To assess dissemination of OXA-23–producing strains of *Acinetobacter baumannii*, we obtained 20 carbapenem-resistant, OXA-23–producing isolates from different regions. Their clonal relationship was assessed by pulsed-field gel electrophoresis and multilocus sequence typing. We identified 8 sequence types, including 4 novel types. All except 2 strains belonged to 2 main European clonal lineages. The *bla*<sub>OXA-23</sub> gene was either located on the chromosome or on plasmids and associated with 4 genetic structures.

*A. baumannii* is a gram-negative organism that is increasingly recognized as a major pathogen causing nosocomial infections, including bacteremia and ventilator-associated pneumonia, particularly in patients admitted to intensive care units (1). Several studies have shown the geographically widespread occurrence of multidrug-resistant *A. baumannii* strains, which suggested a clonal relatedness of these strains. Three international *A. baumannii* clones associated with multidrug resistance (European clones I, II, and III) have been reported (2).

Increasing resistance to carbapenems has been observed worldwide in the past decade, frequently mediated by production of class D β-lactamases with carbapenemase activity. Three acquired class D β-lactamases with carbapenemase gene clusters have been described in *A. baumannii*, which correspond to *bla*<sub>OXA-23</sub>-like, *bla*<sub>OXA-40</sub>-like, and *bla*<sub>OXA-58</sub>-like genes (3). The *bla*<sub>OXA-23</sub> gene, first characterized in Scotland (4), has been increasingly reported worldwide. *A. radioreisens* was recently identified as the progenitor of the *bla*<sub>OXA-23</sub>-like genes (5). Clonal outbreaks of carbapenem-resistant and OXA-23–producing *A. baumannii* have been reported in many countries, such as Bulgaria (6), People’s Republic of China (7), Brazil (8), Iraq (9), Afghanistan (9), and French Polynesia (10).

Genetic acquisition of the *bla*<sub>OXA-23</sub> gene was investigated and transposons Tn2006, Tn2007, and Tn2008 were identified as genetic structures harboring this gene (10–12). In Tn2006, the *bla*<sub>OXA-23</sub> gene is flanked by 2 copies of the insertion sequence IS<sub>Aba1</sub>, which are located in opposite orientations (Figure 1). The functionality of Tn2006 has been recently demonstrated (13). Tn2008 is similar to Tn2006 but lacks the second copy of IS<sub>Aba1</sub> and the *bla*<sub>OXA-23</sub> gene is associated with 1 copy of IS<sub>Aba4</sub> (which differs from IS<sub>Aba1</sub>) in Tn2007 (Figure 1) (11). As reported for strains from United Arab Emirates and Bahrain, the *bla*<sub>OXA-23</sub> gene can be associated with only 1 copy of IS<sub>Aba1</sub> (14,15). We studied the clonal relationship and genomic environment of sequences surrounding the *bla*<sub>OXA-23</sub> gene among a collection of OXA-23–producing isolates from 15 countries.

**Materials and Methods**

**Bacterial Strains and Susceptibility Testing**

Twenty OXA-23–producing *A. baumannii* clinical isolates were obtained from 15 countries. These isolates had been obtained from patients hospitalized in intensive care units from December 2003 through March 2008. Isolates were obtained from tracheal aspirates (n = 3), bile (n = 1), urine (n = 4), wounds (n = 1), respiratory tract (n = 1), blood (n = 4), and sputum (n = 1). The isolates were initially chosen after preliminary pulsed-field gel electrophoresis (PFGE)–based typing had identified 13 pulsotypes. Isolates...
were obtained from France (n = 4), Vietnam (n = 1), New Caledonia (n = 1), Thailand (n = 1), Australia (n = 1), Tahiti (n = 1), Reunion (n = 2), South Africa (n = 1), United Arab Emirates (n = 2), Libya, (n = 1), Bahrain (n = 1), Egypt (n = 1), Belgium (n = 1), Algeria (n = 1), and Brazil (n = 1).

Presence of the bla\textsubscript{OXA-23} gene was screened by PCR by using specific primers (OX-A23-A 5′-GGA ATCCCATGAATAAATATTACCTTCG-3′ and OXA-23-B 5′-CGGTATCCGTTAAATATTTCCAGGTC-3′) and additional sequencing (ABI 3100 sequencer; Applied Biosystems, Foster City, CA, USA). Susceptibility patterns to β-lactam antimicrobial drugs were determined by using a standard disk diffusion method according to published standards (16) and Etest strips (AB Biodisk, Solna, Sweden). Isolates were identified by using 16S rRNA gene sequencing (17).

Clonal Relationships

Isolates were typed by using ApaI macrorestriction analysis and PFGE according to the manufacturer’s recommendations (Bio-Rad, Marnes-la-Coquette, France). Bacteria were grown in a medium appropriate for the strain until an optical density of 0.8 to 1 at 600 nm was reached. One milliliter of cells was centrifuged, washed, and resuspended in 10 mmol/L Tris, pH 7.2, 20 mmol/L NaCl, 50 mmol/L EDTA. Immediately after resuspension, an equal volume of 2% low melting point InCert agarose (Bio-Rad, Marnes-la-Coquette, France). Bac-

Whole-cell DNA of A. baumannii isolates was digested with Apal overnight at room temperature (New England Biolabs, St. Quentin-en-Yvelines, France). Electrophoresis was performed on a 1% agarose gel with 0.5× Tris-borate-EDTA buffer by using a CHEF DRII apparatus (Bio-Rad). Samples were subjected to electrophoresis at 14°C, 6 volts/cm, and a switch angle with 1 linear switch ramp of 3–8 s for 10.5 h, and then for 12–20 s for 10.5 h.

Identification of PCR-based sequence groups was conducted by using 2 multiplex PCR assays designed to selectively amplify group 1 or group 2 alleles of the gene encoding outer-membrane protein A (ompA), the gene encoding part of a pilus assembly system required for biofilm formation (csuE), and the gene encoding the intrinsic carbapenemase gene of A. baumannii (bla\textsubscript{OXA-23}) (18). Clonal relationships were established by multilocus sequence typing (MLST) by using 7 standard housekeeping loci (citrate synthase [gltA], gyrase B [gyrB], glucose dehydrogenase B [gdhB], recombination A [recA], chaperone 60 [cpn60], glucose-6-phosphate isomerase [gpi], and RNA polymerase [rpoD]) as described (18). Sequencing of internal fragments was performed by using BigDye fluorescent terminators and primers described (19). Sequences were compared with the A. baumannii database at the MLST Website (http://mlst.zoo.ox.ac.uk). To supplement epidemiologic results, we performed a second MLST typing using the scheme developed by Nemec et al. (20). Sequences of the 7 housekeeping genes were analyzed by using an A. baumannii database (www.pasteur.fr/recherche/genopole/ PF8/mlst/Abaumannii.html).

Southern Blot Analysis and Location of bla\textsubscript{OXA-23} Gene

Southern blot analysis was performed by using total genomic DNA digested with EcoRI, separated by electro-
phoresis on 0.8% agarose gels, transferred onto Hybond N+ membranes, and hybridized with enhanced chemiluminescence labeled probes overnight at 42°C. The membranes were developed according to the manufacturer’s instructions (GE Healthcare, Saclay, France). Chromosomal or plasmid locations of the β-lactamase gene were assessed by hybridization of I-Ceul–digested genomic DNA with blaOXA-23 and 16S rDNA probes and electrophoresis (20–120 s for 9 h and 60–100 s for 11 h at 14°C and 5 V/cm2) (21). DNA was transferred from an agarose gel to a nylon membrane by capillary transfer. Hybridization, labeling, and detection were conducted as described above. Mating-out assays were performed by using isolates that had plasmid-borne blaOXA-23 as donors and rifampin-resistant A. baumannii BM4547 as recipients as described (22). Transconjugants were selected on trypticase soy agar plates containing ticarcillin (50 mg/L) and rifampin (50 mg/L).

Cloning Experiments
To identify entire transposon structures containing the blaOXA-23 gene in different isolates and determine their location in the target DNA, a cloning procedure was used. Some data had been reported for 6 of 20 isolates (11). Total DNA was digested with either SalI or Sall, ligated into the SalI or Sall sites of plasmid pBK-CMV (kanamycin-resistant cloning vector), and the recombinant plasmids were transformed into Escherichia coli TOP10, as described (14). Recombinant plasmids were selected on trypticase soy agar plates containing amoxicillin (50 mg/L) and kanamycin (30 mg/L). Cloned DNA fragments of several recombinants plasmids were sequenced on both strands by primer walking as described (11).

Results

Clonal Relatedness of the Isolates
Twenty carbapenem-resistant A. baumannii isolates were obtained from 15 countries (Table). All isolates were highly resistant to ticarcillin (MIC ≥256 mg/L) and showed a high level of resistance to ceftazidime (MIC ≥256 mg/L), except isolates Ab14 (MIC 4 mg/L) 861 and DOS (MIC 8 mg/L). All isolates were resistant to imipenem and meropenem (MIC ≥16 mg/L) (Table).

Multiplex PCR for identification of sequence groups showed 10 isolates that belonged to group 1 according to Turton et al. (18), eight that belonged to group 2, and 2 isolates that did not belong to groups 1 or 2. The 10 isolates that belonged to group 1 and corresponded to European clone II (18) were classified into 2 sequence types (STs), ST22 and ST53, according to MLST analysis (18). ST22 (1–3–3–2–2–7–3) was the most frequent type identified. Nine isolates were identified: 2 from France and 1 each from Vietnam, New Caledonia, Thailand, Australia, Ta-
to the A. baumannii recipient strain, except in 1 case (co-resistance to kanamycin and amikacin on a bla\textsubscript{OXA-23} carrying plasmid that originated from isolate 1190). Plasmids carrying the bla\textsubscript{OXA-23} gene in isolates Ab14, DOS, BEL, and 877 were not self-transferable (Table) (24).

**Table. Characteristics of 20 bla\textsubscript{OXA-23} Positive Acinetobacter baumannii clinical isolates**

| Isolate | Origin | Date of isolation | Specimen | EC | ST† | Copy no. of bla\textsubscript{OXA-23} | Genetic location and size, kb | Genetic structure | MIC, µg/mL |
|---------|--------|------------------|----------|----|-----|----------------------------|-----------------------------|------------------|-----------|
| 240     | France | 2003 Dec         | Tracheal aspirate | II | 22/2 | 1 | Chromosome, =200‡ | Tn2006 | 128 >32 >32 |
| 512     | Tahiti | 2004 Mar         | Tracheal aspirate | II | 22/2 | 1 | Chromosome, =200‡ | Tn2006 | 64 >32 >32 |
| 761     | Vietnam | 2005 May        | Bile | II | 22/2 | 1 | Chromosome, =200‡ | Tn2006 | 64 >32 >32 |
| 810     | New Caledonia | 2004 Jun | Blood | II | 22/2 | 1 | Chromosome, =200‡ | Tn2006 | 96 >32 >32 |
| 883     | Reunion | 2006 Jun        | Urine | II | 22/2 | 1 | Chromosome, =200‡ | Tn2006 | 256 >32 >32 |
| Ab13    | France | 2004 Jun | Unknown | II | 22/2 | 2 | Chromosome, =200‡ and plasmid, 70 | Tn2006 | 128 >32 >32 |
| AUS     | Australia | 2004 Oct | Urine | II | 22/2 | 1 | Chromosome, =200‡ | Tn2006 | 96 >32 >32 |
| 859     | South Africa | 2006 Jan | Urine | II | 22/2 | 1 | Chromosome, =200‡ | Tn2006 | 128 >32 >32 |
| 585     | France | 2004 Jul | Tracheal aspirate | II | 53/2 | 1 | Chromosome, =200‡ | Tn2006 | 128 >32 >32 |
| 614     | Libya | 2004 Oct | Unknown | I | 25/20 | 1 | Plasmid, 130 | ISABA\textsubscript{1} | 256 >32 | 16 |
| AS3     | UAE† | 2006 Oct | Blood | I | 25/20 | 1 | Plasmid, 130 | ISABA\textsubscript{1} | 256 >32 | 32 |
| 1190    | Bahrain | 2008 Mar | Blood | I | 25/20 | 1 | Plasmid, 130 | ISABA\textsubscript{1} | 256 >32 | 32 |
| AS1     | UAE | 2006 Jul | Blood | I | 44/1 | 1 | Plasmid, =40‡ >150 | Tn2007 | 4 16 >32 |
| Ab14    | Algeria | 2004 Dec | Unknown | I | 44/1 | 2 | Plasmid, 25, and plasmid, >150 | Tn2007 | 16 >32 |
| 910     | Reunion | 2006 Oct | Unknown | I | New1/1 | 1 | Plasmid, 130 | ISABA\textsubscript{1} | 256 16 | 16 |
| 861     | Egypt | 2005 Nov | Sputum | I | New1/1 | 1 | Plasmid, 130 | ISABA\textsubscript{1} | 8 32 | 32 |
| BEL     | Belgium | 2007 Jul | Respiratory tract | – | New2/1 | 2 | Plasmid, 25, and plasmid, >150 | Tn2007 | 256 32 >32 |
| DOS     | France | 2004 May | Unknown | – | New3/ New4/15 | 1 | Plasmid, 130 | ISABA\textsubscript{1} | 96 >32 >32 |
| 877     | Brazil | 2006 Jul | Wound | – | – | | | |

*EC, European clone; ST, sequence type; UAE, United Arab Emirates; CAZ, ceftazidime; IPM, imipenem; MEM, meropenem. The MIC for ticarcillin was >256 µg/mL for all 20 isolates.
†ST determined by Bartual et al. (19) compared with ST determined by Nemec et al. (20).
‡Size of chromosome band carrying the bla\textsubscript{OXA-23} gene, as determined by using the l-Cue technique.

**Variability of Genetic Structures Flanking the bla\textsubscript{OXA-23} Gene**

The 10 isolates that belonged to European clone II had a bla\textsubscript{OXA-23} gene that was part of Tn2006. The 9-bp direct repeat (DR) that corresponded to duplication of the Tn2006 target site, which was consistent with a transposition event, was identified in the 9 ST22/ST2 isolates. Tn2006 was inserted in different locations on the chromosomes of those isolates (Table). For isolates 240, 512, 810, 859, 883, and Aus, the insertion occurred between 2 genes encoding hypothetical proteins (DR: GTCATTTAA) (Figure 1). In isolate 761, transposon Tn2006 was located between a gene encoding a hypothetical protein and a gene encoding an isoleucyl tRNA synthase (DR: ATTCGCGGG). In isolate 863, Tn2006 was identified between a gene encoding a cytotoxic D terminale oxidase and a putative transposase (DR: ATAATTATT). In isolate 585, Tn2006 was located between a gene encoding a hypothetical protein and a sul gene (DR: ATTCGGGG). The plasmid-borne bla\textsubscript{OXA-23} gene identified in isolate Ab13 was also part of Tn2006 but was inserted into the sul gene that encoded a putative sulfonamide resistance determinant (DR: ATTCGGGG).

Isolates that belonged to European clone I had diverse genetic structures at the origin of bla\textsubscript{OXA-23} acquisition. Two isolates had transposon Tn2006: one on the chromosome (AS1) and 1 on a plasmid (910). Transposon Tn2007 was identified in 3 isolates; it was specific for the same open reading frame in 2 isolates (BEL and Ab14) (Figure 2).
Figure 2. Pulsed-field electrophoresis (PFGE) profiles of Apal-digested genomic DNA from strains of Acinetobacter baumannii. PFGE types, European clone types, and multilocus sequence typing (MLST) results are shown. *ST, sequence type determined by Bartual et al. (19) compared with ST determined by Nemec et al. (20). Lane M, molecular size markers (48.5 kb).

Only 1 copy of ISAbal was identified upstream of the bla\textsubscript{OXA-23} gene in isolates AS3, 1190, 861, and 877. Transposon Tn2008 was identified only in isolate 614 (Figure 1). Sequences of these specific genetic structures have been deposited in Genbank (accession nos. EF127491, EF059914, GQ861438, and GQ861439).

Discussion

This study was conducted to define which features may explain the worldwide dissemination of the bla\textsubscript{OXA-23} gene in A. baumannii. Isolates were from the Middle East, Europe, and Asia; there were no isolates from North America. Except for 2 isolates, the isolates investigated in this study belonged to European clones I or II. Clustering of A. baumannii isolates was determined by MLST and PFGE; our collection was composed of 13 PFGE types corresponding to 9 STs. Eight STs were identified among the OXA-23–producing A. baumannii; the most common STs were ST22/ST2 found in France (n = 2), Vietnam, New Caledonia, Thailand, Australia, Reunion, South Africa, and Tahiti. Spread of bla\textsubscript{OXA-23}–positive A. baumannii isolates that belong to clone ST22 has been demonstrated in South Korea (25). Analysis of the target site of bla\textsubscript{OXA-23} acquisition showed that in the same clone, such as ST22, acquisition of the Tn2006 composite transposon had occurred at different positions in the A. baumannii genome, which suggested that Tn2006-mediated acquisition of bla\textsubscript{OXA-23} may occur as independent events, or that Tn2006 is a structure that is mobile in a given genome. A single clone could have different genetic structures at the origin of the bla\textsubscript{OXA-23} acquisition.

We showed that the bla\textsubscript{OXA-23} gene associated with Tn2006 could be located on the chromosome or a plasmid. This result agrees with our recent findings, which showed that Tn2006 is capable of transposition (13). We have also observed that 5 isolates with different sequence types (ST-New1, ST25) harbored a similar 130-kb plasmid. The same strains with the same genetic structure were identified in 8 countries in different parts of the world.

In conclusion, the current worldwide dissemination of the bla\textsubscript{OXA-23} gene is driven by ≥7 MLST types associated with different genetic structures and plasmids. We have identified complex and dynamic spreading of bla\textsubscript{OXA-23} that will be difficult to control because this spread is not associated with a single entity.

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References

1. Perez F, Hujer AM, Hujer KM, Decker BK, Rather PN, Bonomo RA. Global challenge of multidrug-resistant Acinetobacter baumannii. Antimicrob Agents Chemother. 2007;51:3471–84. DOI: 10.1128/AAC.01464-06
2. Peleg AY, Seifert H, Paterson DL. Acinetobacter baumannii: mechanism and epidemiology. Clin Microbiol Infect. 2006;12:826–36. DOI: 10.1111/j.1469-0691.2006.01456.x
3. Scaife W, Young HK, Paton RH, Aymes GB. Transferable imipenem-resistance in Acinetobacter species from a clinical source. J Antimicrob Chemother. 1995;36:585–7. DOI: 10.1093/jac/36.3.585
4. Poirel L, Nordmann P. Carbapenem resistance in Acinetobacter baumannii: mechanism and epidemiology. Clin Microbiol Infect. 2006;12:585–93. DOI: 10.1111/j.1469-0691.2006.00987.x
5. Poirel L, Figueiredo S, Cattoir V, Carattoli A, Nordmann P. Carbapenem-resistant Acinetobacter baumannii: a silent source of carbapenem resistance for Acinetobacter spp. Antimicrob Agents Chemother. 2008;52:1252–6. DOI: 10.1128/AAC.01304-07
6. Stoeva T, Higgins PG, Bojkova K, Seifert H. Clonal spread of carbapenem-resistant OXA-23-positive Acinetobacter baumannii in a Bulgarian university hospital. Clin Microbiol Infect. 2008;14:723–7. DOI: 10.1111/j.1469-0691.2008.02018.x
7. Zhou H, Pi BR, Yang Q, Yu YS, Chen YG, Li LJ, et al. Dissemination of imipenem-resistant Acinetobacter baumannii strains carrying the ISAbal bla\textsubscript{OXA-23} gene in a Chinese hospital. J Med Microbiol. 2007;56:1076–80. DOI: 10.1099/jmm.0.47206-0
8. Carvalho KR, Carvalho-Assef AP, Peirano G, Santos LC, Pereira MJ, Asensi MD. Dissemination of multidrug-resistant \textit{Acinetobacter baumannii} genotypes carrying \textit{bla}_{OXA-23} collected from hospitals in Rio de Janeiro, Brazil. Int J Antimicrob Agents. 2009;34:25–8. DOI: 10.1016/j.ijantimicag.2008.12.009

9. Calhou JH, Murray CK, Manring MM. Multidrug-resistant organisms in military wounds from Iraq an Afghanistan. Clin Orthop Relat Res. 2008;466:1356–62. DOI: 10.1007/s11999-008-0212-9

10. Naas T, Levy M, Hirschauer C, Marchandin H, Nordmann P. Outbreak of carbapenem OXA-23 in a tertiary care hospital of Papeete, French Polynesia. J Clin Microbiol. 2005;43:4826–9. DOI: 10.1128/JCM.43.9.4826-4829.2005

11. Corvec S, Poirel L, Naas T, Druegon H, Nordmann P. Genetics and expression of the carbapenems-hydrolysing oxacillinase gene \textit{bla}_{OXA-23} in \textit{Acinetobacter baumannii}. Antimicrob Agents Chemother. 2007;51:1530–3. DOI: 10.1128/AAC.01132-06

12. Adams-Haduch JM, Paterson DL, Siddabat HE, Potsok BA, Muto CA, et al. Genetic basis of multidrug resistance in \textit{Acinetobacter baumannii} clinical isolates at a tertiary medical center in Pennsylvania. Antimicrob Agents Chemother. 2008;52:3837–43. DOI: 10.1128/AAC.00570-08

13. Muguier PD, Poirel L, Nordmann P. Functional analysis of insertion sequence \textit{ISAbal}, responsible for genomic plasticity of \textit{Acinetobacter baumannii}. J Bacteriol. 2009;191:2414–8. DOI: 10.1128/JB.01535-06

14. Muguier P, Poirel L, Pitout J, Nordmann P. Carbapenem-resistant and OXA-23 producing \textit{Acinetobacter baumannii} isolates in the United Arab Emirates. Clin Microbiol Infect. 2008;14:879–8. DOI: 10.1111/j.1469-0691.2008.01759.x

15. Muguier PD, Bindayna KM, Poirel L, Nordmann P. Diversity of plasmid-mediated carbapenem-hydrolysing oxacillinases among carbapenem-resistant \textit{Acinetobacter baumannii} isolates from Kingdom of Bahrain. J Antimicrob Chemother. 2009;63:1071–3. DOI: 10.1093/jac/dkp052

16. Clinical and Laboratory Standards Institute. Performance standards for antimicrobial susceptibility testing; 18th informational supplement. M100–S18. Wayne (PA): The Institute; 2008.

17. Dortet L, Legrand P, Soussy CJ, Carroir V. Bacterial identification, clinical significance, and antimicrobial susceptibilities of \textit{Acinetobacter ursingii} and \textit{Acinetobacter schindleri}, two frequently misidentified opportunistic pathogens. J Clin Microbiol. 2006;44:4471–8. DOI: 10.1128/JCM.01535-06

18. Turton JF, Gabriel SN, Valderrey C, Kaufmann ME, Pitt TL. Use of sequence-based typing and multiplex PCR to identify clonal lineages of outbreak strains of \textit{Acinetobacter baumannii}. Clin Microbiol Infect. 2007;13:807–25. DOI: 10.1111/j.1469-0691.2007.01759.x

19. Bartual SG, Seifert H, Hippler C, Lazon MA, Wisplinghoff H, Rodriguez-Valera F. Development of a multilocus sequence typing scheme for characterization of clinical isolates of \textit{Acinetobacter baumannii}. J Clin Microbiol. 2005;43:4382–90. DOI: 10.1128/JCM.43.9.4382-4390.2005

20. Nemec A, Krizova L, Maixnerova M, Diancourt L, Van der Reijden TJK, Brisse S, et al. Emergence of carbapenem resistance in \textit{Acinetobacter baumannii} in the Czech Republic is associated with the spread of multidrug resistant strains of European clone II. J Antimicrob Chemother. 2008;62:484–9. DOI: 10.1093/jac/dkn205

21. Liu SL, Hessel A, Sanderson KE. Genomic mapping with I-CeuI, an intron-encoded endonuclease specific for genes for ribosomal RNA, in \textit{Salmonella} spp., \textit{Escherichia coli}, and other bacteria. Proc Natl Acad Sci U S A. 1993;90:6874–8. DOI: 10.1073/pnas.90.14.6874

22. Poirel L, Guibert M, Bellois S, Naas T, Nordmann P. Integron- and carbencillinase-mediated reduced susceptibility to amoxicillin-clavulanic acid in isolates of multidrug-resistant \textit{Salmonella enterica} serotype typhimurium DT104 from French patients. Antimicrob Agents Chemother. 1999;43:1098–104.

23. Tenover FC, Arbeit RD, Goering RV, Mickelsen PA, Murray BE, Persing DH, et al. Interpreting chromosomal DNA restriction patterns produced by pulsed-field gel electrophoresis: criteria for bacterial strain typing. J Clin Microbiol. 1995;33:2233–9.

24. Bogaerts P, Cuzon G, Naas T, Baurain C, Deplano A, Lissoir B, et al. Carbapenem-resistant \textit{Acinetobacter baumannii} isolates expressing the \textit{bla}_{OXA-23} gene associated with IS\textit{Abad} in Belgium. Antimicrob Agents Chemother. 2008;52:4205–6. DOI: 10.1128/AAC.01121-08

25. Park YK, Choi JY, Jung SI, Park KH, Lee H, Jung DS, et al. Two distinct clones of carbapenem-resistant \textit{Acinetobacter baumannii} isolates from Korean hospitals. Diagn Microbiol Infect Dis. 2009;64:389–95. DOI: 10.1016/j.diagmicrobio.2009.03.029

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