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# Carbapenem-resistant *Acinetobacter baumannii* harboring a plasmid carrying blaOXA-72 in an outbreak involving an intensive care unit and long-term care facilities in Wisconsin.

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## Abstract

**Background:** *Acinetobacter baumannii* is an opportunistic pathogen implicated in a variety of healthcare-associated infections and is a concern in intensive care units. Here we report an outbreak during October 2018 involving patients in an intensive care unit (Facility A) in Wisconsin. Initially, *Acinetobacter baumannii* isolates with matching antimicrobial susceptibility (AST) profiles were identified in 5 patients in Facility A, suggesting the potential spread of a carbapenem resistant *Acinetobacter baumannii* (CRAB).

**Methods:** AST information was collected from three major clinical laboratories in the Wisconsin Clinical Laboratory Network on recent CRAB isolate submissions. An additional 3 isolates from Facility A and 1 isolate from Facility B were found to match the AST profile of the original 5 from Facility A. Isolates were submitted to the Wisconsin State Laboratory of Hygiene where sequencing was performed using both the Illumina MiSeq and the Oxford Nanopore Minion sequencing platforms. To identify if the resistance mechanism was plasmid-borne, genome assemblies were created using a short read and long read hybrid assembly method.

**Results:** Comparison of the 9 isolates by core genome and single nucleotide polymorphisms (SNPs) indicated that 6 of the 9 isolates were closely related, one of which was from Facility B. All six isolates contained a 10,879 bp plasmid carrying two copies of the OXA-24/40-like  $\beta$ -lactamase OXA-72. All 6 plasmids were identical at the nucleotide level, while one isolate had a 5,845 bp region that was reversed and flanked with XerC/XerD-like recombination sites. These plasmids were only 3 SNPs different from a previously published CRAB plasmid pAB120 (JX069966).

**Conclusion:** The combination of an established clinical laboratory network and strong laboratory and epidemiology communication helped identify a potential transmission route of this outbreak. These data helped identify a long-term care facility in Wisconsin (Facility C) as the connecting factor between Facility A and Facility B. Here we demonstrate the value in using AST as a method of prioritizing the use of valuable whole genome sequencing (WGS) resources on potential outbreak isolates. The combination of long read and short read WGS proved useful in the confirmation of outbreak isolates and identification of a plasmid-borne OXA-72.

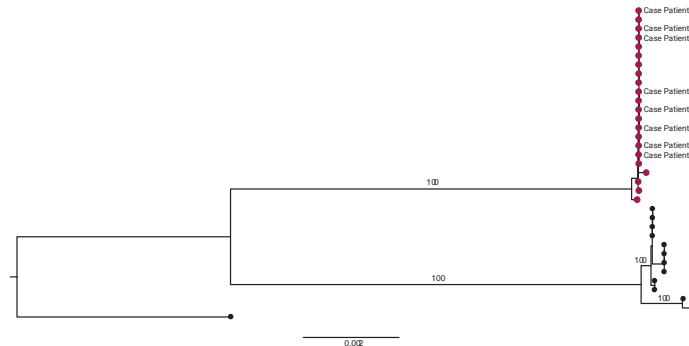
## Antimicrobial Susceptibility (AST) Profile

**Amikacin:** Resistant  
**Aztreonam:** Resistant  
**Cefepime:** Resistant  
**Cefotaxime:** Resistant  
**Ceftazidime:** Resistant  
**Ciprofloxacin:** Resistant  
**Colistin:** Susceptible  
**Doripenem:** Resistant  
**Doxycycline:** Resistant  
**Gentamicin:** Resistant  
**Imipenem:** Resistant  
**Levofloxacin:** Resistant  
**Meropenem:** Resistant  
**Minocycline:** Intermediate  
**Piperacillin-tazobactam:** Resistant  
**Polymyxin-B:** Susceptible  
**Ticarcillin-clavulanate:** Resistant  
**Tobramycin:** Resistant  
**Trimethoprim-sulfamethoxazol:** Resistant

JX069966 - 1. J. Povelonis et al., Spread of carbapenem-resistant *Acinetobacter baumannii* carrying a plasmid with two genes encoding OXA-72 carbapenemase in Lithuanian hospitals. J. Antimicrob. Chemother. 68, 1000-1006 (2013).

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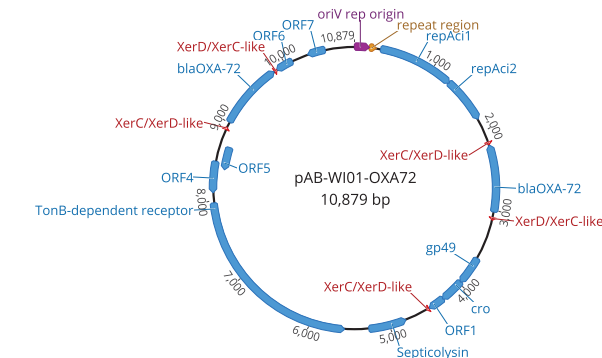
## Core-Genome Maximum Likelihood Tree



## Single Nucleotide Polymorphism (SNP) Difference

	Case Patient 1	Case Patient 2	Case Patient 3	Case Patient 4	Case Patient 5	Case Patient 6	Case Patient 7	Case Patient 8
Case Patient 1	0	3	4	0	5	8	9	5
Case Patient 2	3	0	3	3	4	7	7	2
Case Patient 3	4	3	0	4	5	6	7	3
Case Patient 4	0	3	4	0	5	8	9	4
Case Patient 5	5	4	5	5	0	8	10	4
Case Patient 6	8	7	6	8	8	0	9	7
Case Patient 7	9	7	7	9	10	9	0	9
Case Patient 8	5	2	3	4	4	7	9	0

## OXA-72 Plasmid



## Epidemiological Social-Network

