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Molecular Characterization and Resistance Factors of Circulating *Acinetobacter baumannii* isolates in South-East Michigan

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Introduction

- *Acinetobacter* is a gram-negative ESKAPE pathogen of rising concern
- Carbapenem-resistant *Acinetobacter baumannii CRAb)* is increasing due to widespread use of antibiotics.
- The ***objective*** of this study is to elucidate the molecular epidemiology of circulating antibiotic resistance genes causing multidrug resistant infections by using a combination of whole-genome sequencing and antibiotic susceptibility phenotyping.

Methods

- Bacterial isolates were derived from cultures taken from subjects 48 hours following admission as part of routine clinical care for patients between 2017-2020.
- Isolates were obtained from 16 hospital units (both ICU and non-ICU) across two hospitals in the Detroit area. Whole Genome Sequencing (WGS) was performed using Illumina MiniSeq or Nextseq.
- WgMLST analysis was performed using BioNumerics software v7.6. ResFinder software was used for analysis of antibiotic resistance genes.
- Isolates underwent antibiotic susceptibility testing using a broth microdilution method (VITEK2) and Clinical & Laboratory Standards Institute (CLSI) inhibitory concentration (MIC) cut offs were used to determine resistance phenotypes.

Results

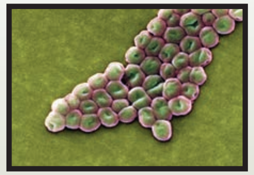

Figure 1: *Acinetobacter baumannii* scanning electron micrograph (SEM). Adapted from CDC/Science PhotoLibrary.

	ST Type		Antimicrobial Susceptibility				Betalactam Genes			
Sample	**Oxford**	**Pasteur**	**Aminoglycoside**	**β-lactam**	**Quinolone**	**Carbapenem**	*blaADC-25*	*blaOXA-23*	*blaOXA-66*	*blaTEM-1D*
1	ST195	ST2	R	R	R	R	99.83	100	100	100
2	ST195	ST2	R	R	R	R	99.83	100	100	100
3	ST195	ST2	R	R	R	R	99.83	100	100	100
4	ST195	ST2	R	R	R	R	99.83	100	100	100
5	ST195	ST2	R	R	R	R	99.83	100	100	100
6	ST195	ST2	R	R	R	R	99.83	100	100	100
7	ST195	ST2	R	R	R	R	99.83	100	100	100
8	ST195	ST2	R	R	R	R	99.83	100	100	100
9	ST195	ST2	R	R	R	R	99.83	100	100	100
10	ST195	ST2	R	R	R	R	99.83	100	100	100
11	ST195	ST2	R	R	R	R	99.83	100	100	100
12	ST208	ST2	R	R	R	R	99.91	100	100	100
13	ST208	ST2	R	R	R	R	99.91	100	100	100
14	ST208	ST2	R	R	R	R	99.83	100	100	100
15	ST208	ST2	R	R	R	R	99.91	100	100	-
16	ST208	ST2	R	R	R	R	99.91	99.64	100	100
17	ST208	ST2	R	R	R	R	99.91	-	100	100
18	ST208	ST2	R	R	R	R	99.91	100	100	100
19	ST208	ST2	R	R	R	R	99.91	100	100	100
20	ST208	ST2	R	R	R	R	99.91	100	100	100
21	ST2768	ST406	R	R	R	R	99.65	100	-	-

Table 1: Molecular characterization of MDR *CRAb* isolates.

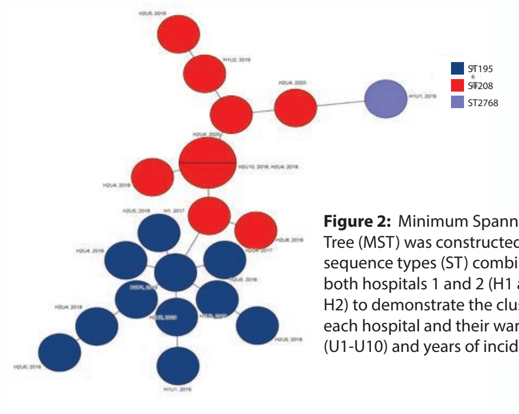

Figure 2: Minimum Spanning Tree (MST) was constructed for all sequence types (ST) combining both hospitals 1 and 2 (H1 and H2) to demonstrate the clusters in each hospital and their wards (U1-U10) and years of incidence.

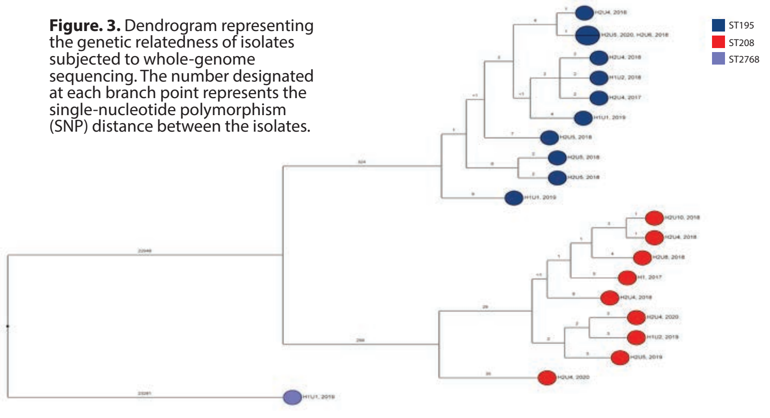

Figure. 3. Dendrogram representing the genetic relatedness of isolates subjected to whole-genome sequencing. The number designated at each branch point represents the single-nucleotide polymorphism (SNP) distance between the isolates.

ST2^{Pas}/ST195^{Ox}			ST2 ^{Pas}/ST208^{Ox}			ST406 ^{Pas}/ST310 like ^{Ox}		
Hospital-ward	**# of isolates**	**Year**	**Hospital-ward**	**# of isolates**	**Year**	**Hospital-ward**	**# of isolates**	**Year**
H1 U1	2	2019 (1), 2020 (1)	**H1 U1**	1	2017 (1)	**H1 U1**	1	2019 (1)
H1 U2	1	2018 (1)	**H1 U2**	1	2018 (1)			
H2 U4	3	2017 (1), 2018 (2)	**H2 U4**	4	2018 (2), 2020 (2)			
H2 U5	4	2018 (3), 2020 (1)	**H2 U5**	1	2019 (1)			
H2 U6	1	2018 (1)						
			H2 U8	1	2018 (1)			
			H2 U10	1	2018 (1)			
Total	11		**Total**	9		**Total**	1	

Table 2: Different Sequence Types (STs) distribution among the two hospitals and wards along with the year of incidence reported.

Conclusions

- The study demonstrated that all MDR CRAb isolates belonged to ST2^{Pas} (ST195^{OX} and ST208^{OX}) carrying multiple beta-lactamase genes including blaOXA-23 gene except one isolate belonging to ST406^{Pas} (ST2768^{OX}) lineage also carry the blaOXA-23 gene.
- Several cases of closely related MDR *CRAb* pairs have been found at hospital H2 in 2018. Potential cases of localized outbreaks of MDR *CRAb* is suspected.
- Continuous surveillance is recommended in limiting the spread of MDR *CRAb* isolates in the healthcare settings.

References

Kyriakidis I, Vasileiou E, Pana ZD, Tragiannidis A. Acinetobacter baumannii Antibiotic Resistance Mechanisms. Pathogens. 2021 Mar 19;10(3):373. doi: 10.3390/pathogens10030373 PMID: 33808905

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