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 rates, and can be intuitively interpreted. Utilization of different metrics could potentially have policy implications in assessing hospital performance on delivery of healthcare to pneumonia patients.

Disclosures. Rajeshwari Nair, PhD, Merck and Company, Inc. (Research Grant or Support)

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 develop permanent dysfunctions. This study aims to identify infants with cCMVi 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 enrollment 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 of birth, 95% 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 did not have laboratory results. A medical record review is being conducted to validate each cCMVi 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) Wei Wang, PhD, Merck (Employee, Shareholder) Merck and Co. Inc. (Consultant)

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 ST358, 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 < 200, 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 Thn401 (a 6 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 ST235 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 ST312 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.