incidence can be explored using agent-based models (ABMs). ABMs can simulate complete systems (e.g., regional healthcare networks) comprised of discrete, unique agents (e.g., patients) which can be represented using a synthetic population, or model-generated representation of the population. We used an ABM of a North Carolina (NC) regional healthcare network to assess the impact of increasing antibiotic risk ratios (RRs) across various locations on healthcare-associated (HA) and community-associated (CA) CDI incidence.

Methods. The ABM describes CDI acquisition and patient movement across 14 network locations (i.e., nodes) (11 short-term acute care hospitals, 1 long-term acute care hospital, 1 nursing home, and the community). We used a sample of 2 million synthetic NC residents as ABM microdata. We updated agent states (i.e., location, antibiotic exposure, C. difficile colonization, CDI status) daily. We applied antibiotic RRs of 1, 5, 8.9 (original model RR), 15, and 20 to agents across the network to simulate varying risk corresponding to different antibiotic classes. We determined network HA-CDI and CA-CDI incidence and percent mean change for each RR.

Results. In this simulation study, HA-CDI incidence increased with increasing antibiotic risk, ranging from 11.3 to 81.4 HA-CDI cases/100,000 person-years for antibiotic RRs of 1 to 20, respectively. On average, the per unit increase in antibiotic RR was 33% for HA-CDI and 6% for CA-CDI (figure).

Conclusion. We used a geospatially explicit ABM to simulate increasing antibiotic risk, corresponding to different antibiotic classes, and to explore the impact on CDI incidence. The per unit increase in antibiotic risk was greater for HA-CDI than CA-CDI due to the higher probability of receiving antibiotics and higher concentration of agents with other CDI risk factors in the healthcare facilities of the ABM. These types of analyses, which deconstruct the interconnectivity of network healthcare facilities and the associated community served by the network, might help inform targeted antibiotic stewardship efforts in certain network locations.

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2441. Automated, Rapid Detection of Potential Healthcare-Acquired Infection Clusters Using Whole-Genome Sequencing Data

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Background. Whole-genome sequencing (WGS) has shown promise in identifying transmissions of healthcare-associated infections (HAIs), but it may be costly to sequence all potential HAIs. By automatically identifying samples likely to be HAIs, WGS can be focused on specific samples. We describe an algorithm that quickly identifies potential HAIs by analyzing patient geotemporal and pathogen microbiology data. This approach systematically triages potential HAI investigations to aid infection control professionals (ICPs) in their workflow.

Methods. This novel algorithm within Philips IntelSpace Epidemiology scores the potential of transmission for pairs of infections. Inputs include microbiology (MB) data (genus- or species-level identification and antimicrobial susceptibility test results) and geotemporal (GT) data (timing of sample collection and shared location stays). From the resulting pairwise scores, clusters of potential HAIs are identified. Leveraging 9 months (June, 2018 – March, 2019) of data from a 900-bed US hospital (i.e., 2,823 samples, 1,814 patients and 13 organisms—of which a subset of 404 samples had WGS performed concomitantly with MB studies), we evaluated the extent to which this algorithm captures genetically similar sample pairs.

Results. Pairwise scores enrich for genetically similar samples when considering MB data only (odds ratio: 17.3), GT only (odds ratio: 6.1) and a combination of both (odds ratio: 19.8), with highly significant P-values for all (P < 10^-10). Considering MB only, 91% of sample groups together in potential transmission clusters. With MB and GT data, this fraction drops to 32.4% (604 samples) forming 178 possible clusters, 17 of which contain fewer than ten samples each. The 5 larger clusters contain 40–64 samples each and span multiple units in the hospital.

Conclusion. The proposed system automatically suggests potential HAI clusters. By combining MB and GT data, the number of samples to review is reduced, enabling ICPs to focus their attention and sequencing efforts. By focusing on a targeted group of higher probability clusters, ICPs may be able to increase their efficiency and effectiveness in controlling the spread of HAIs—thus boosting potential for patient safety and amelioration of cost of care.

Disclosures. All authors: no reported disclosures.

2442. Detection of Prosthetic Hip and Knee Joint Infections Using Administrative Databases – A Validation Study

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Background. Forming large cohorts to study prosthetic joint infections (PJIs) is a challenge without an existing surgical registry, as is the case in Canada. Administrative databases are an option, yet PJIs are insensitive. There is a need to improve the detection of PJIs from within administrative databases.

Methods. Individuals who had a primary arthroplasty at four hospitals in Toronto, Canada from 2010 to 2016 were identified using Canadian Classification of Health Intervention codes (based on the International Classification of Disease, Tenth Revision). Each re-admission to the same hospital until December 31, 2016 was reviewed for the presence of a PJI. The performance characteristics (sensitivity, specificity, positive and negative predictive values) of combinations of diagnostic and procedure codes when compared with the gold standard of chart review were calculated. The primary outcome was the algorithm that maximized sensitivity and positive predictive value.

Results. 27,843 primary arthroplasties were performed with 8,959 readmissions, of which 572 involved a PJI. Median follow-up was 1,285 days (interquartile range (IQR) 614–1,891 days), with median time to first re-admission of 352 days (IQR range 166–725 days). PJIs exhibited a sensitivity of 0.86% (95% confidence interval (95% CI) 0.83–0.89) and positive predictive value (PPV) of 0.89% (95% CI 0.86–0.92). The best performing algorithm is a combination of a PJI code or joint spacer insertion procedure code or insertion of a peripherally inserted central catheter along with an arthroplasty code (sensitivity 0.90%, 95% CI 0.88–0.93 and PPV 0.89%, 95% CI 0.86–0.91). Using timing from primary arthroplasty, spacer insertion codes and presence of a subsequent arthroplasty procedure code identified 66% (71/105) of first stage and 74% (108/146) of debridement with joint retention procedures during the first re-admission for a PJI.

Conclusion. Combinations of diagnosis and procedure codes can reliably identify PJIs from administrative databases. Individual orthopaedic procedure codes and timing from primary arthroplasty can inform the surgical procedure performed. This PJI detection algorithm could be used for PJI surveillance and research.

Disclosures. All authors: no reported disclosures.

2443. Impact of Antimicrobial Stewardship on the Incidence of Carbapenem-Resistant Pseudomonas aeruginosa: A Nonlinear Time-Series Analysis Approach to Identify Carbapenem-Resistant Pseudomonas aeruginosa Among Patients With a Primary Arthroplasty at Four Hospitals in Toronto, Canada

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Conclusion. Combinations of diagnosis and procedure codes can reliably identify PJIs from administrative databases. Individual orthopaedic procedure codes and timing from primary arthroplasty can inform the surgical procedure performed. This PJI detection algorithm could be used for PJI surveillance and research.

Disclosures. All authors: no reported disclosures.
threshold was equivalent to a maximum number of 121 patients to be treated. Below this threshold, i.e. in 2018, CarbUSe including 66 patients treated did not select antimicrobial resistance.

Conclusion. PaCRE could be controlled by reducing the use of carbapenems below minimum thresholds of 6.5 DDD/100 bed-days. In order to avoid the onset of resistance in bacteria, i.e. Pseudomonas aeruginosa, less than 121 patients per month should receive this class of drug. This finding could provide innovative approaches to guide antimicrobial stewardship strategy focused on limiting the spread of PaCRE in hospital populations.

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2444. Infection Prevention in Home Healthcare: Results from a National Study of Home Health Agencies
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Session: 256. HAI: Miscellaneous
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Background. As the population of older Americans with chronic conditions continues to grow, the role of home healthcare (HHHC) services in improving care transitions between acute care and independent living has become a national priority. This has led to the development of value-based purchasing (VBP) initiatives, changes in the Centers for Medicare and Medicaid Services’ Home Health Conditions of Participation, and the Joint Commission’s national patient safety goals for HHHC. We aimed to describe the infection prevention and control (IPC) infrastructure in US home health agencies (HHAs).

Methods. From March to November 2018, we conducted in-depth, phone interviews with 41 staff from 13 HHAs across the United States, including administrators, IPC and quality improvement (QI) personnel, registered nurses and home health aides. In October 2018, we launched a nationwide survey to a random sample of 1,500 HHAs stratified by census region, ownership status and urban/rural location, and achieved a 40% response rate. Transcripts of the qualitative interviews were coded and themes were identified using content analysis. Survey data were analyzed using descriptive statistics.

Results. Themes from the interviews included: 1) Uniqueness of HHHC setting, 2) Importance of staff and patient/caregiver education, (3) Care coordination challenges, and, (4) Keys to success and innovation. From the surveys, we found that, at the majority of HHAs, the staff member in charge of IPC had other responsibilities including QI personnel, registered nurses and home health aides.

Discussion. This work represents a current snapshot of IPC infrastructure and identifies important barriers to IPC in these settings.

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2445. Risk for Readmission and Mortality Amongst LTACH Residents with New-Onset Healthcare-Associated Infections
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Background. Long-term acute care hospitals (LTACH) provide cost-effective alternatives for stable patients requiring ICU-level care. LTACH patients are at increased risk for adverse outcomes including healthcare-associated infections (HAI). There is a paucity of data describing outcomes associated with HAIs in LTACH patients.

Methods. This was a single-center, retrospective study of LTACH patients over a 3 year period. Patients with an HAI (bloodstream [BSI], pneumonia [PNA], urinary tract [UTI], and Clostridiodes difficile [CDI] infections) as defined by NHISS criteria were matched by length of stay (LOS) at the time of inclusion to unexposed patients. Follow-up was 30 days from the date of inclusion. The primary outcome was a composite of unplanned readmission to an acute care hospital or death at the LTACH. Secondary outcomes included all-cause mortality. Patients with HAIs were further evaluated to determine risk factors associated with readmission Antibiotics and cultured organisms were collected. Outcomes were analyzed using Cox proportional hazards model. Variables found to have a P < 0.1 on univariate analysis and those of clinical interest were included in the models.

Results. 250 patients were included, 125 in each group. The distribution of HAIs was 40 BSI, 39 UTI, 26 PNA, and 20 CDI. The incidence of the primary outcome and mortality were 26.0% and 11.6% respectively. HAI was associated with increased risk of the primary outcome, but the effect varied over time: Risk increased seven-fold during the first 5 days (HR, 7.47 [95% CI, 2.86–19.42]) but was smaller and non-significant after day five (HR, 1.94 [95% CI, 0.85–4.43]). Mortality was not significantly different between groups (HR, 1.58 [95% CI, 0.74–3.38]). After adjustment, only hypotension (HR, 2.27 [95% CI 1.21–4.27]) and referral hospital LOS > 28 days (HR, 1.97 [95% CI 1.10–3.53]) were associated with readmission. 37% of cultured organisms were multi-drug resistant. 17% of Enterobacteriaceae were carbapenem resistant. Empiric antibiotics failed to cover in 35% of infections.

Conclusion. HAI was associated with a significant increase in risk of readmission. Exploration of modifiable variables of infection, including hypotension and antibiotic selection, may help to reduce rates of readmission.

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2446. Longitudinal Results and Cost Savings Using a Bundle of C. difficile Infection Prevention Strategies in a Long-Term Care Facility
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Background. Long-term care patients are at high risk of C. difficile infections (CDI) due to advanced age, high comorbidity illness burden, and frequent antibiotic use. Primary infection prevention of CDI is challenging and not frequently studied. Following a period of high CDI incidence, the Long-Term Care facility at Sharp Coronado Hospital implemented a bundle of strategies.

Methods. Patient census, the incidence of CDI (primary and recurrent cases), transfers to acute care and length-of-stay were collected from Jul 2008 through December 2018. In the first phase, 2010, a bundle of CDI prevention strategies was initiated, including an Antimicrobial Stewardship Program (ASP), reduction of acid suppression, and L. acidophilus and S. boulardii probiotics with antibiotic use. From 2012, there was further refinement of the ASP and the probiotic was changed to capsules of a 3-species combination of Lactobacillus acidophilus CL1285, L. casei LBC80R and L. rhamnosus CLR2, 100 Billion CFU daily. In October 2016, a protocol was put in place delegating authority to pharmacists to add probiotics to all antibiotic courses. The average CDI rates were calculated and compared for each time period. The net cost of CDI was calculated from the number of CDI cases, hospital length-of-stay and probiotic purchases.

Results. The incidence of facility-onset CDI cases decreased significantly with each policy change from 7.6 cases/10,000 patient-days (2008–09), to 2.8 (2010–11, p = 0.028), to 0.91 (2012-Q3 2016, p = 0.0015) and to the present incidence 0.24 (Q4 2016–2018, p = 0.048). The annual cost of facility-onset CDI was $214k initially. The annual cost, including the purchase of probiotic, decreased to $161k with introduction

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