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786. Facility Reported vs. CLSI MIC Breakpoint Comparison of Carbapenem Non-susceptible (Carb-NS) *Pseudomonas aeruginosa* (PSA) From 2016-2019: A Multicenter Evaluation

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Session: P-39. HAI: Gram-negatives (MDR-GNR)

Background. CLSI lowered *Pseudomonas aeruginosa* (PSA) Carbapenem (Carb) interpretive breakpoint minimum inhibitory concentrations (MICs) in 2012. It often takes several years for commercial test manufacturers and microbiology labs to incorporate revised breakpoints. We compare facility-reported rates of Carb-NS PSA to the 2012 CLSI MIC breakpoints, using a large nationwide database for isolates tested in 2016-2020 at United States (US) facilities.

Table. Imipenem (IPM)/meropenem (MEM)/doripenem (DOR) interpretation (evaluable isolates) results for PSA.

IPM/MEM/DOR interpretations for PSA			
Interpretation (MIC; µg/mL)	**Facility Reported: n (%)**	**Revised per CLSI: n (%)**	**Underreporting by Facility vs. Revised per CLSI (%)**
I (4)	9,537 (3.7%)	10,335 (4.0%)	7.7%
R (>=8)	29,109 (11.4%)	32,488 (12.7%)	10.4%
S (<=2)	217,198 (84.9%)	213,021 (83.3%)	
Total	**255,844**	**255,844**	

Methods. All adults with a positive non-contaminant PSA culture (first isolate per 30-day period from blood, respiratory, urine, skin/wound, intra-abdominal, or other) in ambulatory and inpatient settings from 298 US hospitals from Q1 2016-Q4 2020 were evaluated (BD Insights Research Database, Becton, Dickinson & Company). Facility-reported Carb-non susceptible (NS) was defined as lab information system feed designations of susceptible (S), intermediate (I) or resistant (R) to imipenem (IPM), meropenem (MEM) and/or doripenem (DOR) per commercial panels. Where available, MICs were interpreted using CLSI 2012 Carb breakpoints (µg/ml) of ≤2 (S), 4 (I), ≥8 (R) for IPM/MEM/DOR. For evaluable PSA isolates we compared susceptibility results as reported by the facility to those using CLSI MIC breakpoints.

Results. Overall, 86.9% (255,844/294,426) of non-duplicate PSA isolates with facility-reported IPM/MEM/DOR susceptibility interpretations also had interpretable MIC results. S rates were 84.9% and 83.3% as reported by facilities and determined by CLSI criteria, respectively (Table). Facilities under-reported Carb-NS by 9.8%, using CLSI criteria as the standard (10.4% and 7.7% of R and I isolates, respectively, were missed by facility reporting).

Conclusion. Systematic application of CLSI breakpoints in 2016-20 would have had minimal impact on PSA S rates in the US. However, facility reporting failed to identify ~10% of Carb-NS isolates. The clinical implications of this observation are unknown. Facilities should know their local epidemiology, decide if under-reporting might be an issue, and assess if there is any impact on their patients.

Disclosures. **Vikas Gupta, PharmD, BCPS**, **Becton, Dickinson and Company** (Employee, Shareholder) **Kalvin Yu, MD**, **BD** (Employee) **Jason M Pogue, PharmD, BCPS, BCIDP**, **Merck** (Consultant)**QPex** (Consultant)**Shionogi** (Consultant)**Utility Therapeutics** (Consultant)**VenatoRX** (Consultant) **Janet Weeks, PhD**, **Becton, Dickinson and Company** (Employee) **Cornelius J. Clancy, MD**, **Merck** (Grant/Research Support)

787. Clinical and Genomic Epidemiology of *mcr-9* Containing Carbapenem-resistant *Enterobacterales* Isolates in Metropolitan Atlanta, 2012-2017

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Session: P-39. HAI: Gram-negatives (MDR-GNR)

Background. Colistin is a last-resort antibiotic for multidrug resistant gram-negative infections. Recently, a new allele of the mobile colistin resistance (*mcr*) gene family designated *mcr-9,* has been reported. However, its clinical and phenotypic significance remains unclear.

Methods. The Centers for Diseases Control and Prevention-funded Georgia Emerging Infections Program (EIP) performs population- and laboratory- based surveillance for CRE isolated from sterile sites or urine in metropolitan Atlanta, GA including standardized chart abstraction. We queried genomes of carbapenem-resistant Enterobacterales (CRE) for *mcr-9* from a convenience sample of Georgia EIP clinical isolates between 2012-2017. Isolates underwent phenotypic characterization by broth microdilution and population analysis profiling. Nine available *E. cloacae* (two *mcr-9* positive, seven *mcr-9* negative) genomes from the National Institutes of Health were included in downstream genomic analysis. Fastq files underwent *de novo* assembly, annotation and AMR and virulence gene prediction, pan-genome association analysis, pairwise comparisons of average nucleotide identity and phylogenetic tree construction based on core genes. We compared characteristics and outcomes of *mcr-9* positive and negative CRE cases.

Results. Among 449 sequenced CRE genomes, thirteen (2.9%) were found to harbor *mcr-9*, all of which were *E. cloacae.* Fourteen *mcr-9* negative E. *cloacae* (n=14) were included as a comparative group. *E. cloacae* was most commonly isolated from the urine (22/24, 86%), and none were community associated. The median colistin MIC, rates of heteroresistance and inducible resistance were similar between *mcr-9* positive and negative isolates (Table 1). 90-day mortality was high in both *mcr-9* positive (31%) and negative (7% cases (p=0.28, Table 1). Phylogenetic analysis revealed no geo-temporal clustering (Figure 1). Plasmid-associated genes were significantly associated with the presence of *mcr-9* (p< 0.001). Phylogeny and average nucleotide identity heatmap of mcr-9 positive and mcr-9 negative E. cloacae.

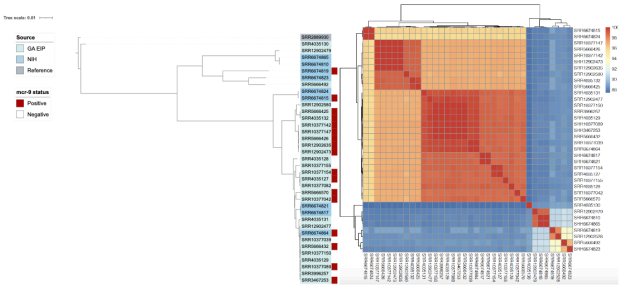

Figure Legend 1: Phylogeny and average nucleotide identity heatmap of mcr-9 positive (n=13) and mcr-9 negative (n=14) E. cloacae from Georgia Emerging Infection program in addition to 9 available E. cloacae (two mcr-9 positive, seven mcr-9 negative) from the National Institutes of Health. A phylogenetic tree based on a core gene alignment containing 1,904 genes defined using Roary v3.13.0. was generated using IQtree v2.0.3. A maximum likelihood tree was generated by running 1,000 bootstrap replicates under the generalized time-reversible model of evolution. The tree was visualized and annotated using Interactive Tree of Life (iTOL) v4. Pairwise comparisons of average nucleotide identity on the assembled genomes were performed with the Mashmap method using fastANI v1.32. Abbreviations: GA EIP: Georgia Emerging Infection Program, NIH: National Institutes of Health,

Table 1: Carbapenem-resistant E. cloacae clinical and microbiological characteristics

	All (n=27)	**MCR-9 positive (n=13)**	**MCR-9 negative * (n=14)**	***P* value**
Culture Source				0.33
Urine	24 (88.9)	12 (92.3)	12 (85.7)	
Blood	2 (7.4)	1 (7.7)	1 (7.1)	
Peritoneal Fluid	1 (3.7)	0 (0.0)	1 (7.1)	
Year				0.62
2012	1 (3.7)	1 (7.7)	0 (0.0)	
2013	8 (29.6)	2 (15.4)	6 (42.9)	
2014	2 (7.4)	1 (7.7)	1 (7.1)	
2015	3 (11.1)	3 (23.1)	0 (0.0)	
2016	9 (33.3)	4 (30.8)	5 (35.7)	
2017	4 (14.9)	2 (15.4)	2 (14.3)	
Infection Onset				0.71
Hospital Onset	3 (11.1)	2 (15.4)	1 (7.1)	
Healthcare Associated-Community Onset	10 (37.0)	4 (30.8)	6 (42.9)	
Long Term Care Facility Onset	14 (51.9	7 (50.0)	7 (53.8)	
Microbiology Characteristics				
Colistin MIC (median[range])**	0.5 [0.249-8.1]	0.5 [0.249-1.00]	0.5 [0.249-8.1]	0.11
Resistant	3 (11.1)	0	3 (21.4)	0.25
Heteroresistant	12 (44.4)	8 (36.4)	4 (27.3)	0.33
Inducible resistance	4 (14.8)	0 (0.0)	1 (12.5)	0.18
Outcomes				
Hospitalization within 29 days after culture	10 (37.0)	5 (38.5)	5 (35.7)	0.86
ICU admission ***^	4 (40.0)	2 (40.0)	2 (40.0)	1.00
In-hospital mortality ^	1 (10.0)	1 (10.0)	0 (0.0)	0.59
90-day Mortality	5 (18.5)	4 (30.8)	1 (7.1)	0.28

*1 mcr-10 positive isolate ** measured by broth microdilution *** Any ICU admission 7 days prior or 6 days after specimen collection ^ among 10 hospitalized patients

Conclusion. The presence of *mcr-9* was not associated with significant changes in colistin resistance or clinical outcomes.

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788. *Enterobacter cloacae* Infection Characteristics and Outcomes in Military Personnel who Sustained Trauma in Iraq and Afghanistan

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