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 (66% to 76%, P < 0.002). In the multivariable analysis, patients with COPD were more likely to be appropriately prescribed 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

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 conducted 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, PPE, personal protective equipment (PPE) use, environmental cleaning, and AS practices. Responses to questions were summarized using frequencies and analyzed using χ² 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 with <90% compliance.

Results. Overall, 25 (61%) facilities nationwide completed the survey. All sites reported having written IP&C and AS 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 in HH (49%), HH adherence (49%), 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, particularly with feedback. Sites with ≥90% compliance with the CMS rule were more likely to report providing prescribers with feedback about their prescribing practices (40%).

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

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Session: 138. Healthcare Epidemiology: Non-acute Care Settings

Background. Acinetobacter baumannii is an important agent of healthcare-acquired infections, particularly in 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 by both 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 and patients, and from multiple patient body sites and high-touch surfaces at admission, and monthly up to 6 months. Ciprofloxacin minimum inhibitory concentration (MIC) 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 591, 620 (3.64%) of visits, and environmental contamination in 267, 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 Cefazidime, Imipenem, Ciprofloxacin Vari Based on the Source of Isolation (Patient, Environment, HCP Hands)

| Isolates            | Patient | Environmental | HCP Hands |
|---------------------|---------|---------------|-----------|
| Total Isolates (%)  | 85      | 454           | 36        |
| Resistant to        |         |               |           |
| Imipenem (%)        | 31 (36%)| 118 (26%), P = 0.047* | 3 (8%) |
| Ciprofloxacin (%)   | 32 (38%)| 128 (28%), P = 0.08* | 5 (14%) |
| Cefazidime (%)      | 30 (35%)| 137 (30%), P = 0.34* | 6 (17%) |

* 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.

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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

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. Male 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 Day 30 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 = 0.01) 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) (fig). Targeting 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.

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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 these genetic distances along with visualization on antimicrobial susceptibilities, and patient location histories and dates were displayed in an interactive interface, Philips Intellispaces Epidemiology (PIE), and reviewed by Infection Prevention.

Results. Among 1,570 patients, 1,393 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, averagng 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 and electronic 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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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), and five from patients with bacteremia (one) and pneumonia (three), were obtained from patients with bacteremia (one) and pneumonia (three), 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 a higher odds ratio (aOR) 8.0; 95% confidence interval [CI] 3.7–18.6) for acquiring 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 carbapenemase genes (NDM, KPC, VIM, IMP, and OXA).

Results. A total of 810 patients were admitted during the study period. The acquisition rate and carbapenem-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 a higher odds ratio (aOR) 8.0; 95% confidence interval [CI] 3.7–18.6). 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 210 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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Table 1: Comparison of DR Isolates

| Organism   | MLST    | KPC Gene | Origin |
|------------|---------|----------|--------|
| K. pneumoniae | ST11 | blaKPC1 | DR     |
| ST1040      | blaKPC1 | NYC, DR patient |        |
| ST507       | blaKPC1 | DR, travel to travel |        |
| Novel ST    | blaKPC1 | DR      |        |
| C. freundii | ST95    |         | DR     |
| E. cloacae  | ST456   |         | NYC, DR patient |