pathogens expressing resistant phenotypes (%R), specifically: MRSA, VRE, CRE, ESBL, CRAsp, and MDR *Pseudomonas,* see Figure.

Figure. National Estimates and Adjusted Trends of % Resistance, by Pathogen

National Estimates and Adjusted* Trends of % Resistance, by Pathogen								
	Methicillin Resistance Among *Staphylococcus aureus*[1]	Vancomycin resistance among *Enterococci*[2]	Carbapenem-resistance among Enterobacteriaceae[3]	ESBL Enterobacteriaceae (ALL)[4]	ESBL Enterobacteriaceae (HO†)[4]	ESBL Enterobacteriaceae (CO‡)[4]	Carbapenem resistance among *Acinetobacter*[5]	MDR among *Pseudomonas*[6]
% R (2012)	53.30%	17.40%	0.70%	8.90%	13.20%	8.30%	36.80%	14.40%
% R (2017)	49.20%	14.60%	0.80%	12.80%	17.10%	12.30%	29.80%	11.30%
Modeled 5-year percent change in %R * (2017 vs 2012)	-9.00% (p<.001)	-20.0% (p<.001)	No significant trend	43.60% (p<.001)	27.30% (p<.001)	49.20% (p<.001)	-16.9% (p=0.03)	-20.2% (p<.001)

*Adjusted for hospital bed size, U.S. census division, urban/rural designation, teaching status, month of discharge, age distributions, and data source
†HO: Hospital-Onset (positive culture on day ≥4)
‡CO: Community-Onset (positive culture on day ≤3)
1 MRSA - % methicillin resistance among Staphylococcus aureus
2 VRE - % vancomycin resistance among Enterococcus spp.
3 CRE - % carbapenem-resistance among Enterobacteriaceae (E. coli, Klebsiella spp., and Enterobacter spp.)
4 ESBL - % extended-spectrum cephalosporin resistance suggestive of extended-spectrum β-lactamase (ESBL)-production in Enterobacteriaceae (with additional estimates based on site of onset)
5 CRAsp - % carbapenem resistance among Acinetobacter spp. (CRAsp),
6 MDR Pseudomonas - % multi-drug resistance among Pseudomonas aeruginosa (MDR Pseudomonas)

Methods. We measured incidence of clinical cultures yielding the bacterial species of interest among hospitalized adults in hospitals submitting data to the Premier Healthcare Database, Cerner Health Facts and BD Insights Research Database from 2012- 2017. Community-onset (CO) cultures were obtained ≤ day 3 of hospitalization; hospital-onset (HO) were obtained ≥ day 4. We determined hospital-specific %R for each species. We generated national estimates using a raking procedure to generate weighted adjustments to match the distribution for all U.S. acute care hospitals based on U.S. census division, bed size, teaching status, and urban/rural designation. We applied a weighted means survey procedure to calculate national estimates for each year. We used weighted multivariable logistic regression adjusting for hospital characteristics to examine trends.

Results. From 2012-2017, the overall number of hospitals contributing data was 890 (over 20% of U.S. hospital hospitalizations annually). National estimates and trends of %R are shown in the Figure. Between 2012-2017, significant annual decreases in %R were observed for MRSA, VRE, CRAsp, and MDR *Pseudomonas.* CRE %R did not change. Overall ESBL %R increased by 44% (CO=49% increase, HO=27% increase).

Conclusion. Reductions in %R were observed among MRSA, VRE, CRAsp, and MDR *Pseudomonas*, suggesting that prevention efforts focused in health care settings are having a disproportionate effect on resistant strains. However, %R remains unacceptably high for all pathogens we studied, and %R among ESBL-producing Enterobacteriaceae has increased, most prominently among CO infections. Continued focus on currently recommended intervention strategies as well as new ones for community onset infections is needed.

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917. Persistence of Multidrug-Resistant Organisms during Occupancy Changes in the Nursing Home Setting, and Impact of Patient Hand Hygiene Assistance

Marco Cassone, MD, PhD[1]; Bonnie Lansing, LPN[1]; Julia Mantey, MPH, MUP[1]; Kristen Gibson, MPH[1]; Kyle Gontjes, MPH[1]; Lona Mody, MD, MS[1]; [1]University of Michigan, Ann Arbor, Michigan

Session: P-43. HAI: Surveillance

Background. We investigated the effect of changes in room occupancy, and patient hand hygiene, on the burden of multidrug-resistant organisms (MDRO) in nursing homes. We assessed: 1/ persistence of MDRO after patients are discharged; and 2/ impact of hand hygiene assistance on colonization and room contamination.

Methods. Prospective cohort study of methicillin-resistant *Staphylococcus aureus* (MRSA), vancomycin-resistant enterococci (VRE) and ceftazidime, ciprofloxacin or meropenem-resistant gram-negative bacilli (rGNB) in 9 single rooms screened three times a week for 34 weeks (five environmental surfaces, plus nares, groin, and hands of enrolled patients). Relative risk (RR) for patient colonization and room contamination were calculated in patient visits based on: 1/ performance of hand hygiene, and 2/ receiving assistance to perform it.

Results. We collected 4670 swabs over a total of 723 visits. Of 143 patient discharges, 31 times the room was swabbed before another patient was admitted (41 total visits), 48 times the next admitted patient was enrolled and available to be swabbed (295 visits), and 64 times the patient was not enrolled but the environment was sampled (387 total visits) (Figure).

Twenty-four (50%) patients were colonized at least once with an MDRO. Rooms were contaminated at least once with MDRO in 72 cases (64%). MDRO persistence during occupancy changes involving at least one screened patient was observed in 21 of 73 cases (29%). In addition, we detected 2 cases of contamination of unoccupied, terminally cleaned rooms with MDRO recovered also in the previous (MRSA) or the following occupancy (VRE).

In 40 occasions, patients performed hand hygiene with assistance from healthcare personnel, while in 169 occasions they performed hand hygiene by themselves. Requiring assistance was a risk factor for patient colonization (27.5% vs. 12.4% not requiring assistance (RR 2.20, 95% CI 1.16-4.18), and for room contamination (37.5% vs. 18.9%, RR 1.97, 95% CI 1.18-3.27) (Table).

Figure. Example of successive changes in room occupancy.

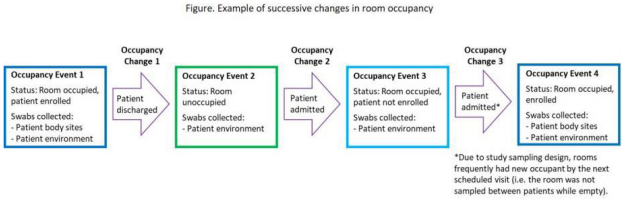

Table. Breakdown of colonization and contamination at each visit according to hand hygiene performance and need for assistance.

Table. Breakdown of colonization and contamination at each visit according to hand hygiene performance and need for assistance.

		Patient colonized			Room contaminated		
		yes	no	RR (95% CI)	yes	no	RR (95% CI)
Performed hand hygiene	yes	32	176	Reference	47	161	Reference
	no	20	67	1.49 (0.91-2.46)	26	61	1.32 (0.88-1.99)
Assisted with hand hygiene	yes	11	29	2.20 (1.16-4.18)	15	25	1.97 (1.18-3.27)
	no	21	147	Reference	32	136	Reference

Conclusion. MDRO can persist during changes in patient occupancy. Patients requiring assistance with hand hygiene experienced a higher MDRO burden. These observations call for further investigation of improved cleaning practices and patient assistance.

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918. Pilot Surveillance for Carbapenemase Gene-positive Organisms Among Hospitalized Solid Organ Transplant Recipients

June L. Chan, PhD[1]; Elizabeth Nazarian, PhD[2]; Kimberlee A. Musser, Ph. D.[3]; Monica Fung, MD, MPH[4]; Sarah B. Doernberg, MD, MAS[5]; Stephanie M. Pouch, MD, MS, FAST[6]; Stephanie M. Pouch, MD, MS, FAST[6]; Surbhi Leekha, MBBS, MPH[7]; Judith A. Anesi, MD[8]; Rosy Priya Kodiyanplakkal, MD[9]; Sarah Turbett; Maroya Spalding Walters, PhD, ScM[10]; Lauren Epstein, MD MSc[11]; Lauren Epstein, MD MSc[11]; [1]NYSDOH/Wadsworth Center, Albany, New York [2]Wadsworth, Albany, NY; [3]Wadsworth Center, New York State Department of Health, Albany, NY; [4]University of California San Francisco, San Francisco, California; [5]University of California, San Francisco, San Francisco, California; [6]Emory University School of Medicine, Atlanta, Georgia; [7]University of Maryland, Baltimore, MD; [8]University of Pennsylvania, Philadelphia, PA; [9]Weill Cornell Medcine, New York, New York; [10]U.S. Centers for Disease Control and Prevention, Atlanta, Georgia; [11]Centers for Disease Control and Prevention, Atlanta, Georgia

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Background. Carbapenemase gene-positive organisms (CPOs) are associated with infections with high mortality rates and have the potential to facilitate epidemic spread of carbapenem resistance. Passive reporting to CDC identified CPOs among organ transplant recipients, potentially representing an emerging reservoir for spread. We aimed to determine the prevalence of CPOs in hospital units where solid organ transplant (SOT) recipients receive care in order to inform public health action to prevent transmission.

Methods. All healthcare facilities identified one medical unit where SOT recipients received inpatient care and conducted point prevalence surveys (PPS) of all consenting patients on 1-2 designated calendar days. We used the Cepheid Xpert® Carba-R assay to identify carbapenemase genes (bla_{KPC}, bla_{NDM}, bla_{VIM}, bla_{IMP}, bla_{OXA-48}) from rectal swabs; carbapenemase-positive swabs were cultured for organisms. All laboratory testing was conducted at the Wadsworth Center, part of CDC's Antibiotic Resistance Laboratory Network.

Results. Five participating hospitals performed nine PPS from September 2019 through June 2020. In total, 154 patients were screened and 92 (60%) were SOT recipients (Table). The most common transplanted organs were kidney (44, 48%) and liver (39, 42%). Carbapenemase genes were detected among 5 (5%) SOT recipients, all from a single healthcare facility; 4 (80%) were bla_{KPC} and 1 (20%) was bla_{NDM}. Of the positive specimens cultured, bla_{KPC} was carried by *Enterobacter cloacae* complex (ECC), *Klebsiella pneumoniae*, and *Klebsiella oxytoca* and bla_{NDM} was carried by *K. oxytoca*; bla_{KPC} was carried by both ECC and *K. pneumoniae* in a single individual. For SOT patients with CPOs, the median interval from transplantation to swab collection was 108 days (range: 12 to 323). CPOs were only detected in 1 (2%) of 62 non-transplant patients.

TABLE. Characteristics of Carbapenemase Gene-positive Organism (CPO) Pilot Surveillance Participants

TABLE: Characteristics of Carbapenemase Gene-positive Organism (CPO) Pilot Surveillance Participants

	Solid Organ Transplant Recipients (N = 92)
Age (median years, range)	57 (18-77)
Male	51 (55%)
Transplant organ[a]	
kidney	44 (48%)
liver	39 (42%)
pancreas	9 (10%)
lung	6 (7%)
Patients with carbapenemase genes detected	5 (5%)
bla $_{KPC}$	4 (80%)
Organisms[b]	*Enterobacter cloacae* complex, *Klebsiella pneumoniae* , *Klebsiella oxytoca*
bla $_{NDM}$	1 (20%)
Organisms[b]	*Klebsiella oxytoca*
Time from transplantation to point prevalence survey (PPS) date among all solid organ transplant (SOT) recipients, N = 92; median days (range)[c]	40 (0-7151)
Time from transplantation to PPS date among SOT recipients with CPOs, N = 5; median days (range)[c]	108 (12-323)

[a]Some patients received dual solid organ transplants.

[b]Carbapenemase genes detected and associated organisms are described.

[c]Time interval represents number of days from transplantation to specimen collection for CPO screening.

Conclusion. Among participating facilities, most did not identify CPOs among patients admitted to transplant units. These findings represent a small number of patients and facilities; additional PPS in areas with varied CPO epidemiology are needed to understand whether SOT recipients should be routinely screened for CPOs.

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919. Understanding Intermittent Detection of Multidrug-Resistant Organisms (MDROs) in Rectally Colonized Patients

Sarah Sansom, DO[1]; Michael Y. Lin, MD, MPH[1]; Michael Schoeny, PhD[1]; Christine Fukuda, MPH[1]; Christine Bassis, PhD[2]; Teppei Shimasaki, MD, MS[1]; Thelma E. Dangana, MBBS[3]; Nicholas M. Moore, PhD[1]; Rachel Yelin, MPH[1]; Sophia Liu, BS[4]; Vincent B. Young, MD, PhD[2]; Yoona Rhee, MD, ScM[1]; Lina Tabith, MBBS[1]; Jianrong Sheng, MD, PhD[1]; Enrique Cornejo Cisneros, MD, MS[1]; John Murray, MS[1]; Kyle Chang, BS[1]; Karen Lolans, BS[1]; Michelle Ariston, BS[1]; William Rotunno, BS[1]; Hazel Ramos, BS[1]; Haiying Li, PharmD[1]; Khaled Aboushaala, MD[1]; Naomi Iwai, BS[1]; Mary K. Hayden, MD[1]; [1]Rush University Medical Center, Berwyn, IL; [2]University of Michigan, Ann Arbor, Michigan; [3]Rush University Medical, Chicago, Illinois; [4]University of Michigan-Ann Arbor, Ann Arbor, Michigan

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Background. MDRO detection in colonized patients may be intermittent for reasons that are incompletely understood. We examined temporal patterns of gut MDRO colonization after initial MDRO detection by rectal swab screening, and determined the relationship of culture positivity to the relative abundance of corresponding MDRO operational taxonomic units (OTUs) identified by 16S rRNA gene sequence analysis.

Methods. Rectal or fecal swabs were collected daily from MICU patients 1/11/2017-1/11/2018. First MICU admissions with ≥2 swabs and MICU stays ≥3 days were studied. Samples were cultured for vancomycin-resistant enterococci (VRE), carbapenem-resistant *Enterobacteriaceae* (CRE) and *P. aeruginosa* (CRPA), and extended-spectrum β-lactamase-producing (ESBL) *Enterobacteriaceae* by selective media. Resistance mechanisms were confirmed by phenotypic methods and/or PCR. Limit of detection was similar for different MDROs (24-52 CFU/sample). OTU categories corresponding to MDRO species were identified by taxonomy and BLAST. Multilevel regression models estimated the association between MDRO detection and relative abundance of the corresponding OTU.

Results. 796 unique patients with 3519 swabs were studied. Median (IQR) age was 64 (51-74) years, MICU length of stay was 5 (3-8) days, and number of samples-per-patient was 3 (2-5). Following initial MDRO detection, the probability of subsequent detection varied by MDRO type, and was highest for VRE and lowest for CRPA [Figure 1]. Within each sample, we found a significant association between MDRO detection and relative abundance of the corresponding OTU [Table 1]. In contrast, relative OTU abundance in the first sample with MDRO detection was not predictive of odds of future MDRO detection (p >0.05 for all comparisons). Carriage of >1 MDRO did not affect the odds of MDRO detection in later samples.

Figure 1. Probability of Subsequent MDRO Detection after First Positive Varies by MDRO Type

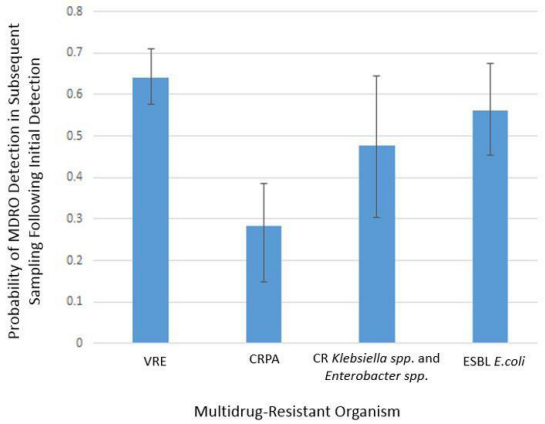

Figure 1: Following initial MDRO detection and controlling for repeated measurements within subject, the estimated probability of MDRO detection in subsequent sampling varied by MDRO type. 95% confidence intervals are represented by black-capped bars.

Table 1. Higher Mean Corresponding OTU Relative Abundance Within Each Sample is Associated with MDRO Detection

Table 1: Relationship of OTU relative abundance and MDRO detection

MDRO	MDRO Detection Status	No. of Samples [a]	Mean OTU Percent Relative Abundance (95% CI) [b]	P- value [c]
VRE (n=155 patients)	Detected	493	26.09 (22.70, 29.48)	<0.0001
	Not Detected	324	1.28 (-2.56, 5.13)	
CRPA (n=27 patients)	Detected	55	12.01 (6.61, 17.41)	<0.0001
	Not Detected	150	1.58 (-2.95, 6.12)	
CR *Klebsiella* and *Enterobacter* spp. (n=34 patients)	Detected	99	15.09 (8.73, 21.45)	0.0013
	Not Detected	96	6.61 (3.69, 12.84)	
ESBL *E. coli* (n=78 patients)	Detected	164	10.51 (6.95, 14.08)	0.0002
	Not Detected	181	4.69 (0.94, 8.45)	

[a] Number of samples following initial MDRO detection.
[b] Operational taxonomic unit (OTU) classification based on 3% sequence differences of 16S rRNA gene sequences of V4 region.
[c] Following initial MDRO detection, comparison of mean relative abundance in subsequent MDRO-detected samples compared to negative samples by multilevel linear model with sample nested within subject.

Conclusion. MDRO culture positivity in rectally colonized patients was correlated with relative abundance of the corresponding OTU in the same sample. Serial detection of different MDRO types was variable, possibly due to distinct microbial community dynamics of different MDRO types. Intermittent failure to detect MDROs could result in misattribution of MDRO acquisition, resulting in inappropriate investigation or intervention.

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920. Use of the Web by State and Territorial Health Departments to Promote the Dissemination of State Antimicrobial Resistance Surveillance Data, United States

Xin Yin, MPH[1]; Keith W. Hamilton, MD[2]; Heather Tate, PhD[3]; Nkuchia M. M'ikanatha, DrPH[4]; [1]Penn State College of Medicine, Hershey, PA; [2]Divison of Infectious Diseases, Philadelphia, Pennsylvania; [3]Food and Drug Administration, Laurel, MD; [4]Pennsylvania Department of Health, Harrisburg, Pennsylvania

Session: P-43. HAI: Surveillance

Background. Antimicrobial resistant (AMR) bacteria pose a serious threat to public health. The national response to this threat includes calls for promoting judicious use of antibiotics in humans and animals and strengthening integrated One Health surveillance of AMR bacteria in humans, animals, and environment. However, the extent to which public health jurisdictions are disseminating surveillance findings to promote judicious use of antimicrobials is unclear.

Methods. We used a standardized web audit tool to manually review and document the presence of AMR-related information on the websites of all public health jurisdictions that participate in national notifiable disease surveillance in the United States. We also emailed a survey to representatives in the 54 jurisdictions that participate in the National Antimicrobial Resistance Monitoring System (NARMS) activities coordinated by the Centers for Disease Control and Prevention. The survey asked questions about AMR-related information on their public health department website.

Results. Of the 37 (68.5%) jurisdictions that responded to the email survey, 26 (70.3%) indicated that their websites have information on appropriate antibiotic use for health professionals, veterinarians and general public, compared to 89.3% from the web survey (Figure). Eleven (29.7%) indicated that they have data on antimicrobial susceptibility for pathogens, or antibiograms, on their websites, compared to 48.2% from the web survey. While 11 (29.7%) jurisdictions indicated that they have highlighted appropriate antimicrobial use on the homepage, the web survey found no reference on the homepage.