Molecular epidemiology of carbapenem-nonsusceptible Acinetobacter baumannii in the United States

Jennifer M. Adams-Haduch
University of Pittsburgh - Main Campus

Ezenwa O. Onuoha
University of Pittsburgh - Main Campus

Tatiana Bogdanovich
University of Pittsburgh - Main Campus

Guo-Bao Tian
University of Pittsburgh - Main Campus

Jonas Marschall
Washington University School of Medicine in St. Louis

See next page for additional authors

Follow this and additional works at: https://digitalcommons.wustl.edu/open_access_pubs

Recommended Citation

This Open Access Publication is brought to you for free and open access by Digital Commons@Becker. It has been accepted for inclusion in Open Access Publications by an authorized administrator of Digital Commons@Becker. For more information, please contact engeszer@wustl.edu.
Molecular Epidemiology of Carbapenem-Nonsusceptible Acinetobacter baumannii in the United States

Jennifer M. Adams-Haduch, Ezenwa O. Onuoha, Tatiana Bogdanovich, Guo-Bao Tian, Jonas Marschall, Carl M. Urban, Brad J. Spellberg, Diane Rhee, Diane C. Halstead, Anthony W. Pascullle and Yohei Doi


Updated information and services can be found at: http://jcm.asm.org/content/49/11/3849

**REFERENCES**

These include:

This article cites 36 articles, 20 of which can be accessed free at: http://jcm.asm.org/content/49/11/3849#ref-list-1

**CONTENT ALERTS**

Receive: RSS Feeds, eTOCs, free email alerts (when new articles cite this article), more»

Information about commercial reprint orders: http://journals.asm.org/site/misc/reprints.xhtml

To subscribe to another ASM Journal go to: http://journals.asm.org/site/subscriptions/
Molecular Epidemiology of Carbapenem-Nonsusceptible Acinetobacter baumannii in the United States

Jennifer M. Adams-Haduch, Ezenwa O. Onuoha, Tatjana Bogdanovich, Guo-Bao Tian, Jonas Marshall, Carl M. Urban, Brad J. Spellberg, Diane Rhee, Diane C. Halstead, Anthony W. Pascuile, and Yohei Doi*

Division of Infectious Diseases, Clinical Microbiology Laboratory, University of Pittsburgh Medical Center, Pittsburgh, Pennsylvania; Animal Disease Prevention and Food Safety Key Laboratory of Sichuan Province, School of Life Sciences, Sichuan University, Chengdu, China; Division of Infectious Diseases, Washington University School of Medicine, St. Louis, Missouri; Infectious Disease Section, New York Hospital Queens, Flushing, New York; Division of General Internal Medicine, Harbor-UCLA Medical Center, Torrance, California; College of Pharmacy, University of Southern Nevada, Henderson, Nevada; and Jacksonville Pathology Consultants, P.A./Baptist Health, Jacksonville, Florida

Received 28 March 2011/Returned for modification 2 May 2011/Accepted 6 September 2011

Acinetobacter baumannii is emerging as an important nosocomial pathogen worldwide. We report molecular epidemiology of 65 carbapenem-nonsusceptible A. baumannii isolates identified from hospitals in New York, Pennsylvania, Florida, Missouri, Nevada, and California between 2008 and 2009. All isolates were subjected to pulsed-field gel electrophoresis (PFGE). Select isolates then underwent multilocus sequence typing (MLST). While the PFGE patterns tended to cluster within each hospital, sequence types (STs) belonging to the clonal complex 92 (CC92) and the pan-European clonal lineage II (EUI; worldwide clonal lineage 2) were predominant in all hospitals. Of them, ST122 and ST208 were the most common and were found in four of the six hospitals. Isolates belonging to the pan-European clonal lineages I and III were identified in one hospital each. Carbapenemase-encoding genes blaOXA-23 and/or ISAbA1-blaOXA-51-like were present among the majority of isolates. These findings suggest that carbapenem-nonsusceptible A. baumannii isolates found in U.S. hospitals constitute part of the global epidemic driven by CC92, but have unique STs other than ST92, which may be spreading by means of patient transfer between health care facilities within the United States.

Over the last decade, Acinetobacter baumannii has emerged to become an important cause of nosocomial infections in many parts of the world (25). Of great concern is the recent, remarkable rise in the frequency of carbapenem-nonsusceptible A. baumannii. According to data from the National Healthcare Safety Network (NHSN) surveillance system, 34% of A. baumannii isolates surveyed from U.S. hospitals between 2006 and 2008 were resistant to carbapenems, along with at least three other classes of antimicrobials, including ampicillin-sulbactam, antipseudomonal penicillins, broad-spectrum cephalosporins, fluoroquinolones, and aminoglycosides (16). In another nationwide survey, nonsusceptibility to carbapenems increased from 22% in 2002 to 52% in 2008 (20). Carbapenem-nonsusceptible A. baumannii infections are difficult to manage, as their therapy relies on salvage agents such as colistin and tigecycline. However, resistance to these agents is emerging among carbapenem-nonsusceptible A. baumannii isolates (8, 24).

Three clonal lineages of A. baumannii, commonly referred to as the pan-European clonal lineages (EUI, EUII, and EUIII), have predominated in many European countries since the 1990s (7). These clonal lineages have subsequently been identified worldwide, including in the United States (14, 36). It has thus been proposed to refer to them as the “worldwide” clonal lineages (WW1, WW2, and WW3) by some investigators (14).

Various molecular typing methods are employed to study the molecular epidemiology of A. baumannii. The most commonly used technique among them is pulsed-field gel electrophoresis (PFGE), which is highly discriminatory. However, PFGE is not well suited for interlaboratory comparisons unless the procedures are meticulously standardized (29), and its interpretation may pose a challenge in nonoutbreak situations (31). Repetitive sequence-based PCR, which is now commercially available, has operating characteristics similar to those of PFGE for A. baumannii (12, 28). Multilocus sequence typing (MLST), on the other hand, compares nucleotide sequences of housekeeping genes among isolates and generates objective and portable data. Three MLST schemes are currently used. The first MLST scheme for A. baumannii was published by Bontu et al. in 2005 (2), and it has subsequently been revised and employed to study the epidemiology of the organism in many countries (11, 13, 15, 17, 21, 23, 26, 28, 30). The second MLST scheme, which shares three of the loci with the original scheme, was developed by Diancourt et al. at the Pasteur Institute (http://www.pasteur.fr/recherche/genopole/PF8/mlst/Abaumannii.html) (6). The third scheme utilizes PCR and mass spectrometry (9). While MLST is an expensive typing method due to the need for DNA sequencing, selective use of
this technique can substantially enhance our understanding of molecular epidemiology across different hospitals and geographic areas.

The primary aim of the present study was to investigate the molecular epidemiology of contemporary carbapenem-nonsusceptible A. baumannii isolates collected from hospitals across the continental United States using MLST.

### MATERIALS AND METHODS

**Bacterial isolates.** A total of 65 carbapenem-nonsusceptible A. baumannii isolates were investigated. Only one isolate per patient was included. All isolates were identified from clinical specimens at hospitals across the United States between 2008 and 2009. The participating hospitals in New York, Pittsburgh, PA, and St. Louis, MO, have an ongoing collection of carbapenem-nonsusceptible A. baumannii isolates. From these hospitals, only one isolate was included for a given month. The hospitals in Jacksonville, FL, Las Vegas, NV, and Torrance, Los Angeles County, CA, collected serial carbapenem-nonsusceptible A. baumannii isolates for this study for 1 or 2 months in 2009. Only one isolate was included from each patient. The isolates were identified as A. baumannii using an automated instrument in each clinical microbiology laboratory (Microscan WalkAway [Siemens Healthcare Diagnostics, Deerfield, IL], Vitek 2 [bioMérieux, Durham, NC], or Phoenix 100 [BD, Franklin Lakes, NJ]). The identification as A. baumannii was subsequently confirmed by detection of blaOXA-51-like by PCR in the research laboratory (34). In addition, nonsusceptibility to carbapenems was confirmed by resistance to imipenem and/or meropenem using the disk diffusion method in the research laboratory located at the University of Pittsburgh.

**Susceptibility testing.** Susceptibility testing was performed following the methodology and breakpoints defined by the Clinical and Laboratory Standards Institute (CLSI) (5). Disk diffusion testing was used for the following agents: ampicillin-sulbactam, piperacillin-tazobactam, ceftazidime, cefepime, imipenem, meropenem, ciprofloxacin, gentamicin, and amikacin. For tigecycline, the Food and Drug Administration (FDA) breakpoints for Enterobacteriaceae (≤14 mm, resistant; ≥19 mm, susceptible) were used. In addition, MICs were determined for imipenem and meropenem using the agar dilution method.

**PFGE and MLST.** Pulsed-field gel electrophoresis (PFGE) was conducted using a CHEF DR III system (Bio-Rad, Hercules, CA) using Apal as the restriction enzyme, as described previously (1). BioNumerics version 6.01 (Applied Maths, Sint-Martens-Latem, Belgium) was used for pattern analysis, which utilizes the unweighted-pair group method. There are currently two multilocus sequence typing (MLST) schemes for A. baumannii which are widely utilized: one described by Bartual et al. (http://pubmlst.org/abaumannii/) (2) and one developed at the Pasteur Institute (http://www.pasteur.fr/mlst) (6). The two schemes share three of the seven loci. For the present study, we primarily used the Bartual scheme with modification of the primer sequences proposed by Martinovich et al. (19). For the purpose of comparison, we then selected one isolate from each sequence type (ST) obtained by the Bartual scheme and determined the corresponding ST based on the Pasteur Institute scheme. The new alleles and STs identified through this study have been deposited into the relevant databases. The relationship among the new and existing STs was surveyed by the use of the eBURST program (http://eburst.mlst.net/) (10).

**PCR and sequencing of carbapenemase-encoding genes.** Detection of blaOXA-51-like and the IS4110blaOXA-51-like complex was performed by PCR using primer sets and conditions described previously (18, 33). The presence of the IS4110blaOXA-51-like complex has been implicated in various degrees of carbapenem resistance in A. baumannii (33). PCR for the blaOXA-23, blaOXA-40, and blaOXA-58 genes, the three major groups of acquired carbapenemase-encoding genes that confer clinically relevant resistance to carbapenems, was conducted using a multiplex scheme (38). For sequencing, the full structural genes of blaOXA-23, blaOXA-40, and blaOXA-58 were amplified using primers described previously (18). Sequencing was performed on a 3730 DNA analyzer (Life Technologies, Carlsbad, CA).

### RESULTS

**Susceptibility of the carbapenem-nonsusceptible A. baumannii isolates.** Of a total of 67 isolates in the initial collection, two were found to be susceptible to both imipenem and meropenem in the research laboratory and were excluded. All of the remaining 65 isolates were positive for blaOXA-51-like by PCR. The numbers of isolates from each participating hospital were as follows: New York, 12; Pittsburgh, 10; St. Louis, 13; Jacksonville, 6; Las Vegas, 14; and Los Angeles, 10. The isolates were identified from various sources, including blood, sputum, bronchoalveolar lavage, wound, and urine specimens.

**Susceptibility testing results of the study isolates are shown in Table 1.** All isolates were nonsusceptible to meropenem, whereas 16 isolates (25%) were susceptible to imipenem by the disk diffusion method. All isolates that were intermediate to meropenem were susceptible to imipenem. Most isolates were nonsusceptible to β-lactams other than carbapenems, including piperacillin-tazobactam, ceftazidime, and cefepime. Of the β-lactams, susceptibility to ampicillin-sulbactam was relatively conserved, with 51% of the isolates being susceptible and another 26% intermediate. All isolates were susceptible to tigecycline when using the breakpoint for Enterobacteriaceae defined by the FDA. The MIC₅₀ and MIC₉₀ of imipenem were 16 and 64 μg/ml, respectively, whereas MIC₅₀ and MIC₉₀ of meropenem were 32 and 128 μg/ml, respectively (Table 2).

**Molecular typing.** The results of PFGE and MLST are summarized in Fig. 1, along with the information on the specimen sources and the hospital locations.

**PFGE.** PFGE was performed on all 65 isolates. Using a cutoff of 80% similarity, the isolates were grouped into 24 clusters (Fig. 1). The largest cluster contained 13 isolates from St. Louis and Pittsburgh. The second and third largest clusters had 7 and 6 isolates from New York and Los Angeles, respectively. Only one other cluster contained isolates from more than one hospital (one isolate each from Pittsburgh and Las Vegas).

**MLST.** At least one isolate from each cluster was selected for MLST. Overall, 36 of the 65 isolates were typed by MLST under the Bartual scheme. The STs

### Table 1: Susceptibility of 65 carbapenem-nonsusceptible A. baumannii isolates determined by the disk diffusion method

<table>
<thead>
<tr>
<th>Antimicrobial</th>
<th>Susceptible</th>
<th>Intermediate</th>
<th>Resistant</th>
</tr>
</thead>
<tbody>
<tr>
<td>Amoxicillin-sulbactam</td>
<td>33 (50.8)</td>
<td>17 (26.2)</td>
<td>15 (23.0)</td>
</tr>
<tr>
<td>Piperacillin-tazobactam</td>
<td>1 (1.5)</td>
<td>0 (0)</td>
<td>64 (98.5)</td>
</tr>
<tr>
<td>Ceftazidime</td>
<td>3 (4.6)</td>
<td>3 (4.6)</td>
<td>59 (90.8)</td>
</tr>
<tr>
<td>Cefepime</td>
<td>2 (3.1)</td>
<td>17 (26.1)</td>
<td>46 (70.8)</td>
</tr>
<tr>
<td>Imipenem</td>
<td>16 (24.6)</td>
<td>8 (12.3)</td>
<td>41 (63.1)</td>
</tr>
<tr>
<td>Meropenem</td>
<td>0 (0)</td>
<td>5 (7.7)</td>
<td>60 (92.3)</td>
</tr>
<tr>
<td>Ciprofloxacin</td>
<td>0 (0)</td>
<td>0 (0)</td>
<td>65 (100)</td>
</tr>
<tr>
<td>Gentamicin</td>
<td>13 (20.0)</td>
<td>0 (0)</td>
<td>52 (80.0)</td>
</tr>
<tr>
<td>Amikacin</td>
<td>16 (24.6)</td>
<td>5 (7.7)</td>
<td>44 (67.7)</td>
</tr>
<tr>
<td>Tigecycline</td>
<td>65 (100)</td>
<td>0 (0)</td>
<td>0 (0)</td>
</tr>
</tbody>
</table>

### Table 2: MICs of imipenem and meropenem for the 65 study isolates determined by the agar dilution method

<table>
<thead>
<tr>
<th>Antimicrobial</th>
<th>No. of isolates with MIC (μg/ml) of:</th>
<th>MIC (μg/ml)*</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>1</td>
<td>2</td>
</tr>
<tr>
<td>Imipenem</td>
<td>1</td>
<td>3</td>
</tr>
<tr>
<td>Meropenem</td>
<td>0</td>
<td>1</td>
</tr>
</tbody>
</table>

*50% and 90%, MIC₅₀ and MIC₉₀, respectively.
FIG. 1. PFGE and MLST results from the carbapenem-nonsusceptible study isolates. STs are based on the Bartual scheme.
based on the Bartual scheme. The five STs representing CC92 of the Pasteur Institute scheme for isolates representing each ST were then conducted MLST based on isolates would be assigned to CC92. If belonging to the same clonal complex, then 55 of the 65 clonal lineages based on MLST. The alleles and STs described in this study are summarized in Table 3.

<p>| TABLE 3. Sequence types and alleles of the carbapenem-nonsusceptible study isolates and select reference strains |
|---|---|---|---|---|---|
| ST by Bartual scheme | MLST by Bartual scheme | ST by Pasteur Institute scheme | MLST by Pasteur Institute scheme | City(ies) or reference strain |</p>
<table>
<thead>
<tr>
<th>gltA</th>
<th>ggyB</th>
<th>glhB</th>
<th>recA</th>
<th>cpn60</th>
<th>gpi</th>
<th>rpoD</th>
<th>Allele</th>
<th>Clonal complex</th>
<th>Allele</th>
<th>Clonal complex</th>
<th>Allele</th>
<th>Clonal complex</th>
</tr>
</thead>
<tbody>
<tr>
<td>122</td>
<td>1</td>
<td>3</td>
<td>61</td>
<td>2</td>
<td>2</td>
<td>7</td>
<td>3</td>
<td>92</td>
<td>2</td>
<td>2</td>
<td>2</td>
<td>2</td>
</tr>
<tr>
<td>123</td>
<td>1</td>
<td>35</td>
<td>61</td>
<td>2</td>
<td>2</td>
<td>3</td>
<td>3</td>
<td>92</td>
<td>2</td>
<td>2</td>
<td>2</td>
<td>2</td>
</tr>
<tr>
<td>124</td>
<td>1</td>
<td>17</td>
<td>60</td>
<td>10</td>
<td>28</td>
<td>66</td>
<td>32</td>
<td>113</td>
<td>79</td>
<td>26</td>
<td>2</td>
<td>2</td>
</tr>
<tr>
<td>203</td>
<td>41</td>
<td>1</td>
<td>72</td>
<td>32</td>
<td>1</td>
<td>98</td>
<td>6</td>
<td>Singleton</td>
<td>124</td>
<td>3</td>
<td>3</td>
<td>2</td>
</tr>
<tr>
<td>204</td>
<td>1</td>
<td>17</td>
<td>61</td>
<td>2</td>
<td>2</td>
<td>99</td>
<td>3</td>
<td>92</td>
<td>2</td>
<td>2</td>
<td>2</td>
<td>2</td>
</tr>
<tr>
<td>205</td>
<td>1</td>
<td>17</td>
<td>60</td>
<td>10</td>
<td>28</td>
<td>99</td>
<td>32</td>
<td>113</td>
<td>79</td>
<td>26</td>
<td>2</td>
<td>2</td>
</tr>
<tr>
<td>206</td>
<td>1</td>
<td>17</td>
<td>72</td>
<td>2</td>
<td>2</td>
<td>99</td>
<td>3</td>
<td>92</td>
<td>2</td>
<td>2</td>
<td>2</td>
<td>2</td>
</tr>
<tr>
<td>207</td>
<td>1</td>
<td>10</td>
<td>53</td>
<td>84</td>
<td>11</td>
<td>4</td>
<td>100</td>
<td>5</td>
<td>Singleton</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>208</td>
<td>1</td>
<td>3</td>
<td>61</td>
<td>2</td>
<td>2</td>
<td>97</td>
<td>3</td>
<td>92</td>
<td>2</td>
<td>2</td>
<td>2</td>
<td>2</td>
</tr>
<tr>
<td>345</td>
<td>46</td>
<td>12</td>
<td>122</td>
<td>1</td>
<td>16</td>
<td>141</td>
<td>50</td>
<td>Singleton</td>
<td>123</td>
<td>3</td>
<td>2</td>
<td>3</td>
</tr>
<tr>
<td>231</td>
<td>10</td>
<td>12</td>
<td>88</td>
<td>11</td>
<td>4</td>
<td>98</td>
<td>5</td>
<td>Singleton</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>207</td>
<td>10</td>
<td>53</td>
<td>84</td>
<td>11</td>
<td>4</td>
<td>100</td>
<td>5</td>
<td>Singleton</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>12</td>
<td>8</td>
<td>4</td>
<td>4</td>
<td>4</td>
<td>4</td>
<td>5</td>
<td>5</td>
<td>Singleton</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>206</td>
<td>1</td>
<td>3</td>
<td>61</td>
<td>2</td>
<td>2</td>
<td>97</td>
<td>3</td>
<td>92</td>
<td>2</td>
<td>2</td>
<td>2</td>
<td>2</td>
</tr>
<tr>
<td>6</td>
<td>1</td>
<td>4</td>
<td>3</td>
<td>2</td>
<td>2</td>
<td>3</td>
<td>3</td>
<td>92</td>
<td>2</td>
<td>2</td>
<td>2</td>
<td>2</td>
</tr>
<tr>
<td>112</td>
<td>1</td>
<td>12</td>
<td>56</td>
<td>36</td>
<td>1</td>
<td>61</td>
<td>26</td>
<td>Singleton</td>
<td>77</td>
<td>3</td>
<td>2</td>
<td>2</td>
</tr>
</tbody>
</table>

 identified included ST122 to -124, which we recently reported in isolates from Pittsburgh (32), as well as ST203 to -208 and ST345, which are new STs that were identified in the present study. The alleles and STs described in this study are summarized in Table 3.

ST122 was the most commonly observed ST, accounting for 14 of 36 isolates that were typed by MLST, followed by ST208, which was identified in 9 isolates. Both ST122 and -208 were found in four of the six hospitals. These STs belong to EUII and clonal complex 92 (CC92). CC92 is the most prevalent clonal complex worldwide, encompassing over 50 STs that have each been identified from many countries, including some from the United States (11, 13, 15, 17, 21, 23, 28, 32, 37). The next most common ST was ST204 (4 isolates), which along with ST206 (1 isolate) comprised isolates from three hospitals and also belonged to CC92. Three isolates belonged to CC113, which is commonly reported from Argentina and Brazil (http://pubmlst.org/abaumannii/). (12a). They included ST124 (1 isolate) and ST205 (2 isolates) from two hospitals. There were seven singleton STs, ST203, ST207, and ST345. ST203 was identified from New York and belonged to EUII. ST207 was identified from Los Angeles as a DLV of STs within CC109, which belongs to EUI. CC109 has been identified worldwide, including Europe, East Asia, and South America (http://pubmlst.org/abaumannii/). ST345, which was found in an isolate from Las Vegas, could not be categorized according to any of the three major pan-European clonal lineages based on MLST.

We only determined ST for approximately half of the study isolates. If we assume that isolates from the same PFGE cluster belong to the same clonal complex, then 55 of the 65 isolates would be assigned to CC92.

(ii) Pasteur Institute scheme. To examine how the two MLST schemes compare, we then conducted MLST based on the Pasteur Institute scheme for isolates representing each ST based on the Bartual scheme. The five STs representing CC92 under the latter scheme were all assigned to ST2 under the Pasteur Institute scheme (Table 3).

**Carbapenemase-encoding genes.** Twenty-seven of the 65 isolates (42%) were positive for blaoxa-23 by PCR. Thirty of them were subjected to sequencing of the entire gene, and they were all consistent with OXA-23, underscoring the homogeneity of this enzyme. blaoxa-23-positive isolates were found from all six hospitals and in multiple STs (ST122 and ST204 to -208). Nine isolates (14%) were positive for blaoxa-40. Seven of them were from ST123 isolates from New York and were found to encode OXA-72 upon sequencing, which is a single-amino-acid variant of OXA-40 (32). The other two isolates were from Pittsburgh (ST122) and Jacksonville (ST124) and encoded OXA-40. None of the isolates was positive for blaoxa-58. Forty-two isolates (65%) were positive for the ISAba1/blaoxa-51-ike complex, which may contribute to carbapenem resistance (33). Two isolates were negative for any of the carbapenemase genes mentioned above.

**DISCUSSION**

It is increasingly recognized that *A. baumannii* is clonal in nature and that a large part of the global epidemic of multidrug-resistant *A. baumannii* is driven by strains that belong to EUII, in particular those defined as CC92 by MLST (11, 15, 17, 21, 23, 28). In the United States, an outbreak of multidrug-resistant *A. baumannii* from a hospital in Houston that took place between 2005 and 2006 was caused by CC92 strains (30). A survey of bacteremic isolates collected from 52 U.S. hospitals between 1998 and 2004 also showed the preponderance of CC92 (37). Carbapenem resistance is becoming more and more common among *A. baumannii* isolates in U.S. hospitals in recent years (16, 20). It poses a substantial clinical challenge as therapeutic options are extremely limited for these organisms. This study was conducted to better understand the molec-
ular epidemiology of carbapenem-nonsusceptible *A. baumannii* in U.S. hospitals, with the aim of identifying predominant clonal lineages currently circulating in this country.

Our analysis revealed CC92 to be the most prevalent clonal complex, identified in isolates from all 6 participating hospitals. Interestingly, however, ST92, the predicted founder of CC92 and reported from a number of European and East Asian countries as well as Australia, was not found in this study. Instead, ST122, ST123, ST204, ST206, and ST208 were identified as CC92 STs, with predominance of ST122 and ST208, both of which were found in 4 of the 6 participating hospitals. While ST123 was only found in the hospital in New York in this study, we previously reported this ST from an isolate in Pittsburgh (32). To our knowledge, these STs have not been identified outside the United States. Furthermore, they share a predicted founder of CC92

Interestingly, however, ST92, the predicted founder of CC92 complexes of carbapenem-nonsusceptible isolates from all hospitals. Globally, *bla*<sub>OXA-23</sub> was the most prevalent acquired carbapenemase-encoding gene that is associated with carbapenem resistance (21). *bla*<sub>OXA-40</sub> and its variant *bla*<sub>OXA-72</sub> were found in isolates from three hospitals. The finding of isolates with *bla*<sub>OXA-23</sub> and *bla*<sub>OXA-72</sub> from the hospital in New York was noteworthy, since a previous comprehensive study describing resistance mechanisms of 40 multidrug-resistant *A. baumannii* isolates collected from hospitals in the area between 2001 and 2006 did not reveal the presence of acquired OXA-type carbapenemase-encoding genes (4). It is thus possible that an ST204 strain with *bla*<sub>OXA-23</sub> and an ST123 strain with *bla*<sub>OXA-72</sub> were introduced in the area between the two study periods.

While the primary scope of this study was molecular epidemiology, we also found that susceptibility to ampicillin-sulbactam was maintained in 33 of 65 isolates, all of which were nonsusceptible to at least one carbapenem tested. They included 12 *bla*<sub>OXA-23</sub>-positive isolates, 2 *bla*<sub>OXA-40</sub>-positive isolates, and 7 *bla*<sub>OXA-72</sub>-positive isolates. Sulbactam, the β-lactamase inhibitor component of this formulation, is known to have intrinsic activity against *A. baumannii*, which is believed to be due to its high affinity to certain penicillin-binding proteins (35). Several clinical studies have suggested that ampicillin-sulbactam may be clinically efficacious in the management of infections due to carbapenem-resistant *A. baumannii* (3, 22). While susceptibility to tigecycline was maintained well, we included only the initial isolate from each patient for this study. Since resistance to tigecycline may develop in subsequent isolates after exposure to this agent (24, 27), our results may underestimate the prevalence of nonsusceptibility on a per case basis.

The limitation of our study was that the isolates were collected in a relatively brief time period at some of the participating hospitals, which may not represent the overall epidemiology of carbapenem-nonsusceptible *A. baumannii* at those hospitals. Based on our findings, we plan to conduct a longitudinal surveillance study to further elucidate the epidemiology of this organism in the United States.

In conclusion, STs representing CC92 appear to be predominant among carbapenem-nonsusceptible *A. baumannii* isolates in U.S. hospitals, suggesting that they constitute part of the global epidemic driven by this clonal complex belonging to EUII. However, the finding that STs in CC92 were not ST92 but predominantly ST122 and ST208, which are thus far unique to the United States, suggests that these organisms may be spreading through transfer of colonized patients between health care facilities within the country.

**ACKNOWLEDGMENTS**

We thank Lenie Drijkshoorn for provision of the pan-European clonal lineage reference strains. We are also grateful to the curators of the MLST databases for their assistance (Sergio Bartual, Hilmar Wisplinghoff, and Laure Diancourt).

This study was funded by the National Institute of Allergy and Infectious Diseases (K22AI80584) and the Pennsylvania Department of Health (grant no. 4100047864).

**REFERENCES**


4. Bratu, S., et al. 2008. Correlation of antimicrobial resistance with β-lactamases, the OmpA-like porin, and efflux pumps in clinical isolates of *Acin-