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

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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

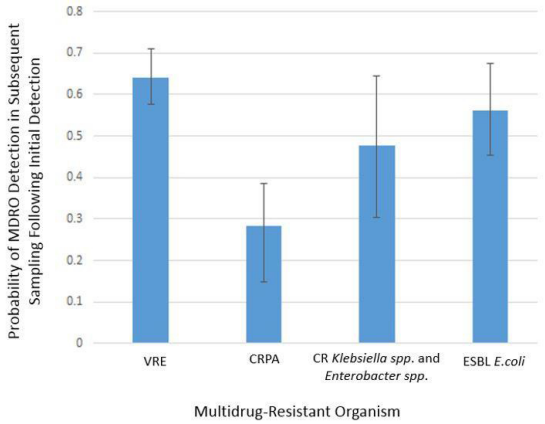

Figure 1: Following initial MDRO detection and controlling for repeated measurements within subject, the estimated probability of MDRO detection in subsequent sampling varied by MDRO type. 95% confidence intervals are represented by black-capped bars.

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

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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.