Results. The study period yielded 1,700 prescriptions after exclusions 1,063 were included in the analysis. Patients aged ≥65 comprised 51% of the population. Older patients had significantly more comorbidities than the younger population. No significant difference was observed for antibiotic indicated (60%), correct drug (50%), or correct duration (75%) between the two age groups. Patients in the ≥65 cohort were statistically significantly more likely to receive an inappropriate dose (86% vs. 76%, $P < 0.002$). In the multivariable analysis, patients with COPD were more likely to be appropriately with antibiotics OR 1.4 (95% CI: 1.03–1.9) compared with those without COPD. Older patients were not more likely to be retreated or admitted for the same indication within 30 days.

Conclusion. Antibiotics were frequently overused in the outpatient setting; however, they were not more frequently used in elderly patients. However, older adults were more likely to be prescribed an antibiotic at an inappropriate dose highlighting the need for increased caution with dosage selection in this population. Stewardship teams caring for elderly patients should be cognizant of dosing in this population.

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1245. Infection Prevention and Control (IP&C) and Antibiotic Stewardship (AS) Practices in Pediatric Long-Term Care Facilities

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Session: 138. Healthcare Epidemiology: Non-acute Care Settings
Friday, October 5, 2018: 12:30 PM

Background. In November 2017, the Centers for Medicare and Medicaid (CMS) implemented a requirement for long-term care facilities (LTCFs) to incorporate AS into their IP&C programs. The purpose of this study was to describe baseline IP&C and AS practices in pediatric LTCFs.

Methods. We modified a survey from the CDC to assess IP&C in pediatric LTCFs. The internet-based survey was distributed to the 41 pLTCFs in the Pediatric Complex Care Association from May to June 2017. The 67-question survey included questions to assess IP&C domains and infrastructure such as written policies, hand and respiratory hygiene (HH), personal protective equipment (PPE) use, environmental cleaning, and AS practices. Responses to questions were summarized using frequencies and analyzed using χ^2 or Fisher's exact tests, as appropriate. The characteristics of sites with ≥90% compliance with the CMS rule, as assessed by 14 relevant survey questions, were compared with those of sites with <90% compliance.

Results. Overall, 25 (61%) facilities nationwide completed the survey. All sites reported having written IP&C policies and most had a person responsible for IP&C (96%); fewer reported reviewing/updating these policies annually (72%). Few sites provided feedback to staff on HH adherence (44%), PPE use (40%), and cleaning/disinfection procedures (44%). Few had written policies on antibiotic prescribing (48%) or provided prescribers with feedback about their prescribing practices (40%). Sites with ≥90% compliance with the CMS rule were more likely to report providing prescribers with feedback (70% vs. 20%, $P = 0.03$), to have provided AS training to clinical (60% vs. 0%, $P < 0.01$) and nursing staff (70% vs. 7%, $P < 0.01$) in the past 12 months, and to provide feedback regarding HH (70% vs. 27%, $P = 0.05$).

Conclusion. While most facilities had implemented some IP&C and AS strategies pertaining to the CMS rule before its enforcement, this survey identified several gaps, especially pertaining to staff feedback for IP&C practices and antibiotic prescribing. Facilities should develop feedback strategies and regularly reinforce the importance of IP&C at employment and during regular trainings.

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1246. *Acinetobacter baumannii* in the Post-Acute Care Setting: Prevalence and Resistance Rates in Patients, Health Care Personnel and the Environment

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Session: 138. Healthcare Epidemiology: Non-acute Care Settings
Friday, October 5, 2018: 12:30 PM

Background. *Acinetobacter baumannii* is an important agent of healthcare-acquired infections, sporting high resistance to major antibiotics in acute care. Since *A. baumannii* is an opportunistic pathogen commonly found in the environment, we aimed to investigate: (1) its prevalence as colonizer on patients, environment, and healthcare personnel (HCP) in Nursing Facilities (NFs) with intermediate intensity of care but high antibiotic pressure and (2) whether resistance rates in colonizing strains vary between patient, environmental, and HCP isolates.

Methods. We analyzed *A. baumannii* patient and HCP colonization and environmental contamination in six NFs in Michigan. Samples were collected from HCPs hands, and from multiple patient body sites and high-touch surfaces at admission, 14 days, and monthly up to 6 months. Ciprofloxacin, imipenem, and ceftazidime resistance was tested according to CLSI guidelines.

Results. 651 patients were screened (average follow-up time was 29 days). Patient colonization with *A. baumannii* was found in 59/1,620 (3.64%) of visits, and environmental contamination in 267/1,620 visits (16.48%) ($P < 0.001$). Interestingly, HCP showed at least as high or possibly higher colonization rates than patients (32/574) (5.25%) ($P = 0.06$). Resistance rates differed significantly between HCP, environmental, and patient isolates, ranging from 35 to 38% for patient isolates, 26 to 30% for environmental isolates, and only 8 to 17% for HCP isolates (table).

Table: Resistance Rates of *Acinetobacter baumannii* to Ceftazidime, Imipenem, Ciprofloxacin Vary Based on the Source of Isolation (Patient, Environment, HCP Hands)

	Patient Isolates	Environmental Isolates	HCP Hands Isolates	Total
Total Isolates	85	454	36	575
Resistant to Imipenem (%)	31 (36%)	118 (26%), P **= 0.047***	3 (8%), $P = 0.002$**	152 (26%)
Ciprofloxacin (%)	32 (38%)	128 (28%), $P = 0.08$*	5 (14%), $P = 0.009$**	165 (29%)
Ceftazidime (%)	30 (35%)	137 (30%), $P = 0.34$*	6 (17%), $P = 0.040$**	173 (30%)

*Patient isolates vs. environmental isolates.

**Patient isolates vs. HCP hands isolates.

Conclusion. In our NFs, *A. baumannii* is more likely to be found on HCPs than on patients. However, HCP isolates have much lower resistance rates. Environmental contamination is alarmingly common, with worrisome resistance rates even in post-acute care settings.

Disclosures. **All authors:** No reported disclosures.

1247. Genomic Epidemiology of MRSA DURING Incarceration at a Large Inner-City Jail

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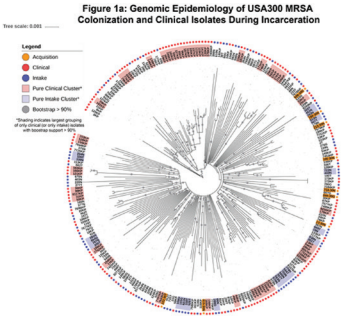
Session: 138. Healthcare Epidemiology: Non-acute Care Settings
Friday, October 5, 2018: 12:30 PM

Background. Congregate settings may facilitate spread of USA300. Jails may be a location where individuals already colonized with MRSA (from preceding exposures) intermingle with others, potentially augmenting spread. We examined the rate of MRSA acquisition during incarceration and characterized the genomic epidemiology of MRSA strains entering the jail, MRSA acquisition isolates, and archived (2015–2017) clinical MRSA isolates from male detainees.

Methods. Males incarcerated at the Cook County Jail were enrolled within 72 hours of intake and surveillance cultures for MRSA carriage (nares, throat, groin) collected. Detainees in jail at Day 30 had cultures repeated to determine MRSA acquisition. A survey was administered and chart review performed to identify predictors of acquisition. Whole-genome sequencing and phylogenetic analysis of isolates were performed with integration of epidemiologic data.

Results. 800 males were enrolled, with 19% colonized with MRSA at jail intake. 143 reached the Day30 visit (82% AA, 7% Hispanic), by which there were 12 MRSA acquisitions detected. Heroin use before entering the jail (OR 3.67, $P = 0.04$) and sharing personal items during incarceration (OR = 4.92, $P = .01$) were significant predictors of acquisition. Sequenced clinical isolates ($n = 175$) (largely skin infections) were more likely to resemble each other genetically than the diverse intake strains ($P < 0.001$) (figure), suggesting clinical isolates may originate from transmission within the jail or be due to more virulent strains. 7/12 (58%) acquisition isolates were within 40 SNVs from another isolate; five were genomically similar to intake isolates and two were similar to clinical isolates. Acquisition strains from those sharing personal items (vs. not) tended to have closer relatedness (19 SNVs vs. 56 SNVs, $P = 0.22$).

Conclusion. There is a high burden of MRSA entering jail. Genomic analysis of acquisition and clinical isolates suggests potential spread of incoming strains and possible networks spread of prevalent strains during incarceration. Sharing of personal items during incarceration is associated with MRSA acquisition and could be a focus of an intervention. Future study of epidemiologic and location data may inform targeting of interventions within the jail.



Disclosures. **All authors:** No reported disclosures.

1248. Genomic Sequencing and Clinical Data Integration for Next-Generation Infection Prevention

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Session: 139. Healthcare Epidemiology: Outbreaks
Friday, October 5, 2018: 12:30 PM

Background. Typical Infection Prevention to detect pathogen transmission in hospitals has relied on observation of (1) uncommon pathogen phenotypes or (2) greater than expected number of pathogen phenotypes in a given timeframe and/or location. Genome sequencing of targeted organisms in conjunction with routine patient geo-temporal information and antibiotic susceptibility data holds promise in identifying transmissions with greater sensitivity and specificity, saving time and effort in reviewing for transmission events.

Methods. In an on-going genomic sequencing surveillance effort in a tertiary care hospital, drug-resistant clinical isolates from the "ESKAPE" pathogens were routinely sequenced in 2017. In parallel, potential clusters were identified for 2017 through conventional Infection Prevention approaches. Groups identified by their genetic distances along with visualizations on antimicrobial susceptibilities, and patient location histories and dates were displayed in an interactive interface, Philips IntelliSpace Epidemiology (PIE), and reviewed by Infection Prevention.

Results. Among 656 patients, 1,239 drug-resistant ESKAPE samples were sequenced. Thirty-eight genetically related groups involving 196 patients were identified. Groups ranged in size from two to 44 patients, primarily consisting of VRE and MRSA. Notably, a review of the 38 groups identified 20 groups where the information at hand suggested a concern for transmission. 16 of the 20 were not previously identified by Infection Prevention. Using PIE to review all 38 groups identified from 1 year's worth of data required 3 hours of time by an Infection Prevention professional, averaging less than 5 minutes per cluster, less than 1 minute per patient, and 11 minutes of review time per actionable opportunity. By conventional means, approximately 23 hours would have been required to review the genomic groups without the aid of the PIE tool.

Conclusion. The use of PIE's genomic-defined groups, along with the integrated clinical data platform, allows for a greater ability, certainty, and speed to detect clusters of organisms representing transmission in the hospital setting. Applied prospectively, PIE can detect transmissions sooner than by conventional means for potential patient safety gains and cost savings.

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1249. Emergence of Diverse Carbapenem-Resistant Enterobacteriaceae (CRE) in the Dominican Republic

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Session: 139. Healthcare Epidemiology: Outbreaks
Friday, October 5, 2018: 12:30 PM

Background. Despite the global threat of CRE, data from resource-limited regions such as the Dominican Republic (DR) are limited. A lack of novel antibiotics and molecular diagnostic tools for outbreak detection, coupled with the role of travel in circulating CRE to and from the DR represent significant challenges to limiting their spread. Here, we report the first molecular characterization of DR CRE isolates and compared them to geographically diverse CRE.

Methods. Isolates from DR (one *Citrobacter freundii*, three *Klebsiella pneumoniae),* obtained from patients with bacteremia (one) and pneumonia (three), were compared with CRE from a New York City hospital in a Dominican neighborhood, including isolates (two *Enterobacter cloacae*, one *K. pneumoniae)* from a patient transferred to NYC from another DR institution. Whole genome sequencing was used to determine multi-locus sequence type (MLST) and resistance gene profiles. Phylogenetic analyses of isolates with same ST were performed.

Results. Isolates from the DR and the Dominican patient were of unique genomic backgrounds including pandemic (*K. pneumoniae* ST11) and novel sequence types, and harbored either bla_{KPC-2} or bla_{KPC-3} (Table 1). Replicon typing suggested that these carbapenemase genes were located on distinct plasmids. Phylogenetic analyses using the NYC collection of ~400 sequenced CRE isolates indicated that DR and NYC *K. pneumoniae* ST307 isolates were related (33 SNPs). Further review showed that both patients had recent admissions in Puerto Rico (PR), highlighting the role of regional spread. *K. pneumoniae* ST11 isolates from DR and NYC, on the other hand, were not found to be closely related (1,418–1,440 SNPs).

Conclusion. Genotyping of DR CRE isolates revealed a high genomic diversity, suggesting multiple introductions. Phylogenetics of *K pneumoniae* ST307 place these within a global context, demonstrating links across the Caribbean and North America. International surveillance studies integrating genomics are needed to track and limit the spread of CRE in resource-limited settings such as DR.

Table 1: Comparison of DR Isolates

Organism	MLST	KPC Gene	Origin
K. pneumoniae	ST11	bla_{KPC-2}	DR
	ST1040	bla_{KPC-3}	NYC, DR patient
	ST307	bla_{KPC-2}	DR, travel to PR
	Novel ST	bla_{KPC-3}	DR
C. freundii	ST95	bla_{KPC-2}	DR
E. cloacae	ST456	bla_{KPC-3}	NYC, DR patient

Disclosures. **A. C. Uhlemann**, Merck: Investigator, Grant recipient.

1250. Prevalence and Risk Factors for Acquiring Carbapenem-Resistant *Enterobacteriaceae* in an Intensive Care Unit at a Tertiary Hospital

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Session: 139. Healthcare Epidemiology: Outbreaks
Friday, October 5, 2018: 12:30 PM

Background. Active surveillance testing of carbapenem-resistant *Enterobacteriaceae* (AST-CRE) is recommended in high-risk settings, such as intensive care units (ICUs), to prevent CRE outbreaks or invasive infections. This study aimed to investigate the effects of AST-CRE by analyzing the prevalence and risk factors for acquiring CRE during the ICU care.

Methods. We conducted AST-CRE on rectal swabs of patients admitted to the ICU in the emergency room at a tertiary hospital in South Korea for 12.5 months. AST-CRE was performed upon admission and weekly thereafter. To assess the risk factors of acquiring AST-CRE during the admission period in adult patients, those colonized with CRE upon admission and aged <18 years were excluded. AST-CRE was performed using Centers for Disease Control and Prevention methods. A polymerase chain reaction assay was performed to detect five carbapenemase genes (NDM, KPC, VIM, IMP, and OXA).

Results. A total of 810 patients were admitted during the study period. The acquisition rate and carbapenemase-producing CRE were 2.6% (21/810) and 42.9% (9/21), respectively. No invasive infection due to CRE was found. The most common species were *Klebsiella pneumoniae* (71.4%, 15/21), and eight KPC and one NDM genes were detected. In CRE-positive patients, in-hospital mortality and length of hospitalization were higher ($P = 0.003$) and longer ($P < 0.001$), respectively. Multivariate analyses showed that male gender (adjusted odds ratio [aOR] 8.0; 95% confidence interval [CI] 1.7–36.8), previous hospitalization in the last year (aOR 5.1; 95% CI 1.6–16.4), co-colonization with multidrug-resistant *Acinetobacter* species (aOR 18.3; 95% CI, 4.2–79.2) and extended-spectrum β-lactamase-producing bacteria (aOR 3.4; 95% CI, 1.1–10.9), and length of ICU admission until CRE detection for ≥10 days (aOR 6.5; 95% CI 2.2–19.2) were independently associated with CRE acquisition.

Conclusion. To prevent CRE outbreak or invasive infections, patients admitted in the ICU should be screened using AST-CRE.

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1251. Contaminated Sinks May be an Environmental Source for Serial Transmission of Carbapenem-Resistant *Enterobacteriaceae* (CRE) to ICU Patients

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