found in 77.3% of *A. baumannii* isolates and OXA-23 was found in 91.1% of carbapenemase-producing *A. baumannii* isolates whereas IMP-4 was found in 9.1% of those isolates (18). This study suggests none or rare incidence of metallo- β -lactamase dissemination in carbapenem-hydrolyzing *A. baumannii* isolates in this study.

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CHAPTER VII

CONCLUSION

Carbapenems are among the drugs of choice for treatment of multidrug-resistant *Acinetobacter baumannii* infections. However, emergence of carbapenem resistance in *A. baumannii* has been reported worldwide. In the present study, the imipenem and meropenem-resistant rates in 501 *A. baumannii* were 82.4% and 81.8%, respectively. MIC₅₀ for imipenem and meropenem were 64 and 32 mg/L, respectively. MIC₉₀ for imipenem and meropenem were 256 and 64 mg/L, respectively. Imipenem-resistant rates of ICUs and non-ICUs isolates were 90.3% and 74.1%, respectively, whereas meropenem-resistant rates were 89.5% and 73.7%, respectively. Imipenem-resistant rates of isolates from sterile and non-sterile specimens were 83.5% and 82.2%, respectively, while meropenem-resistant rates of those were 82.5% and 81.7%, respectively. Carbapenem-resistant rates of *A. baumannii* isolated from patients in ICUs were significantly higher than those in non-ICUs ($P < 0.01$) whereas there was no significant difference in carbapenem-resistant rates in *A. baumannii* isolated from sterile and non sterile clinical specimens ($P = 0.758$).

All carbapenem-resistant *A. baumannii* had carbapenemase activity. Metallo- β -lactamases were not detected in any isolate. The strains with carbapenemase activity were 100% resistant to imipenem whereas 99.3% were resistant and 0.7% were intermediately resistant to meropenem. Screening for carbapenemase genes by multiplex PCR revealed the presence of *bla*_{OXA-23-like}, *bla*_{OXA-24-like}, *bla*_{OXA-51-like} and *bla*_{OXA-58-like} and the absence of *bla*_{IMP-like} and *bla*_{VIM-like}. All 501 *A. baumannii* isolates carried the *bla*_{OXA51-like} gene. The isolates carrying only *bla*_{OXA51-like} were susceptible to carbapenems whereas the isolates carrying *bla*_{OXA-51-like} together with other *bla*_{OXA-like} including *bla*_{OXA-23-like}, *bla*_{OXA-24-like} and *bla*_{OXA-58-like} were resistant to carbapenems. Imipenem MIC of isolates carrying *bla*_{OXA-24-like} together with other *bla*_{OXA-like} showed a high level of carbapenem MIC (128->256 mg/L). The presence of *bla*_{OXA-23-like} were detected in

the majority of carbapenem-resistant *A. baumannii* isolates (93.2%), suggesting that *bla*_{OXA-23-like} plays a major role in carbapenem resistance.

Sequences of ten entire *bla*_{OXA-23-like}, *bla*_{OXA-24-like}, *bla*_{OXA-51-like} and *bla*_{OXA-58-like} were analyzed. The results revealed that *bla*_{OXA-23}, *bla*_{OXA-72} and *bla*_{OXA-58} were identified in 100% of *bla*_{OXA-23-like}, *bla*_{OXA-24-like} and *bla*_{OXA-58-like} groups, respectively. The variations were found in *bla*_{OXA-51-like} group with 50% of *bla*_{OXA-68}, 20% of *bla*_{OXA-66}, 10% each for *bla*_{OXA-64}, *bla*_{OXA-67} and a novel *bla*_{OXA-51-like}. This novel enzyme was found in the isolate A80, which has not yet been reported. Nucleotide and amino acid sequences of this novel enzyme showed 99% identity to *bla*_{OXA-51} and OXA-51. This study demonstrated high prevalence of carbapenem resistance in *A. baumannii* isolates and showed that *bla*_{OXA-23-like} was the major carbapenemase gene associated with carbapenem resistance in our *A. baumannii*-resistant isolates.



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APPENDIX A

REAGENTS AND INSTRUMENTS

A. REAGENTS

Absolute ethanol	(Merck, Germany)
Agarose	(Biorad, USA)
Bacto agar	(Difco, USA)
Boric acid	(Sigma, USA)
Bromthymol blue	(Fluka, Germany)
dNTPs	(Promega, USA)
EDTA	(Amresco, USA)
Ethidium bromide	(Amresco, USA)
Glacial acetic acid	(Merck, Germany)
Miniral oil	(Sigma, USA)
N,N,N,N-tetramethyl- <i>p</i> -phenylenediamine dihydrochloride	(Sigma, U.S.A)
NaCl	(Merck, Germany)
NaHCO ₃	(Merck, Germany)
Na ₂ HPO ₄ *2H ₂ O	(Sigma, USA)
<i>Pfu</i> DNA Polymerase	(Fermentas, USA)
Taq DNA Polymerase	(Fermentas, USA)
Tris	(Amresco, USA)
100 bp DNA ladder	(Fermentas, USA)
100 bp plus DNA ladder	(Fermentas, USA)

B. INSTRUMENTS

ABI prism 310 automated sequencer	(Perkin Elmer, USA)
Automatic pipette	(Gilson, Lyon, France)
Camera Gel Doc™ MZL	(BIO-RAD, USA)
Incubator	(Forma Scientific, USA)
Perkin Elmer GeneAmp PCR system 9600	(Perkin Elmer, USA)
Microcentrifuge	(Eppendorf, USA)
Spectrophotometer	(BIO-RAD, USA)
Water bath	(Mettler, USA)



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APPENDIX B

MEDIA AND ANTIBIOTIC SOLUTION PREPARATION

1. **Sheep blood agar (Oxoid, England)**

Suspend Tryptone Soya agar 40 grams in 1 litre of distilled water. Bring to the boil to dissolve completely. Sterilize by autoclaving at 121°C for 15 minutes. Hold the medium until ~50 °C, then add 5% sheep blood into the medium before pour plate. Once the medium is prepared, store at 4°C.

2. **MacConkey agar**

Suspend 51.5 grams in 1 litre of distilled water. Bring to the boil to dissolve completely. Sterilize by autoclaving at 121°C for 15 minutes. Once the medium is prepared, store at 4°C.

3. **Muller-Hinton II agar (Difco, France)**

Suspend 38 grams of the dehydrated medium in 1,000 ml of distilled water. Dissolve by heating with frequent agitation until complete dissolution. Adjust final volume to 1,000 ml. Sterilize at 121°C (15 lbs. sp) for 15 minutes. Once the medium is prepared, store at 4°C.

4. **Tryptic Soy Broth (Oxoid, England)**

Suspend 30 grams in 1 litre of distilled water. Bring to the boil to dissolve completely. Sterilize by autoclaving at 121°C for 15 minutes. Once the medium is prepared, store at 4°C.

5. LB broth (Pronadisa, Spain)

Suspend 20 grams of the dehydrated medium in 900 ml of distilled water. Dissolve by heating with frequent agitation until complete dissolution. Adjust final volume to 1,000 ml. Sterilize at 121°C (15 lbs. sp) for 15 minutes. Once the medium is prepared, store at 4°C.

6. Tryptone Soya agar (Oxoid, England)

Suspend 40 grams in 1 litre of distilled water. Bring to the boil to dissolve completely. Sterilize by autoclaving at 121°C for 15 minutes. Once the medium is prepared, store at 4°C.

7. Triple Sugar Iron agar (Oxoid, England)

Suspend 65 grams in 1 litre of distilled water. Bring to the boil to dissolve completely. Mix well and distribute into containers. Sterilize by autoclaving at 121°C for 15 minutes. Allow to set as slopes with 2.5 cm butts. Once the medium is prepared, store at 4°C.

8. OF Basal Medium (Difco, France)

Suspend 9.4 grams of the dehydrated medium in 900 ml of distilled water. Dissolve by heating with frequent agitation until complete dissolution. Adjust final volume to 1,000 ml. Add 1% carbohydrate (Glucose). Sterilize at 121°C (15 lbs. sp) for 15 minutes. Once the medium is prepared, store at 4°C.

9. Decarboxylase Base Moeller (Difco, France)

Suspend 10.5 grams of the dehydrated medium in 1,000 ml of distilled water. Dissolve by heating with frequent agitation until complete dissolution. Add 10 grams L-amino acid (Arginine) and dissolve. Sterilize at 121°C (15 lbs. sp) for 15 minutes. Once the medium is prepared, store at 4°C.

10. Nitrate Broth (Difco, France)

Suspend 9 grams in 1 litre of distilled water. Bring to the boil to dissolve completely. Sterilize by autoclaving at 121°C for 15 minutes. Once the medium is prepared, store at 4°C.

11. Malonate broth (BBL, USA)

Suspend 9.8 grams in 1 litre of distilled water. Bring to the boil to dissolve completely. Sterilize by autoclaving at 121°C for 15 minutes. Once the medium is prepared, store at 4°C.

12. Urea Medium (BBL, USA)

Solution A: for	20 ml
Urea agar base (BBL)	2.9 g
Urea	4 g
Distilled water	20 ml

Dissolve in 20 ml of distilled water. Adjust to pH 6.2 Sterilize by filtration (use a 0.22 µm filter).

Solution B: for	80 ml
Bacto agar (Difco)	0.5 g
Distilled water	80 ml

Add the ingredient to 80 ml of distilled water; heat with stirring until the agar is dissolved. Sterilize by autoclaving at 121°C, 15 pounds/inch² pressure, for 15 minutes. Mix solution A, 20 ml with solution B, 80 ml. Aliquot into sterile 1.5 microtube (1 ml/tube). Test the sterility of Urease medium by incubate tubes at 37°C for 24 hours. Store tubes in refrigerator at 4°C until used.

13. Sterile saline solution

Sodium Chloride	8.5 g/L
Distilled water	1 L

Sterilize by autoclaving at 121°C, 15 pounds/inch² pressure, for minutes. Store at room temperature.

14. Antibiotic solution preparation

Imipenem, stock concentration 512 mg/L

- Prepare a stock solution; dissolve 0.1024 g in 10 ml distilled water

Meropenem, stock concentration 512 mg/L

- Prepare a stock solution, dissolve 0.0512 g in 10 ml distilled water.



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APPENDIX C

REAGENTS PREPARATION

1. 10x Tris-borate buffer (TBE)

Tris base	108 g/L
Boric acid	55 g/L
0.5 M EDTA (pH 8.0)	40 ml

Adjust volume to 1 liter with distilled water. The solution was mixed and sterilized by autoclaving at 121°C for 15 min.

2. 0.5 M EDTA (pH 8.0)

Disodium ethylene diamine tetra-acelate 2H ₂ O	186.1 g/L
Distilled water	1 L

Adjust pH to 8.0 and volume to 1 liter. Store at room temperature for no longer than 1 year.

3. 10x TE buffer

Tris	12.11 g/L
0.5 M EDTA	20 ml

Adjust to pH 8.0 by adding conc. HCl. Adjust volume to 1,000 ml and sterilized by autoclaving at 121°C for 15 min.

4. 1 % Agarose gel

Agarose	0.4 g
1x TBE	40 ml

Dissolve by heating in microwave oven and occasional mix unit no granules of agarose are visible.

5. 5x Loading buffer 100 ml

Tris HCl	0.6 g
EDTA	1.68 g
SDS	0.5 g

Bromphenol Blue	0.1 g
Sucrose	40 g

Adjust volume to 100 ml with distilled water. Mix the solution, aliquot into 1.5 microtubes and store at 4°C.

Reagent for DNA Extraction

1.1 Protease K

Reconstituted of protease K (lyophilized) with 1.25 ml protease solvent, stored at -20°C

1.2 Buffer AL (Ready to used)

1.3 Buffer AW1

Buffer AW1 is supplied as a concentrate. Before using for the first time, add the 25 ml of ethanol (96-100%) to buffer AW1 concentrate as indicated on the bottle.

1.4 Buffer AW2

Buffer AW2 is supplied as a concentrate. Before using for the first time, add the 30 ml of ethanol (96-100%) to buffer AW2 concentrate as indicated on the bottle.

1.5 Buffer AE (Ready to used)

Reagent for PCR product purification

Buffer PB (Ready to used)

Buffer PE

Buffer PE is supplied as a concentrate. Before using for the first time, add the 55 ml of ethanol (96-100%) to buffer PE concentrate as indicated on the bottle.

APPENDIX D

THE RESULTS OF ALL TESTS IN THIS STUDY

Results of carbapenem susceptibility, carbapenemase activity and the presence of carbapenemase genes of 501 *A. baumannii* isolates.

No	Strains	MICs (mg/L)		Carbapenemase activity		Presence of carbapenemase genes					
		IMP	MER	M-Hodge test	EDTA disk synergy test	<i>bla</i> _{OXA23} -like	<i>bla</i> _{OXA24} -like	<i>bla</i> _{OXA51} -like	<i>bla</i> _{OXA58} -like	<i>bla</i> _{IMP} -like	<i>bla</i> _{VIM} -like
1	<i>A. baumannii</i> ATCC 19606	2	2	-	-	-	-	+	-	-	-
2	<i>E. coli</i> ATCC 25922	0.25	0.06	ND	ND	ND	ND	ND	ND	ND	ND
3	<i>Ps. aeruginosa</i> ATCC 27853	2	0.5	ND	ND	ND	ND	ND	ND	ND	ND
4	<i>S. aureus</i> ATCC 29213	0.06	0.06	ND	ND	ND	ND	ND	ND	ND	ND
5	<i>E. faecalis</i> ATCC 29212	1	4	ND	ND	ND	ND	ND	ND	ND	ND
6	P4*	64	64	+	+	-	-	-	-	-	+
7	AB 018	0.5	0.25	-	-	-	-	+	-	-	-
8	AB 044	256	128	+	-	+	-	+	-	-	-
9	AB 055	64	16	+	-	+	-	+	-	-	-
10	AB 060	2	2	-	-	-	-	+	-	-	-
11	AB 061	128	32	+	-	+	-	+	-	-	-
12	AB 063	128	32	+	-	+	-	+	-	-	-
13	AB 065	>256	256	+	-	-	+	+	-	-	-
14	AB 066	>256	>256	+	-	+	+	+	-	-	-
15	AB 067	128	32	+	-	+	-	+	-	-	-
16	AB 071	2	2	-	-	-	-	+	-	-	-
17	AB 072	128	32	+	-	+	-	+	-	-	-
18	AB 075	128	16	+	-	+	-	+	-	-	-
19	AB 076	0.5	1	-	-	-	-	+	-	-	-
20	AB 084	32	16	+	-	+	-	+	-	-	-
21	AB 091	0.5	0.12	-	-	-	-	+	-	-	-
22	AB 092	128	32	+	-	+	-	+	-	-	-
23	AB 093	128	64	+	-	+	-	+	-	-	-
24	AB 094	128	64	+	-	+	-	+	-	-	-
25	AB 096	64	64	+	-	+	-	+	-	-	-
26	AB 098	0.5	0.12	-	-	-	-	+	-	-	-
27	AB 099	0.5	0.5	-	-	-	-	+	-	-	-
28	AB 102	64	64	+	-	+	-	+	-	-	-
29	AB 103	128	64	+	-	+	-	+	-	-	-
30	AB 104	64	32	+	-	+	-	+	-	-	-
31	AB 105	64	64	+	-	+	-	+	-	-	-
32	AB 106	128	64	+	-	+	-	+	-	-	-
33	AB 107	256	64	+	-	+	-	+	-	-	-
34	AB 108	256	16	+	-	+	-	+	-	-	-
35	AB 109	64	8	+	-	+	-	+	-	-	-
36	AB 111	0.5	0.25	-	-	-	-	+	-	-	-
37	AB 113	2	2	-	-	-	-	+	-	-	-
38	AB 114	32	16	+	-	+	-	+	-	-	-
39	AB 115	128	64	+	-	+	-	+	-	-	-
40	AB 116	1	0.5	-	-	-	-	+	-	-	-
41	A 001	16	16	+	-	+	-	+	-	-	-
42	A 002	64	16	+	-	+	-	+	-	-	-

Results of carbapenem susceptibility, carbapenemase activity and the presence of carbapenemase genes of *A. baumannii*. (cont.)

No	Strains	MICs (mg/L)		Carbapenemase activity		Presence of carbapenemase genes					
		IMP	MER	M-Hodge test	EDTA disk synergy test	<i>bla</i> _{OXA23} -like	<i>bla</i> _{OXA24} -like	<i>bla</i> _{OXA51} -like	<i>bla</i> _{OXA58} -like	<i>bla</i> _{IMP} -like	<i>bla</i> _{VIM} -like
43	A 003	0.5	0.25	-	-	-	-	+	-	-	-
44	A 004	64	16	+	-	+	-	+	-	-	-
45	A 005	64	16	+	-	+	-	+	-	-	-
46	A 006	64	16	+	-	+	-	+	-	-	-
47	A 007	2	2	-	-	-	-	+	-	-	-
48	A 008	256	64	+	-	+	-	+	-	-	-
49	A 010	64	16	+	-	+	-	+	-	-	-
50	A 011	128	32	+	-	+	-	+	-	-	-
51	A 012	128	32	+	-	+	-	+	-	-	-
52	A 013	128	64	+	-	+	-	+	-	-	-
53	A 014	64	32	+	-	+	-	+	-	-	-
54	A 015	64	32	+	-	+	-	+	-	-	-
55	A 016	64	16	+	-	+	-	+	-	-	-
56	A 017	32	16	+	-	+	-	+	-	-	-
57	A 018	64	16	+	-	+	-	+	-	-	-
58	A 019	16	16	+	-	+	-	+	-	-	-
59	A 021	64	16	+	-	+	-	+	-	-	-
60	A 022	32	16	+	-	+	-	+	-	-	-
61	A 023	128	64	+	-	+	+	+	-	-	-
62	A 024	64	16	+	-	+	-	+	-	-	-
63	A 025	0.5	0.25	-	-	-	-	+	-	-	-
64	A 026	64	16	+	-	+	-	+	-	-	-
65	A 027	128	64	+	-	+	-	+	-	-	-
66	A 028	2	2	-	-	-	-	+	-	-	-
67	A 030	128	64	+	-	+	-	+	-	-	-
68	A 031	128	64	+	-	+	-	+	-	-	-
69	A 032	64	32	+	-	+	-	+	-	-	-
70	A 033	128	64	+	-	-	+	+	+	-	-
71	A 034	64	32	+	-	+	-	+	-	-	-
72	A 035	1	0.25	-	-	-	-	+	-	-	-
73	A 036	1	0.5	-	-	-	-	+	-	-	-
74	A 037	0.5	0.25	-	-	-	-	+	-	-	-
75	A 038	128	64	+	-	+	-	+	-	-	-
76	A 040	64	16	+	-	+	-	+	-	-	-
77	A 041	1	0.5	-	-	-	-	+	-	-	-
78	A 042	2	1	-	-	-	-	+	-	-	-
79	A 043	32	16	+	-	+	-	+	-	-	-
80	A 044	64	32	+	-	+	-	+	-	-	-
81	A 045	32	16	+	-	+	-	+	-	-	-
82	A 046	128	32	+	-	+	-	+	-	-	-
83	A 047	64	16	+	-	+	-	+	-	-	-
84	A 048	32	16	+	-	+	-	+	-	-	-
85	A 049	4	1	-	-	-	-	+	-	-	-
86	A 051	64	16	+	-	+	-	+	-	-	-
87	A 052	64	16	+	-	+	-	+	-	-	-
88	A 053	0.5	0.5	-	-	-	-	+	-	-	-
89	A 054	256	64	+	-	+	-	+	-	-	-
90	A 055	256	256	+	-	-	+	+	+	-	-
91	A 056	1	0.25	-	-	-	-	+	-	-	-
92	A 057	128	16	+	-	+	-	+	-	-	-
93	A 058	1	0.25	-	-	-	-	+	-	-	-
94	A 059	32	16	+	-	+	-	+	-	-	-
95	A 060	2	2	-	-	-	-	+	-	-	-
96	A 064	64	16	+	-	+	-	+	-	-	-
97	A 065	64	16	+	-	+	-	+	-	-	-
98	A 066	16	16	+	-	+	-	+	-	-	-
99	A 067	32	16	+	-	+	-	+	-	-	-
100	A 068	0.5	2	-	-	-	-	+	-	-	-
101	A 070	128	64	+	-	+	+	+	+	-	-

Results of carbapenem susceptibility, carbapenemase activity and the presence of carbapenemase genes of *A. baumannii*. (cont.)

No	Strains	MICs (mg/L)		Carbapenemase activity		Presence of carbapenemase genes					
		IMP	MER	M-Hodge test	EDTA disk synergy test	<i>bla</i> _{OXA23} -like	<i>bla</i> _{OXA24} -like	<i>bla</i> _{OXA51} -like	<i>bla</i> _{OXA58} -like	<i>bla</i> _{IMP} -like	<i>bla</i> _{VIM} -like
102	A 071	1	1	-	-	-	-	+	-	-	-
103	A 072	32	16	+	-	+	-	+	-	-	-
104	A 074	64	32	+	-	+	-	+	-	-	-
105	A 075	64	32	+	-	+	-	+	-	-	-
106	A 077	32	16	+	-	+	-	+	-	-	-
107	A 078	0.5	0.5	-	-	-	-	+	-	-	-
108	A 079	32	32	+	-	+	-	+	-	-	-
109	A 080	0.5	0.5	-	-	-	-	+	-	-	-
110	A 082	0.5	0.5	-	-	-	-	+	-	-	-
111	A 083	256	64	+	-	+	-	+	-	-	-
112	A 084	256	128	+	-	-	+	+	+	-	-
113	A 085	0.5	0.25	-	-	-	-	+	-	-	-
114	A 086	1	0.25	-	-	-	-	+	-	-	-
115	A 087	64	16	+	-	+	-	+	-	-	-
116	A 088	128	64	+	-	+	-	+	-	-	-
117	A 089	64	32	+	-	+	-	+	-	-	-
118	A 090	32	8	+	-	+	-	+	-	-	-
119	A 091	128	32	+	-	+	-	+	-	-	-
120	A 092	128	32	+	-	+	-	+	-	-	-
121	A 093	128	16	+	-	+	-	+	-	-	-
122	A 094	128	64	+	-	-	+	+	+	-	-
123	A 095	128	32	+	-	+	-	+	-	-	-
124	A 096	0.5	0.25	-	-	-	-	+	-	-	-
125	A 098	128	32	+	-	+	-	+	-	-	-
126	A 100	1	0.25	-	-	-	-	+	-	-	-
127	A 101	128	16	+	-	+	-	+	-	-	-
128	A 104	256	64	+	-	+	-	+	-	-	-
129	A 106	>256	64	+	-	+	-	+	-	-	-
130	A 107	128	32	+	-	+	-	+	-	-	-
131	A 108	256	64	+	-	+	-	+	-	-	-
132	A 109	128	64	+	-	-	+	+	+	-	-
133	A 110	256	128	+	-	+	+	+	+	-	-
134	A 111	64	16	+	-	+	-	+	-	-	-
135	A 112	64	16	+	-	+	-	+	-	-	-
136	A 113	128	64	+	-	-	+	+	+	-	-
137	A 114	128	64	+	-	+	-	+	-	-	-
138	A 115	64	16	+	-	+	-	+	-	-	-
139	A 116	128	32	+	-	+	-	+	-	-	-
140	A 118	0.5	0.25	-	-	-	-	+	-	-	-
141	A 119	64	16	+	-	+	-	+	-	-	-
142	A 120	64	16	+	-	+	-	+	-	-	-
143	A 121	64	16	+	-	+	-	+	-	-	-
144	A 122	32	16	+	-	+	-	+	-	-	-
145	A 123	32	16	+	-	+	-	+	-	-	-
146	A 124	64	16	+	-	+	-	+	-	-	-
147	A 125	64	16	+	-	+	-	+	-	-	-
148	A 126	64	16	+	-	+	-	+	-	-	-
149	A 127	0.12	0.12	-	-	-	-	+	-	-	-
150	A 128	64	16	+	-	+	-	+	-	-	-
151	A 129	128	32	+	-	+	+	+	+	-	-
152	A 130	64	16	+	-	+	-	+	-	-	-
153	A 131	128	16	+	-	+	-	+	-	-	-
154	A 133	128	32	+	-	+	-	+	-	-	-
155	A 134	128	32	+	-	+	-	+	-	-	-
156	A 135	64	32	+	-	+	-	+	-	-	-
157	A 136	256	64	+	-	-	+	+	+	-	-
158	A 137	256	64	+	-	-	+	+	+	-	-
159	A 139	128	32	+	-	+	-	+	-	-	-
160	A 140	32	16	+	-	+	-	+	-	-	-

Results of carbapenem susceptibility, carbapenemase activity and the presence of carbapenemase genes of *A. baumannii*. (cont.)

No	Strains	MICs (mg/L)		Carbapenemase activity		Presence of carbapenemase genes					
		IMP	MER	M-Hodge test	EDTA disk synergy test	<i>bla</i> _{OXA23} -like	<i>bla</i> _{OXA24} -like	<i>bla</i> _{OXA51} -like	<i>bla</i> _{OXA58} -like	<i>bla</i> _{IMP} -like	<i>bla</i> _{VIM} -like
161	A 141	>256	256	+	-	+	-	+	-	-	-
162	A 142	64	16	+	-	+	-	+	-	-	-
163	A 144	256	64	+	-	-	+	+	+	-	-
164	A 145	64	16	+	-	+	-	+	-	-	-
165	A 146	>256	128	+	-	-	+	+	-	-	-
166	A 147	32	32	+	-	+	-	+	-	-	-
167	A 148	128	64	+	-	+	-	+	-	-	-
168	A 149	128	32	+	-	+	-	+	-	-	-
169	A 150	256	64	+	-	+	+	+	+	-	-
170	A 151	32	16	+	-	+	-	+	-	-	-
171	A 152	128	32	+	-	+	-	+	-	-	-
172	A 153	1	0.5	-	-	-	-	+	-	-	-
173	A 155	128	32	+	-	+	-	+	-	-	-
174	A 156	64	64	+	-	+	-	+	-	-	-
175	A 157	128	64	+	-	+	-	+	-	-	-
176	A 158	64	32	+	-	+	-	+	-	-	-
177	A 159	0.5	0.25	-	-	-	-	+	-	-	-
178	A 160	128	32	+	-	+	-	+	-	-	-
179	A 161	32	32	+	-	+	-	+	-	-	-
180	A 162	16	32	+	-	+	-	+	-	-	-
181	A 163	32	32	+	-	+	-	+	-	-	-
182	A 164	128	32	+	-	+	-	+	-	-	-
183	A 165	128	64	+	-	-	+	+	+	-	-
184	A 166	2	2	-	-	-	-	+	-	-	-
185	A 167	256	64	+	-	-	+	+	-	-	-
186	A 169	64	16	+	-	+	-	+	-	-	-
187	A 170	128	32	+	-	+	-	+	-	-	-
188	A 171	32	16	+	-	+	-	+	-	-	-
189	A 172	32	16	+	-	+	-	+	-	-	-
190	A 176	0.25	0.25	-	-	-	-	+	-	-	-
191	A 177	256	128	+	-	-	+	+	-	-	-
192	A 178	2	1	-	-	-	-	+	-	-	-
193	A 179	128	32	+	-	+	-	+	-	-	-
194	A 180	128	128	+	-	-	+	+	+	-	-
195	A 181	64	16	+	-	+	-	+	-	-	-
196	A 183	64	32	+	-	+	-	+	-	-	-
197	A 184	2	1	-	-	-	-	+	-	-	-
198	A 185	64	32	+	-	+	-	+	-	-	-
199	A 186	128	32	+	-	+	-	+	-	-	-
200	A 187	128	16	+	-	+	-	+	-	-	-
201	A 188	64	32	+	-	+	-	+	+	-	-
202	A 189	64	32	+	-	+	-	+	-	-	-
203	A 190	64	16	+	-	+	-	+	-	-	-
204	A 191	64	32	+	-	+	-	+	-	-	-
205	A 194	128	32	+	-	+	-	+	-	-	-
206	A 196	128	32	+	-	+	-	+	-	-	-
207	A 198	128	64	+	-	-	+	+	+	-	-
208	A 199	64	32	+	-	+	-	+	-	-	-
209	A 200	64	32	+	-	+	-	+	-	-	-
210	A 201	64	32	+	-	+	-	+	-	-	-
211	A 202	64	32	+	-	+	-	+	-	-	-
212	A 203	16	16	+	-	+	-	+	-	-	-
213	A 204	32	16	+	-	+	-	+	-	-	-
214	A 205	64	32	+	-	+	-	+	-	-	-
215	A 206	32	16	+	-	+	-	+	-	-	-
216	A 207	32	16	+	-	+	-	+	-	-	-
217	A 208	32	16	+	-	+	-	+	-	-	-
218	A 209	32	16	+	-	+	-	+	-	-	-
219	A 210	64	16	+	-	+	-	+	-	-	-
220	A 211	32	16	+	-	+	-	+	-	-	-

Results of carbapenem susceptibility, carbapenemase activity and the presence of carbapenemase genes of *A. baumannii*. (cont.)

No	Strains	MICs (mg/L)		Carbapenemase activity		Presence of carbapenemase genes					
		IMP	MER	M-Hodge test	EDTA disk synergy test	<i>bla</i> _{OXA23} -like	<i>bla</i> _{OXA24} -like	<i>bla</i> _{OXAS1} -like	<i>bla</i> _{OXAS6} -like	<i>bla</i> _{IMP} -like	<i>bla</i> _{VIM} -like
221	A 212	128	32	+	-	+	-	+	-	-	-
222	A 213	64	16	+	-	+	-	+	-	-	-
223	A 214	64	16	+	-	+	-	+	-	-	-
224	A 215	32	16	+	-	+	-	+	-	-	-
225	A 216	64	16	+	-	+	-	+	-	-	-
226	A 217	64	32	+	-	+	-	+	-	-	-
227	A 218	64	32	+	-	+	-	+	-	-	-
228	A 219	16	16	+	-	+	-	+	-	-	-
229	A 220	32	16	+	-	+	-	+	-	-	-
230	A 221	32	16	+	-	+	-	+	-	-	-
231	A 222	64	16	+	-	+	-	+	-	-	-
232	A 223	2	1	-	-	-	-	+	-	-	-
233	A 226	128	32	+	-	+	-	+	-	-	-
234	A 228	32	16	+	-	+	-	+	-	-	-
235	A 229	64	32	+	-	+	-	+	-	-	-
236	A 230	32	16	+	-	+	-	+	-	-	-
237	A 231	32	16	+	-	+	-	+	-	-	-
238	A 232	32	16	+	-	+	-	+	-	-	-
239	A 233	2	1	-	-	-	-	+	-	-	-
240	A 234	128	64	+	-	+	-	+	-	-	-
241	A 235	32	16	+	-	+	-	+	-	-	-
242	A 236	128	64	+	-	+	-	+	-	-	-
243	A 237	1	1	-	-	-	-	+	-	-	-
244	A 238	256	64	+	-	+	+	+	+	-	-
245	A 240	32	16	+	-	+	-	+	-	-	-
246	A 241	64	16	+	-	+	-	+	-	-	-
247	A 242	256	64	+	-	+	+	+	+	-	-
248	A 243	64	16	+	-	+	-	+	-	-	-
249	A 244	64	16	+	-	+	-	+	-	-	-
250	A 245	32	16	+	-	+	-	+	-	-	-
251	A 246	32	16	+	-	+	-	+	-	-	-
252	A 247	128	32	+	-	+	-	+	-	-	-
253	A 249	256	64	+	-	+	-	+	-	-	-
254	A 250	128	32	+	-	+	-	+	+	-	-
255	A 251	16	32	+	-	+	-	+	-	-	-
256	A 252	0.5	1	-	-	-	-	+	-	-	-
257	A 253	128	32	+	-	+	-	+	-	-	-
258	A 257	64	32	+	-	+	-	+	-	-	-
259	A 258	128	32	+	-	+	-	+	-	-	-
260	A 259	64	16	+	-	+	-	+	-	-	-
261	A 260	64	16	+	-	+	-	+	-	-	-
262	A 262	64	16	+	-	+	-	+	+	-	-
263	A 263	64	32	+	-	+	-	+	-	-	-
264	A 265	256	64	+	-	+	+	+	+	-	-
265	A 266	32	16	+	-	+	-	+	+	-	-
266	A 267	2	1	-	-	-	-	+	-	-	-
267	A 268	64	16	+	-	+	-	+	-	-	-
268	A 269	32	16	+	-	+	-	+	-	-	-
269	A 270	128	32	+	-	+	-	+	-	-	-
270	A 271	256	64	+	-	+	+	+	-	-	-
271	A 272	32	16	+	-	+	-	+	-	-	-
272	A 274	64	16	+	-	+	-	+	-	-	-
273	A 275	64	16	+	-	+	-	+	-	-	-
274	A 277	64	32	+	-	+	-	+	-	-	-
275	A 278	64	16	+	-	+	-	+	-	-	-
276	A 280	64	16	+	-	+	-	+	-	-	-
277	A 281	0.5	0.5	-	-	-	-	+	-	-	-
278	A 285	128	32	+	-	+	-	+	-	-	-
279	A 286	64	16	+	-	+	-	+	-	-	-
280	A 288	128	64	+	-	-	+	+	+	-	-

Results of carbapenem susceptibility, carbapenemase activity and the presence of carbapenemase genes of *A. baumannii*. (cont.)

No	Strains	MICs (mg/L)		Carbapenemase activity		Presence of carbapenemase genes					
		IMP	MER	M-Hodge test	EDTA disk synergy test	<i>bla</i> _{OXA13} -like	<i>bla</i> _{OXA24} -like	<i>bla</i> _{OXAS1} -like	<i>bla</i> _{OXAS6} -like	<i>bla</i> _{IMP} -like	<i>bla</i> _{VIM} -like
281	A 289	128	32	+	-	+	-	+	+	-	-
282	A 290	1	1	-	-	-	-	+	-	-	-
283	A 291	128	32	+	-	+	-	+	+	-	-
284	A 292	64	16	+	-	+	-	+	+	-	-
285	A 293	2	1	-	-	-	-	+	-	-	-
286	A 296	64	16	+	-	+	-	+	-	-	-
287	A 297	0.5	0.5	-	-	-	-	+	-	-	-
288	A 298	128	32	+	-	+	-	+	-	-	-
289	A 300	128	32	+	-	+	-	+	-	-	-
290	A 302	64	16	+	-	+	-	+	-	-	-
291	A 303	128	64	+	-	-	+	+	+	-	-
292	A 305	32	32	+	-	+	-	+	-	-	-
293	A 307	32	16	+	-	+	-	+	-	-	-
294	A 308	0.5	0.25	-	-	-	-	+	-	-	-
295	A 309	0.5	0.5	-	-	-	-	+	-	-	-
296	A 310	32	16	+	-	+	-	+	-	-	-
297	A 311	256	64	+	-	+	-	+	-	-	-
298	A 312	64	32	+	-	+	-	+	-	-	-
299	A 314	0.25	0.25	-	-	-	-	+	-	-	-
300	A 315	64	32	+	-	+	-	+	-	-	-
301	A 316	64	32	+	-	+	-	+	-	-	-
302	A 317	64	32	+	-	+	-	+	-	-	-
303	A 318	128	32	+	-	+	-	+	-	-	-
304	A 320	64	16	+	-	+	-	+	-	-	-
305	A 321	64	32	+	-	+	-	+	-	-	-
306	A 322	128	32	+	-	+	-	+	-	-	-
307	A 323	256	64	+	-	+	+	+	+	-	-
308	A 324	64	16	+	-	+	-	+	-	-	-
309	A 325	128	32	+	-	+	-	+	-	-	-
310	A 327	64	16	+	-	+	-	+	-	-	-
311	A 328	64	16	+	-	+	-	+	-	-	-
312	A 329	64	32	+	-	+	-	+	-	-	-
313	A 332	32	16	+	-	+	-	+	-	-	-
314	A 334	64	32	+	-	+	-	+	-	-	-
315	A 335	128	32	+	-	+	-	+	-	-	-
316	A 337	32	32	+	-	+	-	+	-	-	-
317	A 338	0.5	0.5	-	-	-	-	+	-	-	-
318	A 339	128	32	+	-	+	-	+	-	-	-
319	A 341	0.5	2	-	-	-	-	+	-	-	-
320	A 342	128	32	+	-	+	-	+	-	-	-
321	A 343	128	32	+	-	+	-	+	-	-	-
322	A 345	32	16	+	-	+	-	+	-	-	-
323	A 346	64	16	+	-	+	-	+	-	-	-
324	A 347	128	32	+	-	+	-	+	-	-	-
325	A 348	32	16	+	-	+	-	+	-	-	-
326	A 350	1	0.25	-	-	-	-	+	-	-	-
327	A 351	128	32	+	-	+	-	+	-	-	-
328	A 352	32	32	+	-	+	-	+	-	-	-
329	A 354	128	32	+	-	+	-	+	-	-	-
330	A 356	128	32	+	-	+	-	+	-	-	-
331	A 357	1	0.25	-	-	-	-	+	-	-	-
332	A 358	1	0.12	-	-	-	-	+	-	-	-
333	A 360	64	32	+	-	+	-	+	-	-	-
334	A 362	64	16	+	-	+	-	+	-	-	-
335	A 364	2	2	-	-	-	-	+	-	-	-
336	A 365	64	64	+	-	+	-	+	-	-	-
337	A 368	32	32	+	-	+	-	+	-	-	-
338	A 369	128	32	+	-	+	-	+	-	-	-
339	A 370	128	32	+	-	+	-	+	-	-	-
340	A 371	128	32	+	-	+	-	+	-	-	-

Results of carbapenem susceptibility, carbapenemase activity and the presence of carbapenemase genes of *A. baumannii*. (cont.)

No	Strains	MICs (mg/L)		Carbapenemase activity		Presence of carbapenemase genes					
		IMP	MER	M-Hodge test	EDTA disk synergy test	<i>bla</i> _{OXA23} -like	<i>bla</i> _{OXA24} -like	<i>bla</i> _{OXA51} -like	<i>bla</i> _{OXA58} -like	<i>bla</i> _{IMP} -like	<i>bla</i> _{VIM} -like
341	A 372	64	16	+	-	+	-	+	-	-	-
342	A 373	64	64	+	-	+	-	+	-	-	-
343	A 374	32	16	+	-	+	-	+	-	-	-
344	A 375	128	64	+	-	+	-	+	-	-	-
345	A 377	256	128	+	-	-	+	+	+	-	-
346	A 378	256	64	+	-	+	-	+	-	-	-
347	A 380	2	4	-	-	-	-	+	-	-	-
348	A 381	32	32	+	-	+	-	+	-	-	-
349	A 382	256	64	+	-	-	+	+	+	-	-
350	A 383	128	64	+	-	+	-	+	-	-	-
351	A 384	256	32	+	-	-	+	+	+	-	-
352	A 385	1	0.5	-	-	-	-	+	-	-	-
353	A 386	256	32	+	-	+	-	+	-	-	-
354	A 387	64	32	+	-	+	-	+	-	-	-
355	A 388	256	32	+	-	+	-	+	-	-	-
356	A 389	256	64	+	-	+	+	+	+	-	-
357	A 390	128	32	+	-	+	-	+	-	-	-
358	A 392	0.5	1	-	-	-	-	+	-	-	-
359	A 393	256	32	+	-	+	-	+	-	-	-
360	A 394	128	32	+	-	+	-	+	-	-	-
361	A 397	256	64	+	-	+	-	+	-	-	-
362	A 398	2	0.5	-	-	-	-	+	-	-	-
363	A 399	128	32	+	-	+	-	+	-	-	-
364	A 400	0.5	0.5	-	-	-	-	+	-	-	-
365	A 401	256	64	+	-	-	+	+	+	-	-
366	A 402	256	128	+	-	+	+	+	+	-	-
367	A 403	128	32	+	-	+	-	+	-	-	-
368	A 404	64	32	+	-	+	-	+	-	-	-
369	A 405	4	4	-	-	-	-	+	-	-	-
370	A 408	32	16	+	-	+	-	+	-	-	-
371	A 409	32	16	+	-	+	-	+	-	-	-
372	A 410	128	32	+	-	+	-	+	-	-	-
373	A 412	256	64	+	-	+	-	+	-	-	-
374	A 415	128	32	+	-	+	-	+	-	-	-
375	A 416	64	32	+	-	+	-	+	-	-	-
376	A 419	0.5	0.25	-	-	-	-	+	-	-	-
377	A 420	128	32	+	-	+	-	+	-	-	-
378	A 421	32	16	+	-	+	-	+	-	-	-
379	A 422	1	0.5	-	-	-	-	+	-	-	-
380	A 423	256	64	+	-	+	+	+	+	-	-
381	A 424	64	16	+	-	+	-	+	-	-	-
382	A 425	256	128	+	-	-	+	+	+	-	-
383	A 426	256	128	+	-	-	+	+	+	-	-
384	A 427	256	64	+	-	-	+	+	+	-	-
385	A 428	256	64	+	-	+	-	+	-	-	-
386	A 429	256	64	+	-	-	+	+	+	-	-
387	A 430	0.5	0.25	-	-	-	-	+	-	-	-
388	A 431	256	64	+	-	+	-	+	-	-	-
389	A 432	>256	32	+	-	+	-	+	-	-	-
390	A 433	>256	64	+	-	+	-	+	-	-	-
391	A 434	128	16	+	-	+	-	+	-	-	-
392	A 435	256	64	+	-	-	+	+	+	-	-
393	A 436	256	64	+	-	+	-	+	-	-	-
394	A 437	128	64	+	-	-	+	+	+	-	-
395	A 438	64	16	+	-	+	-	+	-	-	-
396	A 439	256	128	+	-	+	-	+	-	-	-
397	A 440	32	16	+	-	+	-	+	-	-	-
398	A 441	64	32	+	-	+	-	+	-	-	-
399	A 442	64	16	+	-	+	-	+	-	-	-
400	A 443	64	16	+	-	+	-	+	-	-	-

Results of carbapenem susceptibility, carbapenemase activity and the presence of carbapenemase genes of *A. baumannii*. (cont.)

No	Strains	MICs (mg/L)		Carbapenemase activity		Presence of carbapenemase genes					
		IMP	MER	M-Hodge test	EDTA disk synergy test	<i>bla</i> _{OXA23} -like	<i>bla</i> _{OXA24} -like	<i>bla</i> _{OXA51} -like	<i>bla</i> _{OXA58} -like	<i>bla</i> _{IMP} -like	<i>bla</i> _{VIM} -like
401	A 444	128	64	+	-	+	-	+	-	-	-
402	A 446	256	128	+	-	+	+	+	+	-	-
403	A 449	32	16	+	-	+	-	+	-	-	-
404	A 450	64	32	+	-	+	-	+	-	-	-
405	A 453	64	16	+	-	+	-	+	-	-	-
406	A 455	32	16	+	-	+	-	+	-	-	-
407	A 456	32	16	+	-	+	-	+	-	-	-
408	A 458	128	16	+	-	+	-	+	-	-	-
409	A 459	128	16	+	-	+	-	+	-	-	-
410	A 460	64	64	+	-	+	-	+	-	-	-
411	A 461	64	16	+	-	+	-	+	-	-	-
412	A 462	64	16	+	-	+	-	+	-	-	-
413	A 465	128	64	+	-	+	-	+	-	-	-
414	A 466	128	16	+	-	+	-	+	-	-	-
415	A 467	128	16	+	-	+	-	+	-	-	-
416	A 468	64	32	+	-	+	-	+	-	-	-
417	A 469	128	64	+	-	+	-	+	-	-	-
418	A 470	256	128	+	-	+	+	+	+	-	-
419	A 471	256	128	+	-	+	+	+	+	-	-
420	A 472	256	128	+	-	+	+	+	+	-	-
421	A 473	1	0.5	-	-	-	-	+	-	-	-
422	A 474	0.5	0.25	-	-	-	-	+	-	-	-
423	A 475	32	8	+	-	+	-	+	-	-	-
424	A 479	64	16	+	-	+	-	+	-	-	-
425	A 480	0.5	0.5	-	-	-	-	+	-	-	-
426	A 481	64	32	+	-	+	-	+	-	-	-
427	A 482	64	32	+	-	+	-	+	-	-	-
428	A 483	0.5	0.5	-	-	-	-	+	-	-	-
429	A 486	64	32	+	-	+	-	+	-	-	-
430	A 487	64	16	+	-	+	-	+	-	-	-
431	A 488	0.5	1	-	-	-	-	+	-	-	-
432	A 489	32	16	+	-	+	-	+	-	-	-
433	A 493	1	0.12	-	-	-	-	+	-	-	-
434	A 494	0.5	0.5	-	-	-	-	+	-	-	-
435	A 495	64	32	+	-	+	-	+	-	-	-
436	A 496	0.5	1	-	-	-	-	+	-	-	-
437	A 497	32	32	+	-	+	-	+	-	-	-
438	A 498	32	16	+	-	+	-	+	-	-	-
439	A 499	64	16	+	-	+	-	+	-	-	-
440	A 500	>256	64	+	-	+	-	+	-	-	-
441	A 502	1	0.25	-	-	-	-	+	-	-	-
442	A 503	64	64	+	-	+	-	+	-	-	-
443	A 504	0.5	0.25	-	-	-	-	+	-	-	-
444	A 505	0.5	0.25	-	-	-	-	+	-	-	-
445	A 506	64	32	+	-	+	-	+	-	-	-
446	A 507	64	32	+	-	+	-	+	-	-	-
447	A 508	0.5	1	-	-	-	-	+	-	-	-
448	A 510	128	32	+	-	+	-	+	-	-	-
449	A 511	64	16	+	-	+	-	+	-	-	-
450	A 512	128	64	+	-	+	+	+	-	-	-
451	A 513	64	32	+	-	+	-	+	-	-	-
452	A 514	0.5	0.25	-	-	-	-	+	-	-	-
453	A 515	128	64	+	-	+	-	+	-	-	-
454	A 516	256	64	+	-	+	-	+	-	-	-
455	A 517	128	32	+	-	+	-	+	-	-	-
456	A 518	256	32	+	-	+	-	+	-	-	-
457	A 519	>256	64	+	-	+	+	+	-	-	-
458	A 522	128	16	+	-	+	-	+	-	-	-
459	A 523	128	32	+	-	+	-	+	-	-	-
460	A 524	128	32	+	-	+	-	+	-	-	-

Results of carbapenem susceptibility, carbapenemase activity and the presence of carbapenemase genes of *A. baumannii*. (cont.)

No	Strains	MICs (mg/L)		Carbapenemase activity		Presence of carbapenemase genes					
		IMP	MER	M-Hodge test	EDTA disk synergy test	<i>bla</i> _{OXA23} -like	<i>bla</i> _{OXA24} -like	<i>bla</i> _{OXA51} -like	<i>bla</i> _{OXA58} -like	<i>bla</i> _{IMP} -like	<i>bla</i> _{VIM} -like
461	A 526	128	32	+	-	+	-	+	-	-	-
462	A 527	128	32	+	-	+	-	+	-	-	-
463	A 528	128	16	+	-	+	-	+	-	-	-
464	A 529	256	32	+	-	+	-	+	-	-	-
465	A 530	128	32	+	-	+	-	+	-	-	-
466	A 531	128	32	+	-	+	-	+	-	-	-
467	A 532	128	32	+	-	+	-	+	-	-	-
468	A 535	128	32	+	-	+	-	+	-	-	-
469	A 536	4	0.5	-	-	-	-	+	-	-	-
470	A 537	>256	128	+	-	+	+	+	-	-	-
471	A 538	128	16	+	-	+	-	+	-	-	-
472	A 539	256	32	+	-	+	-	+	-	-	-
473	A 540	1	0.5	-	-	-	-	+	-	-	-
474	A 541	256	32	+	-	+	-	+	-	-	-
475	A 542	64	16	+	-	+	-	+	-	-	-
476	A 543	128	32	+	-	+	-	+	-	-	-
477	A 544	128	32	+	-	+	-	+	-	-	-
478	A 546	1	0.25	-	-	-	-	+	-	-	-
479	A 548	256	64	+	-	+	-	+	-	-	-
480	A 549	1	0.25	-	-	-	-	+	-	-	-
481	A 551	128	32	+	-	+	-	+	-	-	-
482	A 554	256	64	+	-	+	-	+	-	-	-
483	A 557	128	16	+	-	+	-	+	-	-	-
484	A 558	2	0.5	-	-	-	-	+	-	-	-
485	A 559	>256	128	+	-	+	+	+	+	-	-
486	A 560	128	32	+	-	+	-	+	-	-	-
487	A 562	256	32	+	-	+	-	+	-	-	-
488	A 563	256	32	+	-	+	-	+	-	-	-
489	A 564	4	1	-	-	-	-	+	-	-	-
490	A 565	1	1	-	-	-	-	+	-	-	-
491	A 566	64	16	+	-	+	-	+	-	-	-
492	A 567	256	64	+	-	+	-	+	-	-	-
493	A 568	256	32	+	-	+	-	+	-	-	-
494	A 569	256	32	+	-	+	-	+	-	-	-
495	A 570	128	32	+	-	+	-	+	-	-	-
496	A 571	256	32	+	-	+	-	+	-	-	-
497	A 573	64	16	+	-	+	-	+	-	-	-
498	A 574	256	64	+	-	+	-	+	-	-	-
499	A 575	128	32	+	-	+	-	+	-	-	-
500	A 576	256	32	+	-	+	-	+	-	-	-
501	A 577	64	32	+	-	+	-	+	-	-	-

+ = positive , - = negative

^a P4 = *Pseudomonas aeruginosa* (lab strain) that carried *bla*_{VIM-like}

601 720

OXA-23 AATATGCTTC TTTTAGAAGA GAGTAATGGC TACAAAATTT TTGGAAAGAC TGGTTGGGCA ATGGATATAA AACCACAAGT GGGCTGGTTG ACCGGCTGGG TTGAGCAGCC AGATGGAAAA

A66 AATATGCTTC TTTTAGAAGA GAGTAATGGC TACAAAATTT TTGGAAAGAC TGGTTGGGCA ATGGATATAA AACCACAAGT GGGCTGGTTG ACCGGCTGGG TTGAGCAGCC AGATGGAAAA

A67 AATATGCTTC TTTTAGAAGA GAGTAATGGC TACAAAATTT TTGGAAAGAC TGGTTGGGCA ATGGATATAA AACCACAAGT GGGCTGGTTG ACCGGCTGGG TTGAGCAGCC AGATGGAAAA

A72 AATATGCTTC TTTTAGAAGA GAGTAATGGC TACAAAATTT TTGGAAAGAC TGGTTGGGCA ATGGATATAA AACCACAAGT GGGCTGGTTG ACCGGCTGGG TTGAGCAGCC AGATGGAAAA

A266 AATATGCTTC TTTTAGAAGA GAGTAATGGC TACAAAATTT TTGGAAAGAC TGGTTGGGCA ATGGATATAA AACCACAAGT GGGCTGGTTG ACCGGCTGGG TTGAGCAGCC AGATGGAAAA

A74 AATATGCTTC TTTTAGAAGA GAGTAATGGC TACAAAATTT TTGGAAAGAC TGGTTGGGCA ATGGATATAA AACCACAAGT GGGCTGGTTG ACCGGCTGGG TTGAGCAGCC AGATGGAAAA

A150 AATATGCTTC TTTTAGAAGA GAGTAATGGC TACAAAATTT TTGGAAAGAC TGGTTGGGCA ATGGATATAA AACCACAAGT GGGCTGGTTG ACCGGCTGGG TTGAGCAGCC AGATGGAAAA

A472 AATATGCTTC TTTTAGAAGA GAGTAATGGC TACAAAATTT TTGGAAAGAC TGGTTGGGCA ATGGATATAA AACCACAAGT GGGCTGGTTG ACCGGCTGGG TTGAGCAGCC AGATGGAAAA

A446 AATATGCTTC TTTTAGAAGA GAGTAATGGC TACAAAATTT TTGGAAAGAC TGGTTGGGCA ATGGATATAA AACCACAAGT GGGCTGGTTG ACCGGCTGGG TTGAGCAGCC AGATGGAAAA

A433 AATATGCTTC TTTTAGAAGA GAGTAATGGC TACAAAATTT TTGGAAAGAC TGGTTGGGCA ATGGATATAA AACCACAAGT GGGCTGGTTG ACCGGCTGGG TTGAGCAGCC AGATGGAAAA

A519 AATATGCTTC TTTTAGAAGA GAGTAATGGC TACAAAATTT TTGGAAAGAC TGGTTGGGCA ATGGATATAA AACCACAAGT GGGCTGGTTG ACCGGCTGGG TTGAGCAGCC AGATGGAAAA

Consensus AATATGCTTC TTTTAGAAGA GAGTAATGGC TACAAAATTT TTGGAAAGAC TGGTTGGGCA ATGGATATAA AACCACAAGT GGGCTGGTTG ACCGGCTGGG TTGAGCAGCC AGATGGAAAA

721 822

OXA-23 ATTGTCGCTT TTGCATTAAT TATGGAAATG CCGTCAGAAA TGCCGGCATC TATACGTAAT GAATTATTGA TGAAATCATT AAAACAGCTG AATATTATTT AA

A66 ATTGTCGCTT TTGCATTAAT TATGGAAATG CCGTCAGAAA TGCCGGCATC TATACGTAAT GAATTATTGA TGAAATCATT AAAACAGCTG AATATTATTT AA

A67 ATTGTCGCTT TTGCATTAAT TATGGAAATG CCGTCAGAAA TGCCGGCATC TATACGTAAT GAATTATTGA TGAAATCATT AAAACAGCTG AATATTATTT AA

A72 ATTGTCGCTT TTGCATTAAT TATGGAAATG CCGTCAGAAA TGCCGGCATC TATACGTAAT GAATTATTGA TGAAATCATT AAAACAGCTG AATATTATTT AA

A266 ATTGTCGCTT TTGCATTAAT TATGGAAATG CCGTCAGAAA TGCCGGCATC TATACGTAAT GAATTATTGA TGAAATCATT AAAACAGCTG AATATTATTT AA

A74 ATTGTCGCTT TTGCATTAAT TATGGAAATG CCGTCAGAAA TGCCGGCATC TATACGTAAT GAATTATTGA TGAAATCATT AAAACAGCTG AATATTATTT AA

A150 ATTGTCGCTT TTGCATTAAT TATGGAAATG CCGTCAGAAA TGCCGGCATC TATACGTAAT GAATTATTGA TGAAATCATT AAAACAGCTG AATATTATTT AA

A472 ATTGTCGCTT TTGCATTAAT TATGGAAATG CCGTCAGAAA TGCCGGCATC TATACGTAAT GAATTATTGA TGAAATCATT AAAACAGCTG AATATTATTT AA

A446 ATTGTCGCTT TTGCATTAAT TATGGAAATG CCGTCAGAAA TGCCGGCATC TATACGTAAT GAATTATTGA TGAAATCATT AAAACAGCTG AATATTATTT AA

A433 ATTGTCGCTT TTGCATTAAT TATGGAAATG CCGTCAGAAA TGCCGGCATC TATACGTAAT GAATTATTGA TGAAATCATT AAAACAGCTG AATATTATTT AA

A519 ATTGTCGCTT TTGCATTAAT TATGGAAATG CCGTCAGAAA TGCCGGCATC TATACGTAAT GAATTATTGA TGAAATCATT AAAACAGCTG AATATTATTT AA

Consensus ATTGTCGCTT TTGCATTAAT TATGGAAATG CCGTCAGAAA TGCCGGCATC TATACGTAAT GAATTATTGA TGAAATCATT AAAACAGCTG AATATTATTT AA

ศูนย์วิทยทรัพยากร
จุฬาลงกรณ์มหาวิทยาลัย

3. OXA-51 GROUP

- A80

	1											120
OXA-51	ATGAACATTA	AAACACTCTT	ACTTATAACA	AGCGCTATTT	TTATTTTCAGC	CTGCTCACCT	TATATAGTGA	CTGCTAATCC	AAATCACAGC	GCTTCAAAAT	CTGATGAAAA	AGCAGAGAAA
OXA-132
OXA-99
A80
OXA-64G.....G.....
OXA-111T.....T.....
OXA-67G.....A.....A.....
OXA-86A.....A.....
OXA-87A.....A.....
OXA-100G.....A.....A.....
OXA-70G.....A.....
OXA-106G.....A.....
OXA-71G.C.....
OXA-113G.C.....
OXA-93G.C.....A.....
OXA-68G.....
OXA-128G.....
OXA-78G.....
OXA-77G.....C.....
OXA-91G.....
OXA-89
OXA-75C.....	.G.....T.....
OXA-65G.....
OXA-90G.....
OXA-88G.....A.....
OXA-95G.....C.....
OXA-108G.....A.....
OXA-130G.....A.....
OXA-66G.....T.....
OXA-83G.....T.....
OXA-79G.....T.....
OXA-76G.....T.....
OXA-80G.....T.....
OXA-109G.....T.....
OXA-131G.....T.....
OXA-84G.....T.....
OXA-82G.....T.....
OXA-115G.....T.....


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OXA-89 .....T.
OXA-75 .....T.
OXA-65 .....C.....A.....G.....A.
OXA-90 .....C.....A.....G.....
OXA-88 .....C.....G.....
OXA-95 .....C.....A.....G.....
OXA-108 .....C.....A.....G.....
OXA-130 .....C.....A.....G.....
OXA-66 .....C.....A.....G.....
OXA-83 .....C.....C.....A.....G.....
OXA-79 .....C.....A.....G.....
OXA-76 .....C.....A.....G.....
OXA-80 .....C.....TA.....G.....
OXA-109 .....C.....AA.....G.....
OXA-131 .....C.....G.....A.....G.....
OXA-84 .....C.....T.A.....G.....
OXA-82 .....C.....A.....G.....A.
OXA-115 .....C.....TA.....G.....
OXA-94 .....C.....G.....
OXA-69 .....G.....
OXA-110 .....C.....G.....
OXA-112 .....G.....
OXA-92 .....G.....
OXA-107 .....G.....
OXA-116 .....T.
OXA-117 .....T.
OXA-104 .....G.....GAG...G.....G.....G.....C.G.G..C..C...C..G.....G..AGC..C...A..C..G..C...C..G...T..C...
Consensus .....t.....ttc...t.....g...t.....a...t.a.t.t.t.t...a...t..a..c...tct.g...g..t...t.t...t..a...c.t...

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481

600

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OXA-51 CAAGTCGATA ATTTTGGCT GGTGGGTCTT TAAAAATTA CTCCTCAGCA AGAGGCACAG TTTGCTTACA AGCTAGCTAA TAAAACGCTT CCATTTAGCC CAAAAGTCCA AGATGAAGTG
OXA-132 .....
OXA-99 .....
A80 .....
OXA-64 .....
OXA-111 .....C.....
OXA-67 .....T.....
OXA-86 .....T.....
OXA-87 .....T.....C.....
OXA-100 .....G.....A.....
OXA-70 .....A.....
OXA-106 .....A.....
OXA-71 .....A.....
OXA-113 .....G.....A.....

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OXA-104 ..C.....G.TAG... G...C.G...C..T..G.. .AGC..G..CA.... .C..... CC.G.....G C.G..C...C .G
 Consensus ..t.....a.ctc... t...t.a...a..a..t... .tct..t..ag.... .t..... tt.a....a t.a..t...t .atag

- **A74**

1 120
 OXA-64 ATGAACATTA AAGCACTCTT ACTTATAACA AGCGCTATTT TTATTTTCAGC CTGCTCACCT TATATAGTGA CTGCTAATCC AAATCACAGC GCTTCAAAAT CTGATGAAAA AGGAGAGAAA
 A74 ATGAACATTA AAGCACTCTT ACTTATAACA AGCGCTATTT TTATTTTCAGC CTGCTCACCT TATATAGTGA CTGCTAATCC AAATCACAGC GCTTCAAAAT CTGATGAAAA AGGAGAGAAA
 Consensus ATGAACATTA AAGCACTCTT ACTTATAACA AGCGCTATTT TTATTTTCAGC CTGCTCACCT TATATAGTGA CTGCTAATCC AAATCACAGC GCTTCAAAAT CTGATGAAAA AGGAGAGAAA

121 240
 OXA-64 ATTA AAAAATT TATTTAACGA AGCACACACT ACGGGTGT TT TAGTTATCCA ACAAGGCCAA ACTCAACAAA GCTATGGTAA TGATCTTGCT CGTGCTTCGA CCGAGTATGT ACCTGCTTCG
 A74 ATTA AAAAATT TATTTAACGA AGCACACACT ACGGGTGT TT TAGTTATCCA ACAAGGCCAA ACTCAACAAA GCTATGGTAA TGATCTTGCT CGTGCTTCGA CCGAGTATGT ACCTGCTTCG
 Consensus ATTA AAAAATT TATTTAACGA AGCACACACT ACGGGTGT TT TAGTTATCCA ACAAGGCCAA ACTCAACAAA GCTATGGTAA TGATCTTGCT CGTGCTTCGA CCGAGTATGT ACCTGCTTCG

241 360
 OXA-64 ACCTTCAAAA TGCTTAATGC TTTGATCGGC CTTGAGCACC ATAAGGCAAC CACCACAGAA GTATTTAAGT GGGACGGGCA AAAAAGGCTA TTCCAGAAAT GGGAAAAGGA CATGACCCTA
 A74 ACCTTCAAAA TGCTTAATGC TTTGATCGGC CTTGAGCACC ATAAGGCAAC CACCACAGAA GTATTTAAGT GGGACGGGCA AAAAAGGCTA TTCCAGAAAT GGGAAAAGGA CATGACCCTA
 Consensus ACCTTCAAAA TGCTTAATGC TTTGATCGGC CTTGAGCACC ATAAGGCAAC CACCACAGAA GTATTTAAGT GGGACGGGCA AAAAAGGCTA TTCCAGAAAT GGGAAAAGGA CATGACCCTA

361 480
 OXA-64 GGCGATGCTA TGAAAGCTTC CGCTATTCCG GTTTATCAAG ATTTAGCTCG TCGTATTGGA CTTGAACTCA TGTCTAAGGA AGTGAAGCGT GTTGGTTATG GCAATGCAGA TATCGGTACC
 A74 GGCGATGCTA TGAAAGCTTC CGCTATTCCG GTTTATCAAG ATTTAGCTCG TCGTATTGGA CTTGAACTCA TGTCTAAGGA AGTGAAGCGT GTTGGTTATG GCAATGCAGA TATCGGTACC
 Consensus GGCGATGCTA TGAAAGCTTC CGCTATTCCG GTTTATCAAG ATTTAGCTCG TCGTATTGGA CTTGAACTCA TGTCTAAGGA AGTGAAGCGT GTTGGTTATG GCAATGCAGA TATCGGTACC

481 600
 OXA-64 CAAGTCGATA ATTTTGGCT GGTGGTCCCT TAAAAATTA CTCCTCAGCA AGAGGCACAG TTTGCTTACA AGCTAGCTAA TAAAACGCTT CCATTTAGCC CAAAAGTCCA AGATGAAGTG
 A74 CAAGTCGATA ATTTTGGCT GGTGGTCCCT TAAAAATTA CTCCTCAGCA AGAGGCACAG TTTGCTTACA AGCTAGCTAA TAAAACGCTT CCATTTAGCC CAAAAGTCCA AGATGAAGTG
 Consensus CAAGTCGATA ATTTTGGCT GGTGGTCCCT TAAAAATTA CTCCTCAGCA AGAGGCACAG TTTGCTTACA AGCTAGCTAA TAAAACGCTT CCATTTAGCC CAAAAGTCCA AGATGAAGTG

601 720
 OXA-64 CAATCCATGT TATTCATAGA AGAAAAGAAAT GGAAATAAAA TATACGCAAA AAGTGGTTGG GGATGGGATG TAGACCCACA AGTAGGCTGG TTAAGTGGAT GGGTTGTTCA GCCTCAAGGG
 A74 CAATCCATGT TATTCATAGA AGAAAAGAAAT GGAAATAAAA TATACGCAAA AAGTGGTTGG GGATGGGATG TAGACCCACA AGTAGGCTGG TTAAGTGGAT GGGTTGTTCA GCCTCAAGGG
 Consensus CAATCCATGT TATTCATAGA AGAAAAGAAAT GGAAATAAAA TATACGCAAA AAGTGGTTGG GGATGGGATG TAGACCCACA AGTAGGCTGG TTAAGTGGAT GGGTTGTTCA GCCTCAAGGG

721 825
 OXA-64 AATATTGTAG CGTTCTCCCT TAACTTAGAA ATGAAAAAAG GAATACCTAG CTCTGTTCGA AAAGAGATTA CTTATAAAAAG TTTAGAACAA TTAGGTATTT TATAG
 A74 AATATTGTAG CGTTCTCCCT TAACTTAGAA ATGAAAAAAG GAATACCTAG CTCTGTTCGA AAAGAGATTA CTTATAAAAAG TTTAGAACAA TTAGGTATTT TATAG
 Consensus AATATTGTAG CGTTCTCCCT TAACTTAGAA ATGAAAAAAG GAATACCTAG CTCTGTTCGA AAAGAGATTA CTTATAAAAAG TTTAGAACAA TTAGGTATTT TATAG

APPENDIX F

AMINO ACID SEQUENCES ALIGNMENT OF OXA-TYPE CARBAPENEMASE AND METALLO β -LACTAMASES

OXA-TYPE CARBAPENEMASES

1. OXA-23 GROUP

	1											120
OXA-23	MNKYFTCYVV	ASLFLSGCTV	QHNLINEPVS	QIVQGHQVI	HQYFDEKNTS	GVLVIQTDKK	INLYGNALSR	ANTEYVPAST	FKMLNALIGL	ENQKTDINEI	FKWRGKRSF	TAWEKDMLG
OXA-27A.....
OXA-49
Consensusc.....
	121											240
OXA-23	EAMKLSAVPV	YQELARRIGL	DLMQKEVKRI	GFGNAEIGQQ	VDNFWLVGPL	KVTPIQEVEF	VSQLAHTQLP	FSEKVQANVK	NMLLLEESNG	YRIFGRTGWA	-MDIKPQVGW	LTGWVEQPDG
OXA-27
OXA-49E.....A.....
Consensusk.....
	241			274								
OXA-23	KIVAFALNME	MRSEMPASIR	NELLMKSLKQ	LNII								
OXA-27K.....								
OXA-49								
Consensusn.....								

2. OXA-24 GROUP

	1											120
OXA24	MKKFILPIFS	ISILVLSLAC	SSIKTKSEDN	FHISSQQHEK	AIKSYFDEAQ	TQGVIIIEG	KNLSTYGNAL	ARANKEYVPA	STFKMLNALI	GLENHKATTN	EIFKWDGKKR	TYPMWERDMT
OXA-33
OXA-40
OXA-26
OXA-72
OXA-25
Consensus
	121											240
OXA24	LGEAMALSAV	PVYQELARRT	GLELMQKEVK	RVNFGNTNIG	TOVDNFWLVG	PLKITPVQEV	NFADDLAHR	LPFKLETQEE	VKKMLLIEV	NGSKIYAKSG	WGMGVTPQVG	WLTGWVEQAN
OXA-33
OXA-40
OXA-26
OXA-72D.....
OXA-25E.....
Consensusk.....g.....
	241			275								
OXA24	GKKIPFSLNL	EMKEGMSGSI	RNEITYKSLE	NLGII								
OXA-33								
OXA-40								
OXA-26T.....								
OXA-72								
OXA-25L.....								
ConsensusS.....S.....								

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3. OXA-51 GROUP

	1											120
OXA-51	MNIKTLILLIT	SAIFISACSP	YIVTANPNHS	ASKSDEHAEK	IKNFLNEVHT	TGVLVIQOQG	TQOSYGNDLA	RASTEYVPAS	TFKMLNALIG	LEHHKATTE	VFKWDGQKRL	FPEWEKMTL
OXA-64	...A...G..A..
OXA-71	...A...A..T...
OXA-111S.....A..
OXA-67	...A...	.T.....	T.....A..	I.....
OXA-100	...A...	.T.....	T.....A..	I.....
OXA-86T.....	T.....A..I.....	I.....
OXA-87T.....	T.....A..I.....	I.....
OXA-65	...A...A..K...
OXA-88	...A...K...A..K...
OXA-66	...A...V...A..K...
OXA-82	...A...V...A..K...
OXA-76	...A...V...A..K...
OXA-80	...A...V...A..K...
OXA-109	...A...V...A..K...
OXA-79	...A...V...A..K...
OXA-95	...A.F...A..K...
OXA-108	...A...T.....A..K...
OXA94	...QA...S.....A..K...
OXA-69	...A...D.....A..E...N...
OXA-110	...A...D.....A..E...N...
OXA-107	...A...D.....A..E...N...
OXA-112	...A...D.....A..E...N...
OXA-68	...A...A..N...
OXA-77	...A...S.....A..N...
OXA-91	...A...S.....A..N...
OXA-104	...A...A..K...N...
OXA-78	...A...S.....A..A...N...
OXA-93	...A...	.T.....A..SN...
OXA-70	...A...K...A..N...
OXA-106	...A...K...A..N...
OXA-75	...QA...Y...A..N...
Consensus	...ka...	...a...	...t...	...a...	...e...	...a...!	...q...#...



	121											240
OXA-51	GDAMKASAIP	VYQDLARRIG	LELMSKEVKR	VGYGNADIGT	QVDNFWLVGP	LKITPQQEAO	FAYKLANKTL	PFSPKVQDEV	QSMLFIEEKN	GNKIYAKSGW	GWDVDPQVGV	LTGWVVQPQG
OXA-64
OXA-71
OXA-111M.....
OXA-67L.....
OXA-100Q.....
OXA-86L.....
OXA-87L.A.....
OXA-65Q.....N.....
OXA-88Q.....N.....
OXA-66Q.....N.....
OXA-82V.....Q.....N.....
OXA-76Q.....N.....
OXA-80L.....Q.....N.....
OXA-109Q.....Q.....N.....
OXA-79Q.....G.N.....
OXA-95Q.....
OXA-108T.....V.....Q.....
OXA94Q.....N.....H.....
OXA-69Q.....N.....
OXA-110L.....Q.....N.....
OXA-107V.....Q.....N.....
OXA-112Q.....N.....
OXA-68N.....QE.....N.....
OXA-77P.....N.....Q.....N.....
OXA-91N.....Q.....
OXA-104N.....Q.....
OXA-78N.....Q.....N.....
OXA-93N.....Q.....N.....
OXA-70N.....Q.H.....
OXA-106N.....Q.....
OXA-75N.....L.....Q.....N.....
Consensusk.....q.....#.....

	241		274
OXA-51	NIVAFSLNLE	MKRGIPSSVR	KEITYKSLEQ LGIL
OXA-64
OXA-71
OXA-111
OXA-67
OXA-100
OXA-86
OXA-87
OXA-65
OXA-88
OXA-66
OXA-82
OXA-76K
OXA-80
OXA-109
OXA-79
OXA-95
OXA-108
OXA94
OXA-69
OXA-110
OXA-107
OXA-112P.....
OXA-68
OXA-77
OXA-91
OXA-104
OXA-78T.....
OXA-93
OXA-70
OXA-106
OXA-75S.....RG.....
Consensus



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4. OXA-58 GROUP

	1											120
OXA-58	MKLLKILSLV	CLISISIGACA	EHSMSRAKTS	TIPQVNSII	DQNVQALFNE	ISADAVFVTY	DGQNIKKYGT	HLDRAKTAYI	PASTFKIANA	LIGLENHKAT	STEIFKWDGK	PRFFKAWDKD
OXA-96
OXA-97G..
Consensusa..
	121											240
OXA-58	FTLGEAMQAS	TVPVYQELAR	RIGPSLMQSE	LQRIGYGNMQ	IGTEVDQFWL	KGPLTITPIQ	EVKFVYDLAQ	GQLPFKPEVQ	QQVKEMLYVE	RRGENRLYAK	SGWGMVDPQ	VGWYVGFVEK
OXA-96	M.....
OXA-97
Consensus	i.....
	241			280								
OXA-58	ADGQVAFAL	NMQMKAGDDI	ALRKQLSLDV	LDKLGVFHYL								
OXA-96								
OXA-97								
Consensus								

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AMINO ACID SEQUENCES ALIGNMENT OF 4 SUBGROUPS IN OXA-TYPE CARBAPENEMASE

```

1
OXA-23  MNKYFTCY VVASLFLSGC TVQHNLINET PSQI-VQGH- -NQVIHQYFD EKNTSGVLVI QTDKKINLYG NALSranTEY VPASTFmLN ALIGLENQKT DINEIFKWK G EKRSTAWEK
OXA24  MKKFILPIFS ISILVLSLAC SSIKTKSEDN FHIS-SQGH- -EKAIKSYFD EAQTQGVIII KEGKNLSTYG NALARANKEY VPASTFmLN ALIGLENHKA TTNEIFKWDG KKRTPMWEK
OXA-51  MNIKTLLL ITSALFISAC SPYIVTANPN HSASKSDEK- -AEKIKNLFN EVHTTGVLVI QQQQTQSSYG NDLARASTEY VPASTFmLN ALIGLEHKA TTTEVFKWDG QKRLFPEWEK
OXA-58  MKLLKILSL VCLSISIGAC AEHSMSRAKT STIPQVNSI IDQNVQALFN EISADAVFVT YDQNIKKYG THLDRAKTAY IPASTFRAN ALIGLENHKA TSTEIFKWDG KPRFFKAWDK
Consensus ..k..k.l.l !..sisisaC .....t ..i..v#... ..q.!..lF# E..t.gV.!i ..gqni..YG n.L.RA.teY !PASTFmLn ALIGLEnKa t.tE!FKWdG kkr.%.aW#K

121
OXA-23  DMTLGEAMKL SAVPVYQELA RRIGLDLMQK EVKRIGFGNA EIGQQVDNFW LVGPLKVTPI QEVFVSOLA HTQLPFSEKV QANVKNMLL EESNGYKIFG KTGWAMDIKP QVGWLTGWVE
OXA24  DMTLGEAMAL SAVPVYQELA RRTGLELMQK EVKRVNFGNT NIGTQVDNFW LVGPKITPV QEVNFADDLA HNRLPFKLET QEVKMLLI KEVNGSKIYA KSGWGMGVT QVGWLTGWVE
OXA-51  DMTLGDAMKA SAIPVYQDLA RRIGLELSK EVKRVGYGNA DIGTQVDNFW LVGPKITPQ QEAQFAYKLA NKTLPFSPKV QEVQSMFLI EEKNGNKIYA KSGWGDVDP QVGWLTGWVV
OXA-58  DFTLGEAMQA STVPVYQELA RRIGPSLMQS ELQRIGYGNM QIGTEVDQFW LKGPLTITPI QEVKVVYDLA QGQLPFKPEV QQVKEMLYV ERRGENRLYA KSGWMAVDP QVGWYVGFVE
Consensus DmTLG#AM.a Sa!PVYQ#LA RRIGL.LMqk Evkrig#GN. #IGt#VD#FW LvGPLk!TPI QEv.FvydLA ..qLPfkpev Q.#Vk.ML.. ee.ngnki#a KsgWgm.!dP QVGWltGwVe

241
OXA-23  QPDGKIVAFa LNMEMRSEMP ASIRNELLMK SLKQLNII
OXA24  QANGKIPFS LNLEMKEGMS GSIRNEITYK SLENLGI
OXA-51  QPQGNIVAFS LNLEMKKIP SSVRKEITYK SLEQLGIL
OXA-58  KADGQVAFa LNMQMKAGDD IALRKQLSLD VLDKLGVFHY L
Consensus qa#G..!aFa LNS#Mk.g.. .s.Rk#l..k sL..Lg!...

281

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METALLO β -LACTAMASES

IMP-TYPE CARBAPENEMASES

	1												120
IMP-1	MSKLSVFFIF	LFCSIATAAE	SLPDLKIEKL	DEGVYVHTSF	EEVNGWGVVP	KHGLVVLVNA	EAYLIDTPFT	AKDTEKLVTW	FVERGYKIKG	SISSHFHSDS	TGGIEWLNSR	SIPTYASELT	
IMP-6	
IMP-4	P.....
IMP-5	...F...M.	...TA...
IMP-2	.K..F.LCVC	FL...TA.GA	R.....	E.....S	T D.....	.T.....	N.....	T.....
IMP-11	.K..F.LC..	..L..TASG.	V.....	E....L....	..S....TN	D.....	N.....	A..G..FT..	.V.....
Consensus	.k..f.lcif	lfc..taage	#....v....	..n.....#.	#.....	ak.....	..e..%k..	s!.....
	121												240
IMP-1	NELLKKDGRV	QATNSFSGVN	YWLVKNKIEV	FYPGPGHTPD	NVVVWLPERK	ILFGGCFIKP	YGLGNLGDAN	IEAWPKSAKL	LKSKYGKAKL	VVPSHSEVGD	ASLLKLTLEQ	AVKGLNESKK	
IMP-6
IMP-4K..G...L.....	L.....	.I.....
IMP-5K...AS	..K.....NR	V.....V..	V.....	.M.....
IMP-2K.....SQK.....V..	D.....	L.....	I..M..V....	..S...I..R.W..
IMP-11N...SIQN.V..	D.....	D...LK.....	I..M...V....	..SG..I..NW..K...
Consensus#...	..k...s.vsn...!q.	v.....k!!	d.....g...	le.....i	m...g...	..ss...i.#l.w..n...
	241												
IMP-1	PSKPSN												
IMP-6												
IMP-4	...L..												
IMP-5												
IMP-2	..Q...												
IMP-11	..LL...												
Consensus	..s.p..												

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AMINO ACID SEQUENCES ALIGNMENT OF METALLO β -LACTAMASES

```

1
IMP-1  MSKLSV  FFIFLFCISIA  --TAAESLP-  -----  --DLKIEKLD  EGVYVHTSFE  EVNGWGVVVK  HGLVVLVNAE  AYLIIDTPFTA  KDTEKLVTF  VER-GYKIKG  SSSHFHSDS
SIM-1  MRTLLI  LCLFGTLNTA  --FAEEAQP-  -----  --DLKIEKIE  EGIYLHTSFQ  EYKGFGLVVK  QGLVVLNHHK  AYLIIDTPASA  GDTEKLVNWL  EKN-DFTVNG  SISTHFHDDS
GIM-1  MKNVLV  FLILLVALPA  --LAQGHKP-  -----  ---LEVIKIE  DGVYLHTSEK  NIEGYGLVDS  NGLVVLNHNQ  AYIIDTPWSE  EDTKLLLSWA  TDR-GYQVMA  SISTHSHEDR
VIM-1  MLKVISSLV  YMTASVMAVA  SPLAHSGEPS  GEYPTVNEIP  VGEVRLYQIA  DGVVSHIATQ  SFDG-AVYPS  NGLIVRDGDE  LLLIDTAWGA  KNTAALLAEI  EKQIGLPVTR  AVSTHFHDDR
SPM-1  MNSPKS  RALLGFMGAF  CLLLAVGAPL  SAKSSDHVDL  PYNLTATKID  SDVFVVTDRD  FYSSNVLVAK  ---MLDGT-  VVIVSSPFEN  LGTQTLMDWV  AKTMKPKRVV  AINTHFHLDG
Consensus  ....m.s.lv  ...l..m.a  ..la..g.P.  .....  ...l...ki.  .g!..ht...  ...g..lv.k  .gl.vldg..  ..i!dtp...  ..T..L..w.  .k..g..v..  a!stHFH.D.

121
IMP-1  TGGIEWLNSR  SIPTYASELT  NELLKKDGKV  Q-----  -----  -----ATNSF  SGVNYW---L  VKNKIEVFYP  GPGHTPDNVV  VWLPERKILF  GGCFIKPY--  -GLGNLGDAN
SIM-1  TAGIEWLNTK  SIPTYASKLT  NELLNKNGKT  Q-----  -----  -----AKHSF  DKESFW---L  VKNKIEVFYP  GPGHTQDNEV  VWIPNKKILF  GGCFIKPN--  -GLGNLSDAN
GIM-1  TAGIKLLNSK  SIPTYTSELT  KKLLAREGKP  V-----  -----  -----PTHYF  KDFEFT---L  GNGLIELYYP  GAGHTEDNIV  AWLPKSKILF  GGCLVRSHEW  EGLGYVGDAS
VIM-1  VGGVDVLRRAA  GVATYASPST  RRLAEAEAGNE  I-----  -----  -----PTHSL  EGLSSSGDAV  RFGPVELFYP  GAAHSTDNLV  VYVPSANVLY  GGCVAHELSS  TSAGNVADAD
SPM-1  TGGNEIYKMM  GAETWSSDLT  KQLRLEENKK  DRIKAAEFYK  NEDLKRRIILS  SHVPADNVF  DLKQGGVFSF  SNELVEVSFP  GPAHSPDNVV  VYFPKPKLLF  GGCMIKPKK-  --LGYLGDAN
Consensus  tgG.e.l...  g..Ty.S.lT  k.L...#gk.  .....  .....  .....ath.f  .....  .n.l!E...P  GpaHs.DN.V  vy.Pk.k.L%  GGC.!kp.e.  ..lGylgDAN

241
IMP-1  IEAWPKSAKL  LSKYKAKL  VVPSHSEVGD  ASLLKLTLEQ  AVKGLNESKK  PSKPSN
SIM-1  LEAWPGSAKK  MISKYSKAKL  VIPSHSEIGD  ASLLKLTWEQ  AIKGLNESKS  KPPLIN
GIM-1  ISSWADSIKN  IVSKKYPQIM  VVPGHGKVG  SDILDHTIDL  AESASNKLMQ  PTAEASAD
VIM-1  LAEWPTSVR  IQKHYPEAEV  VIPGHGLPGG  LDLLQHTANV  VKAHKNRSVA  E
SPM-1  VKAWPDSARR  L--KKFDAKI  VIPGHGEWGG  PEMVNKTIKV  AEKAVGEMRL
Consensus  ..aWpdSa.r  ...kk..ak.  V!PgHge.Gg  ...l..Ti.v  aeka.ne...  .....

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1. 64 codon on DNA

First Position	Second Position				Third Position
	T	C	A	G	
T	F	S	Y	C	T
	F	S	Y	C	C
	L	S	STOP CODON	STOP CODON	A
	L	S	STOP CODON	W	G
C	L	P	H	R	T
	L	P	H	R	C
	L	P	Q	R	A
	L	P	Q	R	G
A	I	T	N	S	T
	I	T	N	S	C
	I	T	K	R	A
	M	T	K	R	G
G	V	A	D	G	T
	V	A	D	G	C
	V	A	E	G	A
	V	A	E	G	G

Abbreviation: A, alanine; C, cysteine; D, aspartic acid; E, glutamic acid; F, phenylalanine; G, glycine; H, histidine; I, isoleucine; K, lysine; L, leucine; M, methionine; N, asparagine; P, proline; Q, glutamine; R, arginine; S, serine; T, threonine; V, valine; W, tryptophan; Y, tyrosine

BIOGRAPHY

Mrs. Napawan Punakabutra was born on December 31, 1974 in Bangkok, Thailand. She graduated with the Bachelor degree of Science (Microbiology) from the Faculty of Science, Kasetsart University in 1996. She is currently a member of Bacteriology Unit, Department of Microbiology, King Chulalongkorn Memorial Hospital and was given the opportunity to pursue her MS degree in the Inter-Department of Medical Microbiology, Faculty of Graduate School, Chulalongkorn University since 2005.



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