

Solid line: March 16th, surveillance halted in 3 out of 4 outpatient clinics due to SARS-CoV-2 restrictions

Dashed line: March 23rd, stay-at-home implementation in Nashville, TN

Conclusion. Most medical encounters in infants are due to viral pathogens, with RSV, RV/EV, and flu being the most common. However, distributions differed by clinical setting, with RSV being the most frequently detected in the IP and ED settings, and second to RV/EV in the OP setting. Continued active viral ARI surveillance in various clinical settings is warranted. Preventative measures such as vaccines and infection control measures deserve study to reduce viral ARI burden.

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914. Epidemiology of Patients with ESKAPE Pathogen Bloodstream Infection in the US Military Health System

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Session: P-43. HAI: Surveillance

Background. Bloodstream infections (BSI) are associated with both inpatient mortality and substantial morbidity in the United States. We sought to characterize the epidemiology of BSIs with ESKAPE pathogens on patients served by the United States Military Healthcare System (MHS), which actively prospectively captures clinical and microbiological data from US service members and their beneficiaries.

Methods. We performed a retrospective analysis of MHS patients with blood cultures positive for ESKAPE pathogens (*E. faecium, S. aureus, K. pneumoniae, A. bau-mannii, P. aeruginosa,* and *Enterobacter spp.*), as well as *Neisseria gonorrhoeae* and *Raoultella spp.* between January 2010 and December 2015. Microbiological data from the Navy and Marine Core Public Health Center was retrospectively collated with clinical and demographic data from the MHS Data Repository.

Results. We identified 7,404 patients who experienced 8,791 episodes of ESKAPE (including *N. gonorrhoeae* and *Raoultella spp.*) BSI. The patients were predominately

active duty (N=688) or retired (N=2,517) Armed Forces service members and their dependents (N=2,361). Further, 59.4% were male and 47.5% were >65 years old. A total of 5,594 (75.5%) of BSI episodes were associated with hospital admission, with an average length of stay of 14.9 days (SD of 27.5 days) and 47.4% (N=2,650) of those admissions were associated with an ICU stay averaging 8.6 days (SD of 18.0 days). The most common pathogens detected were *E. coli* (34.6%, N= 3,042) followed by *S. aureus* (28.0%,N=2,464), with 7.6% and 40.7% of isolates resistant to ceftriaxone and methicillin, respectively. We found a larger proportion of *E. coli* BSI in females (47.4% versus 26.2%) and *S. aureus* BSI in males (32% versus 21.9%). The frequency of *A. baumannii* BSI in younger patients, ages 18-30, was an average 4.5 fold higher than in older age groups (30-50, 50-65 and >65).

Conclusion. We noted epidemiological differences in the burden of ESKAPE pathogen BSIs, in various populations including sex and age specific risk factors in a population served by the MHS. Further work is underway to evaluate risk factors for infection and outcomes with pathogens with in vitro resistance controlling for factors such as age, gender, co-morbid diseases and severity of illness.

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915. Global 2018 Surveillance of Eravacycline Against Gram-positive Pathogens, Including Resistant Isolates

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Session: P-43. HAI: Surveillance

Background. Eravacycline (ERV) is a fully-synthetic, fluorocycline antibacterial approved by the FDA and EMA for the treatment of complicated intra-abdominal infections (cIAI) in patients \geq 18 years of age. The purpose of this study was to further monitor the *in vitro* activity of ERV against Gram-positive pathogens, such as *Staphylococcus aureus* (including methicillin-resistant *S. aureus*, MRSA), *Enterococcus* spp. (including vancomycin-resistant *Enterococcus*, VRE) and *Streptococcus* spp.

Methods. Isolates were collected globally during 2018 from various body sites. Minimum inhibitory concentrations (MICs) were determined by CLSI broth microdilution. Antibiotic susceptibility was determined using the most recent CLSI breakpoints (30th ed CLSI M100 document), except for ERV and tigecycline (TGC) where FDA breakpoints from 2018 and 2005, respectively, were applied. **Results.** Summary MIC data for ERV and select comparators are shown in the

Results. Summary MIC data for ERV and select comparators are shown in the Table. ERV MIC_{5090} for *Enterococcus* spp were 0.06/0.12 µg/mL and were not affected by the presence of vancomycin resistant mechanisms. The MIC_{90} of ERV against VRE was 2-fold lower than TGC, at a value of 0.12 µg/mL. ERV MIC_{90} values for methicillin-susceptible *S. aureus* (MSSA) was 0.12 µg/mL and for MRSA was 0.25 µg/mL. Generally, for all pathogens, ERV MIC_{90} values were 2- to 4-fold lower than TGC. Table

Organisms (N)	ERV MIC 50/90	TGC MIC _{50/90}	VAN MIC 50/90	DAP MIC 50/90
Enterococcus spp (985)	0.06/0.12	0.12/0.25	1/>16	2/2
E. faecalis (502)	0.06/0.12	0.12/0.25	1/2	1/2
E. faecium (483)	0.06/0.06	0.06/0.25	1/>16	2/4
VRE (189)	0.06/0.12	0.06/0.25	>16/>16	2/4
S. aureus (520)	0.06/0.12	0.25/0.25	1/1	0.25/0.5
MSSA (308)	0.06/0.12	0.25/0.25	1/1	0.25/0.5
MRSA (212)	0.06/0.25	0.25/0.5	1/1	0.5/0.5
Streptococcus anginosus group ^a (48)	0.015/0.03	0.03/0.06	0.5/1	0.25/0.5

isolates; ^aS. anginosus, S. constellatus, S. intermedius

Conclusion. ERV *in vitro* activity was demonstrated for clinically important Gram-positive pathogens, including resistant isolates. Overall, ERV demonstrated lower MIC_{90} values than comparators for all organisms. This 2018 global surveillance highlights ERV's utility against Gram-positive organisms and further underscores its role in cIAI, where these pathogens play a causative role.

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916. National Estimates of the Proportion of Bacterial Pathogens Expressing Resistant Phenotypes in US Hospitals, 2012-2017

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Session: P-43. HAI: Surveillance

Background. In 2019, CDC updated national estimates of antibiotic resistance. In this abstract we provide national estimates of and trends in proportion of bacterial

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

National Estimates a		ds of % Resistance, b	y Pathogen					
	Methicillin Resistance Among Staphylococcus gureus 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 Acinetobocter ⁵	MDR among Pseudomonas [®]
% 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 hospit †HO: Hospital-Onset			ural designation, teach	ning status, month of	discharge, age distr	ibutions, and data so	ource	

CO: Community-Onset (positive culture on day ≤3) 1 MPCA - 5 methicilin registrance among Stanbudgeoccur at 1 MPCA - 5 methicilin registrance

2 VRE - % vancomycin resistance among Enterococcus spp.

3 UKE - % carbapenem-resistance among Enterobacteriaceae (E. coli, Kiebsielia spp., and Enterobacter spp.) 4 ESBL - % extended-spectrum cephalosporin resistance suggestive of extended-spectrum β-lactamase (ESBL)-production in Enterobacteriaceae (with add

RAsp - % carbapenem resistance among Acinetobacter spp. (CRAsp),

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 \leq day 3 of hospitalization; hospital-onset (HO) were obtained \geq 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, PhD¹; Bonnie Lansing, LPN¹; Julia Mantey, MPH, MUP¹;

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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.

Figure. Example of successive changes in room occ



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

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

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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_{NDM} , bla_{IMP} , $bla_{\text{OXA-sb}}$) 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.

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