and public health need. Patients may have multiple isolates. The 7 AR Lab Network regional laboratories used matrix-assisted laser desorption ionization-time of flight (MALDI-TOF) or DNA sequencing for species identification. AFST was performed using broth microdilution for azoles and echinocandins (anidulafungin and micafungin) and Etest for amphotericin B. This analysis focuses on non-*albicans Candida* species with Clinical and Laboratory Standards Institute M60 minimum inhibitory concentration breakpoints and *C. auris*, which has CDC-proposed tentative breakpoints.

Results: Participation increased from healthcare facilities from 2 states submitting in 2016 to 35 states in 2019. Species identification was performed on 5,234 non-*albicans* isolates. AFST was performed on 4,222 (81%) isolates, including 2,395 *C. glabrata*, 815 *C. auris*, 267 *C. parapsilosis*, 125 *C. tropicalis*, 35 *C. guilliermondii*, and 32 *C. krusei*. Of isolates with AFST and body site indicated, 22% (900/4,102) were from blood. We found 85% of *C. auris*, 8% of *C. glabrata*, and 5% of *C. parapsilosis* isolates were resistant to azoles; 33% of *C. auris* isolates were resistant to amphotericin B; and 2% of *C. glabrata*, 1% of *C. auris*, and 1% of *C. parapsilosis* isolates were resistant to echinocandins. Although intrinsically resistant to fluconazole, *C. krusei* isolates were not resistant to voriconazole. Multidrug resistance was present in 32% of *C. auris* and 1% of *C. glabrata* isolates.

Conclusion: AR Lab Network has expanded access to rapid *Candida* testing, including AFST, and provides real-time surveillance. Results can be used to detect emerging species and resistance and guide public health action and healthcare practices.

Disclosures: **All Authors**: No reported disclosures

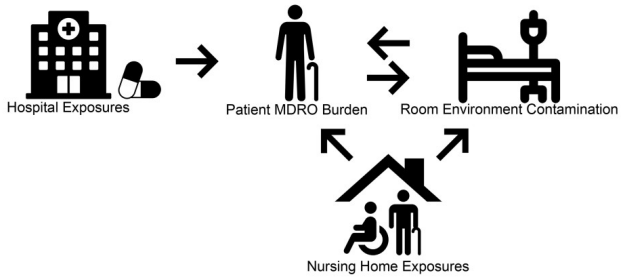
156. How Does Exposure to C. Diffogenic Antibiotics Impact Multidrug-resistant Organism Colonization and Environment Contamination in Nursing Homes?

Kyle J. Gontjes, MPH[1]; Kristen Gibson, MPH[2]; Bonnie Lansing, LPN[2]; Julia Mantey, MPH, MUP[2]; Karen Jones, MPH, RN, CIC[2]; Marco Cassone, MD, PhD[2]; Joyce Wang, PHD[2]; John Mills, MD[2]; Lona Mody, MD, MS[2]; Payal K. Patel, MD, MPH[2]; [1]University of Michigan Medical School, Ann Arbor, Michigan; [2]University of Michigan, Ann Arbor, Michigan

Session: O-30. MDRO Epidemiology and Transmission

Background: Antimicrobial stewardship program (ASP) outcomes are often measured in the acute care setting, less is known about the effect of acute care antibiotic exposures on multidrug-resistant organism (MDROs) colonization of nursing home (NH) patients. We assessed exposure to antibiotics commonly associated with *Clostridioides difficile* (C. diffogenic agents) on post-acute care patient colonization and room environment contamination (Figure 1).

Figure 1. Conceptual Diagram of Hospital Antibiotic Exposure's Influence on Patient Colonization and Room Environment Contamination with Multidrug-Resistant Organisms



Methods: MDRO surveillance of post-acute care patients in 6 NHs between 2013–16. We screened patient hands, nares, oropharynx, groin, perianal area, and high-touch room environment surfaces for methicillin-resistant *Staphylococcus aureus* (MRSA), vancomycin-resistant enterococci (VRE), and resistant Gram-negative bacilli (rGNB). C. diffogenic agents were defined as fluoroquinolones, 3rd/4th generation cephalosporins, penicillin combinations, lincosamides, and carbapenems. Multivariable logistic regression was used to assess whether hospital antibiotic exposure is an independent risk factor for MDRO colonization and room environment contamination on study enrollment.

Results: We enrolled 618 patients: average age was 74.4 years; 57.4% female; 62.3% white; 9.9% had indwelling devices (Table 1). Three hundred-fifty patients (56.6%) were MDRO colonized on enrollment: 98 (15.9%), MRSA; 208 (33.7%); VRE; 196 (31.7%), rGNB. Sixty-eight percent of patient rooms were MDRO contaminated: 166 (26.9%), MRSA; 293, (47.4%). VRE; 182 (29.5%), rGNB.

A majority (59.4%) of patients were exposed to an antibiotic before admission. Of which, 239 (65.1%) were exposed to a C. diffogenic antibiotic. In multivariable analysis, C. diffogenic antibiotic exposure was an independent risk factor for MDRO colonization (OR, 1.94; 95% CI, 1.35–2.79), MDRO room environment contamination (OR, 1.94; 95% CI, 1.43–2.63), VRE colonization (OR, 4.23; 95% CI, 2.59–6.90), and VRE room environment contamination (OR, 2.58; 95% CI, 2.00–3.33).

Table 1. Clinical Characteristics and MDRO Burden on Study Enrollment, Stratified by Hospital Antibiotic Exposure Status

Characteristic	All Patients (N=618)	No Antibiotic Exposure History (N=251)[1]	Low-Risk Antibiotic Exposure History (N=128)[1]	High-Risk Antibiotic Exposure History (N=239)[1]
Patient Characteristics				
Age, y, mean (SD)	74.4 (12.1)	74.5 (12.8)	73.9 (11.2)	74.5 (11.9)
Male Sex, No. (%)	263 (42.6)	104 (41.4)	61 (47.7)	98 (41.0)
Non-Hispanic White, No. (%)	385 (62.3)	135 (53.8)	91 (71.1)	159 (66.5)
Charlson Comorbidity Score, mean (SD)	2.6 (2.1)	2.6 (2.1)	2.3 (2.0)	2.7 (2.1)
Physical Self-Maintenance Score, mean (SD)	14.3 (4.5)	14.1 (4.2)	13.6 (4.4)	14.9 (4.8)
Indwelling Device Use, No. (%)[2]	61 (9.9)	15 (6.0)	13 (10.2)	33 (13.8)
Hospital Stay > 2 weeks, No. (%)	60 (9.7)	12 (4.8)	12 (9.4)	36 (15.1)
NH Days to Enrollment, mean (SD)	5.6 (3.0)	5.7 (3.1)	5.0 (2.9)	5.7 (2.9)
Proximal Outcome: Patient Colonization				
Any MDRO Colonization, No. (%)	350 (56.6)	119 (47.4)	71 (55.5)	160 (67.0)
MRSA, No. (%)	98 (15.9)	42 (16.7)	15 (11.7)	41 (17.2)
VRE, No. (%)	208 (33.7)	46 (18.3)	44 (34.4)	118 (49.4)
rGNB, No. (%)	196 (31.7)	71 (28.3)	40 (31.3)	85 (35.6)
Distal Outcome: Room Environment Contamination				
Any MDRO Contamination, No. (%)	418 (67.6)	150 (59.8)	87 (68.0)	181 (75.7)
MRSA, No. (%)	166 (26.9)	63 (25.1)	32 (25.0)	71 (29.7)
VRE, No. (%)	293 (47.4)	87 (34.7)	66 (51.6)	140 (58.6)
rGNB, No. (%)	182 (29.5)	77 (30.7)	32 (25.0)	73 (30.5)

[1] High-risk antibiotic exposure was defined as exposure to one or more of the following antibiotics that predispose patients to a high-risk of *Clostridioides difficile* infection prior to admission to the nursing facility: fluoroquinolones, 3rd/4th generation cephalosporins, penicillin combinations, lincosamides, and carbapenems. Patients without a high-risk antibiotic exposure, but with exposure to other antibiotics were classified as having a low-risk antibiotic exposure history.

[2] Indwelling device use was defined as the presence of a feeding tube or indwelling urinary catheter on study enrollment.

Notes: MDRO, multidrug-resistant organism; MRSA, methicillin-resistant *Staphylococcus aureus*; NH, nursing home; rGNB, resistant Gram-negative bacilli; SD, standard deviation; VRE, vancomycin-resistant enterococci.

Multivariable Analysis of Hospital Antibiotic Exposure Status as Risk Factor for Proximal and Distal MDRO Outcomes

Characteristic	Any MDRO aOR (95% CI)[1]	MRSA aOR (95% CI)[1]	VRE aOR (95% CI)[1]	rGNB aOR (95% CI)[1]
Proximal Outcome: Patient Colonization				
No Antibiotic Exposure	1.00 (Referent)	1.00 (Referent)	1.00 (Referent)	1.00 (Referent)
Low-Risk Exposure History[2]	1.34 (0.91-1.96)	**0.66 (0.44-0.98)**	**2.54 (1.42-4.56)**	1.10 (0.77-1.55)
High Risk Exposure History[2]	**1.94 (1.35-2.79)**	0.94 (0.51-1.73)	**4.23 (2.59-6.90)**	1.22 (0.80-1.85)
Distal Outcome: Room Environment Contamination				
No Antibiotic Exposure	1.00 (Referent)	1.00 (Referent)	1.00 (Referent)	1.00 (Referent)
Low-Risk Exposure History[2]	1.45 (0.79-2.64)	0.96 (0.55-1.67)	**2.24 (1.21-4.14)**	0.77 (0.43-1.38)
High Risk Exposure History[2]	**1.94 (1.43-2.63)**	1.19 (0.89-1.60)	**2.58 (2.00-3.33)**	0.91 (0.53-1.56)

[1] Multivariable logistic regression model was adjusted for age, sex, race, Charlson Comorbidity Index score, Physical Self-Maintenance score, indwelling device (urinary catheter or feeding tube) present on enrollment, hospital stay greater than 14 days, and nursing home days to enrollment. All regression analyses were cluster adjusted.

[2] High-risk antibiotic exposure was defined as exposure to one or more of the following antibiotics that predispose patients to a high-risk of *Clostridioides difficile* infection prior to admission to the nursing facility: fluoroquinolones, 3rd/4th generation cephalosporins, penicillin combinations, lincosamides, and carbapenems. Patients without a high-risk antibiotic exposure, but with exposure to other antibiotics were classified as having a low-risk antibiotic exposure history.

Notes: aOR, adjusted odds ratio; Bold, p < 0.05; CI, confidence interval; MDRO, multidrug-resistant organism; MRSA, methicillin-resistant *Staphylococcus aureus*; rGNB, resistant Gram-negative bacilli; VRE, vancomycin-resistant enterococci.

Conclusion: Hospital exposure to antibiotics is associated with an increased risk of VRE colonization and room environment contamination on NH study enrollment. These observations highlight the potential influence of hospital-based ASPs on MDRO prevalence and transmission in NHs.

Disclosures: **All Authors**: No reported disclosures

157. patient to Environment Transmission of Multidrug-resistant Bacteria Within Intensive Care Units

Matthew J. Ziegler, MD MSCE[1]; Brendan Kelly, MD, MSCE[2]; Michael Z. David, MD PhD[2]; Lauren Dutcher, MD[1]; Pam C. Tolomeo, MPH, CCRP[1]; Selamawit Bekele, BS[1]; Sean Loughrey, BS[1]; Emily Reesey, MS[1]; Laurel Glaser, MD, PhD[1]; Ebbing Lautenbach, MD, MPH, MSCE[1]; [1]University of Pennsylvania, Philadelphia, Pennsylvania; [2]Hospital of the University of Pennsylvania, Philadelphia, Pennsylvania

For the Centers for Disease Control and Prevention (CDC) Prevention Epicenters Program

Session: O-30. MDRO Epidemiology and Transmission

Background: Identifying risk factors for environmental contamination with multidrug-resistant organisms (MDROs) is essential to prioritize methods for prevention of hospital transmission.

Methods: Patients admitted to an ICU with an MDRO detected on clinical culture in the prior 30 days were enrolled. Patients (4 body sites) and high-touch objects (HTO) (3 composite sites) in ICU rooms were sampled. Environmental transmission was defined by shared MDRO species cultured on patient and HTO cultures obtained on multiple time points during the patient's stay. Risk factors for environmental transmission were identified with logistic regression.

Results: Forty-five patients were included (median 2 days of longitudinal sampling [IQR 1–4 days]). Enrollment anatomic cultures included extended-spectrum beta-lactamase-producing Enterobacterales (ESBLE) (n=12, 27%), carbapenem-resistant organisms (CRO) (n=4, 9%), methicillin-resistant *S.aureus* (MRSA) (n=11, 24%), vancomycin-resistant Enterococci (VRE) (n=4, 9%), and *C.difficile* (CDIFF) (n=14, 31%). Patient colonization during serial sampling was common with CRO (n=21, 47%), ESBLE (n=16, 36%), and VRE (n=16, 36%) and less so with MRSA (n=7, 16%) and CDIFF (n=5, 11%). Detection of MDROs on environmental surfaces was also common with identification of CRO in 47% of patient rooms (n=21) and ESBLE in 29% (n=13); MRSA (n=2, 4%), VRE (n=9, 20%), and CDIFF (n=3, 7%) were rarer. Patient to environment transmission was observed in 40% of rooms (n=18). Thirteen (29%) rooms had foreign MDRO contamination (i.e., one not detected on a body culture), most (n=10) with CRO. Environmental MDROs were most common in bathroom/

sinks (n=22), followed by surfaces near the patient (n=10), and least common surfaces often touched by staff within the room (n=6).

On multivariable logistic regression, naïve to clustering by patient, recent receipt of a proton pump inhibitor (OR 2.35, 95% CI 1.00 – 5.52, P=0.049) and presence of one or more wounds (OR 2.56, 95% CI 1.05 – 6.26, P=0.038) were significantly associated with environmental transmission (OR 1.56, 95% CI 1.01 – 2.43, P=0.046) (Table 1).

TABLE 1. Logistic regression for detection of patient to environment transmission of multi-drug resistant organisms

Variable	Bivariable OR (95% CI)	P-Value	Multivariable OR (95% CI)	P-Value
Patient characteristics				
Sedated	1.02 (0.41 – 2.55)	0.96		
Wound present	2.71 (1.19 – 6.17)	0.02	2.56 (1.05 – 6.26)	0.04
Bedfast[a]	2.35 (0.82 – 6.69)	0.11		
Diarrhea[b]	0.79 (0.37 – 1.71)	0.56		
Invasive devices present				
Mechanical ventilation	1.67 (0.80 – 3.46)	0.17		
Central venous catheter	1.86 (0.85 – 24.05)	0.12		
Urinary catheter	1.09 (0.52 – 2.28)	0.82		
Rectal tube	2.44 (1.07 – 5.56)	0.03		
Medication use				
Broad-spectrum antibiotic use[c]	1.09 (0.97 – 1.05)	0.64		
Laxative[d]	1.18 (0.49 – 2.86)	0.71		
Proton pump inhibitor[d]	2.59 (1.21 – 5.53)	0.01	2.35 (1.03 – 5.52)	0.049

NOTE. Model developed naïve to clustering by patient; OR, odds ratio, CI; confidence interval

[a]Bedfast determined by a mobility score of 1 on daily Braden score assessment

[b]As documented by medical staff

[c]Number of anti-pseudomonal antibiotic days within the prior 30 days

[d]Within 3 days

Conclusion: MDRO contamination of patient rooms is common with detection of organisms attributed to, and foreign to, the occupant.

Disclosures: Michael Z. David, MD PhD, GSK (Consultant)

158. Intra- and Inter-hospital Epidemiology of Carbapenem-resistant *klebsiella Pneumoniae* in US Hospitals

Courtney Luterbach, PhD, MS[1]; Liang Chen, PhD[2]; Blake Hanson, PhD[3]; Michelle Earley, MS[4]; Lauren Komarow, MS[4]; Gregory Weston, MD MSCR[5]; Eric Cober, MD[6]; Julia Garcia Diaz, MD, MSc, FACP, FIDSA, CPI[7]; Keith S. Kaye, MD, MPH[8]; W. Charles Huskins, MD, MSc[9]; Jason C. Gallagher, PharmD[10]; Robert A. Bonomo, MD[11]; Cesar A. Arias, MD, MSc, PhD, FIDSA[12]; Barry N. Kreiswirth, PhD[13]; David van Duin, MD, PhD[14]; [1]University of North Carolina Chapel Hill, Chapel Hill, North Carolina; [2]Hackensack-Meridian Health Center for Discovery and Innovation, Nutley, NJ, USA, Nutley, New Jersey; [3]University of Texas Health Science Center, Houston, Texas; [4]George Washington University, Rockville, Maryland; [5]Montefiore Medical Center and Albert Einstein College of Medicine, Bronx, New York; [6]Cleveland Clinic, Cleveland, Ohio; [7]University of Queensland/Ochsner Clinical School, New Orleans, Louisiana; [8]University of Michigan Medical School, Ann Arbor, Michigan; [9]Mayo Clinic College of Medicine and Science, Rochester, Minnesota; [10]Temple University School of Pharmacy, Philadelphia, Pennsylvania; [11]Louis Stokes Cleveland VA Medical Center, Cleveland, Ohio; [12]CARMiG, UTHealth and Center for Infectious Diseases, UTHealth School of Public Health, HOU, TX; Molecular Genetics and Antimicrobial Resistance Unit and International Center for Microbial Genomics, Universidad El Bosque, BOG, COL, Houston, Texas; [13]Hackensack Meridian Health, Nutley, New Jersey; [14]University of North Carolina, Chapel Hill, North Carolina

Session: O-30. MDRO Epidemiology and Transmission

Background: Carbapenem-resistant Enterobacterales (CRE) and specifically *Klebsiella pneumoniae* (CRKp) are a global threat. CRE rapidly spreading in a healthcare network may infect a distinct patient cohort or have higher virulence. We determined the impact of cluster assignment of CRKp on transmission dynamics and clinical outcomes.

Methods: CRACKLE-2 is a multi-site, prospective, observational cohort study of hospitalized patients with a clinical CRE culture from any anatomic site. We analyzed 351 patients enrolled 4/30/2016–8/31/2017 in 42 US hospitals with clonal group 258 CRKp. Static clusters were set as ≤ 21 core single nucleotide polymorphisms (SNPs), identified by Snippy, and sharing a recent common ancestor, using a maximum likelihood phylogeny (RAxML v8.2.4). Dynamic clusters were set as > 80% probability of being within 3 transmissions by the R program transcluster (λ = 4, β = 1.6). Clinical outcome was assessed by desirability of outcome ranking with best outcome as alive without events and worst outcome as death. Events were no clinical response, unsuccessful discharge, and adverse events. We compared patients in and out of clusters. For patients in clusters, we also compared intra- vs inter-hospital clusters.

Results: In total, there were 49 static (median: 5, IQR: 2, 8) and 45 dynamic clusters (median: 5, IQR: 2, 20). For static clusters, 176 patients (50%) were in clusters with 82 (47%) patients in intra-hospital clusters. A higher proportion of patients in clusters, vs not in clusters, had a CRKp culture > 3 days from admission ($P = 0.037$). More patients in inter-hospital, vs intra-hospital, clusters had diabetes ($P = 0.02$). For dynamic clusters, 179 patients (51%) were in clusters with 69 (39%) patients in intra-hospital clusters. A lower proportion of patients in clusters, vs not in clusters, had CRKp isolated from urine ($P = 0.04$). More patients in inter-hospital, vs intra-hospital, clusters had a CRKp culture 3 days from admission ($P = 0.04$). Clinical outcomes were the same for patients in clusters vs not in clusters for static and dynamic clusters.

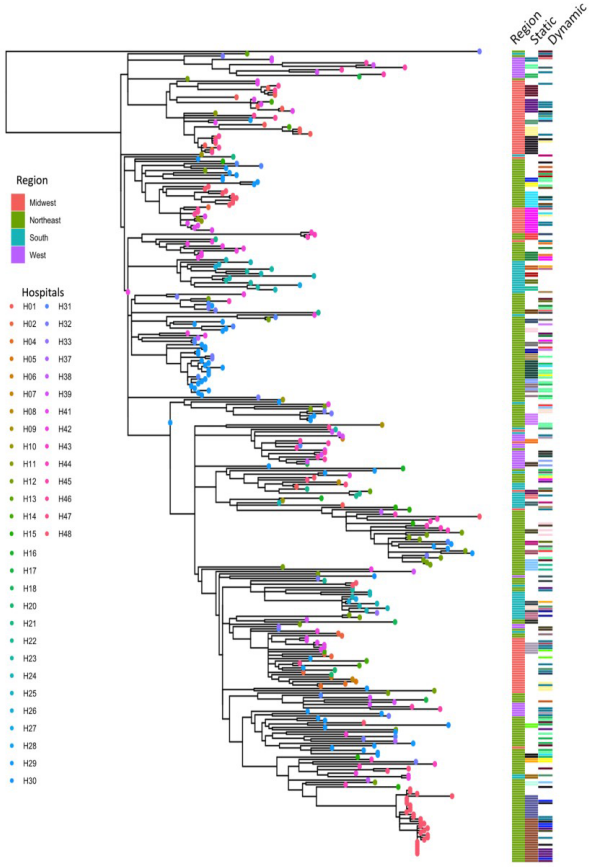


Figure 1. Phylogenetic population structure of *K. pneumoniae* CG258 strains. Panels from left to right indicate core SNP maximum likelihood phylogenetic tree, region of isolation, static CRKp clusters and dynamic CRKp clusters. Hospitals of isolation are colored at the nodes of the tree. For static clusters, each color represents a group of *K. pneumoniae* CG258 genomes differing by ≤ 21 core SNPs and sharing a recent common ancestor. For dynamic clusters, each color represent a group of *K. pneumoniae* CG258 genomes with >80% probability of being within 3 transmission.

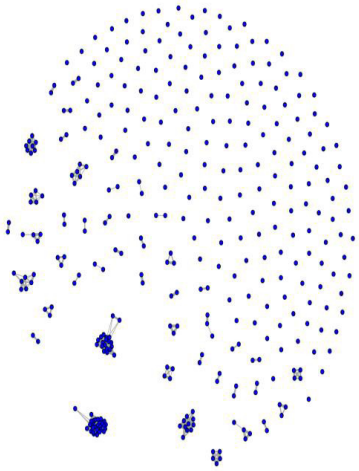


Figure 2. Dynamic cluster structure of *K. pneumoniae* CG258 strains. Individual CRKp strains (circles) were clustered based on SNPs and date of culture isolation with the edges between nodes indicating a > 80% probability of being within 3 transmissions. Edge thickness represents the number of likely transmissions between isolates with the thinnest edge representing 3 transmissions.