home time. Using the home time metric, 35.5% of hospitals were reclassified as high performers compared with their average or poor performance on the RSRR or RSMR metric.

Conclusion. Home time is a novel, patient-centered, hospital-level metric that can be easily calculated using claims data, accounts for differences in post-discharge mortality and can be intuitively interpreted. Utilization of this metric could potentially have policy implications in assessing hospital performance on delivery of healthcare to pneumonia patients.

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829. Identification of Congenital Cytomegalovirus Infection Using Real-World Healthcare Data

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Session: P-35. HAI: Epidemiologic Methods

Background. Infants with congenital cytomegalovirus infection (cCMVi) may present with symptoms such as sensorineural hearing loss (SNHL) during the neonatal period and/or develop permanent disability. This study aims to identify infants with cCMV using information available in an electronic healthcare database in Israel.

Methods. We performed a retrospective study in Maccabi Healthcare Services (MHS, 2.4-million-member healthcare system) among infants with ≥30 days continuous enrolment since birth and linked maternal data of women aged 18–44 years in 2013–2017. Data were obtained on diagnosis codes (DX; ICD-9-CM) of CMV and SNHL and dispensed valganciclovir treatment (Tx) within 90 days after birth. To help inform the timing of the CMV infection (congenital vs. postnatal) data on maternal CMV testing history were also obtained among infants whose earliest CMV Dx was at age 22–90 days.

Results. The study included 171,952 infants linked to 128,264 mothers (167,879 pregnancies). A total of 461 infants (0.3%) had a CMV Dx within 90 days, 81.3% of which (n=375) were diagnosed within 21 days. Among all infants with a CMV Dx within 90 days, 70.5% had a CMV Dx within 30 days. 108 also had dispensed Tx (n=101) and/or SNHL Dx (n=16). Among infants diagnosed at age 22–90 days without evidence of prior Tx or SNHL (n=69), 12 had a record of primary maternal CMV infection in pregnancy, 8 had mothers who were CMV seronegative at the start of pregnancy without follow-up test results, and 49 had a laboratory test result that was negative. A medical record review is being conducted to validate each cCMV case definition in the MHS database.

Conclusion. In large Israeli healthcare system, 0.3% of infants had a CMV Dx in their electronic health records suggestive of potential cCMVi. Case review is ongoing to validate these codes and help inform analyses on the clinical and economic burden of cCMVi in this population where awareness of CMV is high but newborn screening is not universal.

Disclosures. Morgan Marks, PhD, ScM, Merck and Co. Inc. (Employee), Shareholder), Wei Wang, PhD, Merck (Employee), Anushua Sinha, MD, MPH, Merck & Co. (Employee), Merck & Co. (Shareholder), Merck & Co. (Consultant)

830. The effect of a long-stay patient on transmission of a pathogen to shorter-stay patients in a small multi-bed hospital unit: Implications for infection control

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Session: P-35. HAI: Epidemiologic Methods

Background. Objective: To quantify the effect of a long-stay patient in a hospital unit on the likelihood of colonization of that patient and other patients in the unit.

Prolonged hospital and intensive care unit (ICU) stays have been found to be risk factors for colonization and infection with bacteria such as carbapenem-resistant Enterobacteriaceae (CRE) for which there are limited treatment options and high mortality rates, making prevention of transmission and infection important public health objectives. Many studies have shown that long-stay patients (such as inpatients, residents, or skilled nursing facility patients) are at higher risk for hospital-acquired infections than short-stay patients, but the impact of long-stay patients on short-stay patients in the same hospital unit has not received as much attention. Here, we consider a mathematical model of pathogen transmission within a hospital unit and assess the impact at different patient-patient transmission rates of a single long-stay patient on the probability that any other patient leaves the unit colonized with a pathogen.

Methods. We estimated the increased risk caused by a colonized long-stay patient on colonization of other patients using an ordinary differential equation Markov model with three mechanisms of colonization (pre-existing colonization, environmental transmission, and patient-patient transmission) with parameters previously estimated from a 13-bed hospital rehabilitation unit to evaluate the probability of exiting colonized.

Results. A single colonized long-stay patient increases the probability of each other patient exiting the unit colonized from 10.4% to 17.3%, a relative increase in risk of 1.4, and increases the expected number of colonized patients within the unit from 1.37 to 2.07 (not including the long-stay colonized patient).

Probability of exiting colonized from a unit with a long-stay, initially colonized patient versus the probability of exiting colonized from a unit with no long-stay patient.

The solid black line indicates a unit with regular turnover, whereas the dashed black line indicates a unit with a single long-stay, initially colonized patient. The vertical line shows the value of γ = 0.002 inferred from data from a 13-bed rehabilitation unit, and the shaded regime indicates the uncertainty in this estimate (0.000329, 0.003729).

Conclusion. Colonized long-stay patients pose a risk to other uncolonized patients in the unit, especially at higher patient-patient transmission rates. Potential long-stay patients should be screened for CRE at entry and periodically during their stay because they are both at high risk of colonization and also of transmitting bacteria to other patients. Consider increased surveillance, isolation, and/or decolonization of long-stay patients.

Disclosures. All Authors: No reported disclosures

831. Analysis of a Worldwide Collection of Klebsiella pneumoniae CC258 with Reference to Carbapenemase Production Using the 1928 Core Genome (cg) Multilocus Sequence Type (MLST) Reveals Endemicity and Global Dissemination of Clones

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Session: P-36. HAI: Gram-negatives (MDR-GNR)

Background. K. pneumoniae (KPN) has emerged as a major hospital associated pathogen in the recent years. Clonal complex (CC) 258 constitutes an international epidemic clone responsible for spread of extended spectrum beta-lactamases (ESBL) and carbapenemases. We evaluated the core genome (cg) MLST, resistance (R) gene and plasmid profiles of a worldwide collection of KPN using the 1928 bioinformatic cloud platform.

Methods. A total of 155 KPN clinical isolates (CC258, n=129; non-CC258, n=26) collected from 19 countries during 2018 of SENTRY Program were analyzed. Isolates included carbapenem resistant (CR; n=120) and non-CR (n=35). Whole genome sequencing FASTQ files were uploaded to the 1928 pipeline for analysis.

Results. Most CC258 isolates belonged to ST258, ST11 and ST512 (Table), and separated from unrelated ST by allelic distance (ad) >2000. cgMLST grouped together isolates from the same STs, and those from similar geographies had greater homology, except isolates from US showed greater heterogeneity (ad 620). Applying an ad cutoff of < 100, ST258 isolates grouped in 4 clades with a predominance of either KPC-2 or -3. An ad cutoff of < 200 identified 7 clades within ST11 that were related by geography and R genes. Among CC258 isolates KPC was the major carbapenemase (58.1%) and associated with Tn4401 (α or β in 84% KPC). NDM-1 was detected (8.5%) only in ST11 and ST395. KPC-2 was more prevalent in Latin America and the isolates were closely related (ad 104) among ST258 compared to ST11 (ad 355). KPC-3 CC258 isolates showed ad of 164 and were from Italy, Russia, Greece, and US. CTX-M-14 was prevalent in ST258 while CTX-M-15 was common in other STs, except ST512 which carried no CTX-M despite clustering within ST258.

Conclusion. 1928 generated cgMLST showed good correlation with MLST in classifying all KPN isolates. ST258 isolates showed tight clustering, no NDM genes and distribution in the Americas while ST11 showed global dissemination and diversity of carbapenemases.
Table 1

832. Assessment of Risk Factors Associated with Wide-resistance Gram-negative Bacteria Infections

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Session: P-36. HAI: Gram-negatives (MDR-GNR)

Background. Enterobacteria and multidrug-resistant non-fermenting Gram-negative bacilli present a challenge in the management of invasive infections, leading to mortality rates due to their limited therapeutic arsenal. The objective of this work was to analyze risk factors that may be associated with these infections, for a better situational mapping and assertive decision-making in a university hospital in Brazil.

Methods. The study was conducted between January and September 2019, with 167 patients in contact isolation at a university hospital in Brazil. Potential outcome-related variables for wide-resistance Gram-negative bacteria (BGN) infections were evaluated. Risk factors were identified from univariate statistical analysis using Fisher’s test.

Results. 51 (30.5%) out of 167 patients in contact isolation evolved with wide-resistance BGN infection. Risk factors in univariate analysis were age, hospital unit and previous use of invasive devices. Patients aged up to 59 years were more likely to progress to infection than those aged over 60 years (p = 0.0274, OR 2.2, 95% CI 1.1-4.5). Those admitted to the oncology unit (p < 0.001, OR 32.5, CI 9.1-116.3) and intensive care unit (p < 0.001, OR 28.6, CI 3.5-225.9) units were more likely to develop this type of infection. The least likely were those admitted to a kidney transplant unit (p = 0.0034, OR 15.33, CI 1.8-131.0). Prior use of mechanical ventilation (p = 0.0058, OR 12.2, CI 2.0-76.1) and delayed bladder catheter (p = 0.0266, OR 5.0, CI 1.2-20.1) in patients with respiratory and urinary tract infection, respectively, were also reported as risk factors related to these infections. The gender of the patients was not significant for the study.

Conclusion. This study determined that variables such as age, hospitalization unit, use of mechanical ventilation and delayed bladder catheter could be considered important risk factors in triggering the infectious process by wide-resistant gram-negative bacteria. Thus, the analysis of these factors becomes a great foundation to prevent the development of multiresistant pathogens through prevention strategies, prophylaxis management and more targeted empirical therapies.

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833. Characteristics and Utilization Patterns of Colistin Compared with Newer Agents in Gram-negative Infections

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Session: P-36. HAI: Gram-negatives (MDR-GNR)

Background. Colistin has resurfaced in light of Gram-negative (GN) resistance. New antibiotics to treat antibiotic resistant GN infections (eg, ceftazidime-avibactam, cefepime-tazobactam, meropenem-vaborbactam [new agents]), have recently been approved but their use vs colistin is unclear. We compared the overall use of colistin and new agents from 2014 to 2018 in patient days on therapy (PDOT).

Methods. Data on non-cystic fibrosis patients from the Premier Healthcare Database was used. PDOT was tabulated quarterly for Premier hospitals and projected to the US population. A subset of data from 2016 to 2018 with microbiologically confirmed GN (MCGN) infections was selected for adult inpatients receiving ≥3 days of therapy with colistin, new agents, carbapenems, or extended-spectrum cephalosporins. The index infection was defined either as the first carbapenem-resistant (CR) or -sensitive infection if no CR infection occurred. Patients could be treated with ≥1 antibiotic per infection. Utilization was examined by pathogen and patient characteristics.

Results. PDOT with colistin decreased from 2015 to 2018 while new agents have increased (Figure). During 2015-2018, colistin and any of 3 new agents were used by 3,320 and 5,781 inpatients, respectively, of whom, 649 (20%) and 1,284 (22%) had MCGN pathogens. Colistin-treated patients were sicker than patients treated with new agents (Table), underlying renal disease was present in 34.5% vs 36.3%, and median length of stay of 17 vs 15 days, respectively. Mean total hospital cost was $93,815 vs $84,013 for colistin and new agents, respectively. Mortality was greater in colistin patients (18% vs 12%; p < 0.0001). CR infections constituted similar proportions of colistin and new agent use (79% vs 75%). Colistin accounted for 15.2% of CR carbapenem treatments and 9.7% of CR Enterobacteriaceae (CRE) treatments compared with 4.5% and 12.8%, respectively, for new agents.

Figure. Projected Inpatient PDOT

Table.

834. Clinical Outcomes with Carbapenem-Resistant Pseudomonas aeruginosa that Retain Susceptibility to Traditional Antipseudomonal β-lactams: Atlanta, 2016-2018

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Session: P-36. HAI: Gram-negatives (MDR-GNR)

Background. Carbapenem-resistant Pseudomonas aeruginosa (CRPA) often results from multiple mechanisms, creating unique phenotypic patterns of resistance including retaining susceptibility to traditional antipseudomonal β-lactams: ceftazidime, cefepime, aztreonam.