

# Genetic Analysis of Antibiotic Resistance Profiles of *Acinetobacter baumannii* Using Whole Genome Sequencing

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## Introduction

- Acinetobacter spp.* is a gram-negative coccobacilli involved in many healthcare-associated infections (HAIs), especially in the critically ill hospitalized patients.
- These infections are increasingly difficult to treat as they are known to quickly develop resistance to commonly used antibiotics. Therefore, surveillance studies are important and provide a snapshot of prevalent antibiotic resistance profiles in an area.
- In this study, we sought to characterize antibiotic resistance patterns in clinical *Acinetobacter* isolates by performing whole genome sequencing (WGS) and whole genome multi-locus sequence typing (wgMLST) analysis, and *in silico* analysis for antibiotic resistance genes.



Adapted from: <https://www.sciencephoto.com/media/843265/view/acinetobacter-baumannii-bacteria-illustration>

## Methods

- The *Acinetobacter* isolates were provided from two tertiary Detroit area hospitals from patients admitted to 16 different intensive care units (ICU) and non-ICU wards between 2017-2019.
- Samples were subjected to WGS using the NextSeq instrument (Illumina). The contigs were *de novo* assembled using SPAdes (v3.7.1) and wgMLST analysis was performed using BioNumerics software v7.6.
- The genomic sequence for each isolate was uploaded in ResFinder 3.2 and known antibiotic resistance genes were analyzed.

Hospital	Unit	ST	ST	ST	ST	ST	ST	ST	ST
Hospital 1	Unit A	ST2	ST15	ST36			ST119		ST406
	Unit B	ST2		ST36	ST49	ST93		ST212	ST406
	Unit C	ST2	ST15						ST406
	Unit D								ST406
	Unit E								ST406
	Unit F								ST406
Hospital 2	Unit G	ST2						ST214	ST406
	Unit H	ST2	ST15						ST427
	Unit I	ST2						ST268	ST427
	Unit J	ST2						ST395	
	Unit K	ST2							
	Unit L	ST2							

Table 1: Sequence Types (ST) arranged by hospital and by unit. Geographic room locations are not represented here; arranged for visual clarity only.

Hospital 1		
Sequence Type (ST)	Total No. of Isolates	Resistance to Antibiotic Drugs
ST2	11	β-lactam, aminoglycoside, sulphonamide, phenicol, macrolide, tetracycline
ST15	2	β-lactam, aminoglycoside, sulphonamide
ST36	2	β-lactam
ST49	1	β-lactam
ST93	5	β-lactam
ST119	2	β-lactam
ST212	1	β-lactam
ST406	4	β-lactam, aminoglycoside, sulphonamide
ST667	1	β-lactam

Table 2: ST and genetic resistance expression in Hospital 1

Hospital 2		
Sequence Type (ST)	Total No. of Isolates	Resistance to Antibiotic Drugs
ST2	20	β-lactam, aminoglycoside, sulphonamide, phenicol, macrolide, tetracycline
ST15	1	β-lactam, aminoglycoside, sulphonamide
ST20	1	β-lactam, aminoglycoside, sulphonamide, phenicol, macrolide, tetracycline
ST214	1	β-lactam
ST268	1	β-lactam
ST395	1	β-lactam
ST406	1	β-lactam, aminoglycoside, sulphonamide
ST427	2	β-lactam

Table 3: ST and genetic resistance expression in Hospital 2

Hospital 1:		
Antibiotic Drugs	Antibiotic Resistance Genes	% of isolates with Antibiotic Resistance Genes
Aminoglycoside	aadA1	72
	aadA2	9
	armA	72
	ant(2'')-Ia	9
	aph(3'')-Ib	81
	aph(3')-Via	9
	aph(3')-Ia	81
	aph(6)-Id	81
	aac(3)-Ia	9
Aminoglycoside/Quinolone	aac(6')-Ib3	63
	aac(6')-Ib-cr	63
Phenicol	catB8	63
Macrolide	mph(E)	72
	msr(E)	72
Sulphonamide	sul1	90
	sul2	9
Tetracycline	tet(B)	81
	blaADC-25	100
	blaOXA-23	27
	blaOXA-66	81
	blaOXA-82	18
Betalactam	blaTEM-1D	72

Table 4: ST resistance genes breakdown by percentage present in Hospital 1

Hospital 2:		
Antibiotic Drugs	Antibiotic Resistance Genes	% of isolates with Antibiotic Resistance Genes
Aminoglycoside	aadA1	30
	aadA2	15
	armA	70
	ant(2'')-Ia	15
	aph(3'')-Ib	80
	aph(3')-Via	40
	aph(3')-Ia	70
	aph(6)-Id	80
	aac(3)-Ia	5
Aminoglycoside/Quinolone	aac(6')-Ib3	25
	aac(6')-Ib-cr	30
Phenicol	catB8	30
Macrolide	mph(E)	80
	msr(E)	80
Sulphonamide	sul1	40
	sul2	10
Tetracycline	tet(B)	80
	blaADC-25	100
Betalactam	blaOXA-223	5
	blaOXA-23	80
	blaOXA-66	20
	blaOXA-82	15
	blaTEM-1D	35

Table 5: ST resistance genes breakdown by percentage present in Hospital 2

## Results

- ST2 was the most prevalent sequence type (ST) accounting for 52% in both hospitals. Please check poster by Chatterjee *et al.* and as presented in Table 1.
- The most common resistance gene found is blaADC-25 conferring resistance to beta-lactams across all STs. See tables 2 and 3.
- Sulfonamide (sul1) and macrolide resistance (mphE/msrE) among STs were also common. See tables 4 and 5.
- ST2 in H2 exhibited the presence of the maximum number of resistance genes including resistance to aminoglycosides, macrolides (2), tetracyclines (tetB), beta-lactams, fluoroquinolones (aac(6')-Ib-cr), sulphonamides (sul1, sul2). See table 5.
- ST2 had a slightly different resistance profile of beta-lactams in H1 when compared to H2. See tables 4 and 5.
- ST406 and ST15 exhibited similar antibiotic profiles in both hospitals and a single isolate of ST20 from H2 is highly antibiotic resistant. See tables 2 and 3.

## Conclusions

- Acinetobacter* infection is a known HAI problem which has necessitated emerging new treatments.
- We provide a snapshot of resistance genes identified. All the hospital isolates demonstrated resistance to beta-lactams and some with similar antibiotic resistance profiles.
- No colistin resistance genes were identified by *in silico* analysis.
- In future practices, monitoring for genetic subtypes and encoded genetic resistance may prove useful for better infection control practices and clinical practice.

## Acknowledgements

Funding- This project is supported by AHRQ 1R01HS024709-04, 1R03 HS 027667-01 and support was also provided by the Central Texas Veterans Healthcare System (CTVHCS) facility during the study period.