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Background. In 2010, a multispecies outbreak of IMP type carbapenemase-producing Enterobacteriaceae (IMP-CPE) occurred at a large acute care hospital in Japan. The outbreak continued for years involving more than 100 patients mainly in surgical wards.

Methods. Because of the long period of the outbreak, investigation were focused on hospitalized patients whose clinical samples were positive for IMP-CPE between July 2013 and March 2014. A case–control study was conducted for cases who underwent abdominal surgery with controls from whom meropenem-susceptible Enterobacteriaceae were isolated. Pulsed-field gel electrophoresis (PFGE) was used for molecular typing. To evaluate genetic relationship among IMP-CPE isolates of different species, plasmid analysis using S1 nuclease to separate plasmid and chromosomal DNA followed by plasmid DNA extraction and whole-genome sequencing (WGS) was conducted.

Results. During the study period, 22 cases were identified and 22 IMP-CPE isolates which consisted of eight *Escherichia coli*, five *Klebsiella oxytoca*, five *Enterobacter cloacae*, three *Klebsiella pneumoniae* and one *Enterobacter aerogenes* were obtained. All five isolates of *K. oxytoca* had similar PFGE profiles which suggested clonal transmission. However, PFGE profiles of *E. coli*, *E. cloacae* and *K. pneumoniae* isolates were diverse. Plasmid analysis revealed that all 22 isolates shared ca. 50 kb IncN plasmid with bla_{IMP-6} which implies interspecies transmission of it The case–control study which adjusted by days of hospitalization with 11 cases and 24 controls revealed that pancreato-duodenectomy (adjusted odds ratio (aOR) = 6.4, 95% confidence interval (CI) 1.3–32.4) and enteric fistula (aOR = 8.0, 95% CI 1.5–41.9) were associated with IMP-CPE acquisition. Use of endoscopy within the past six months was not associated with IMP-CPE (aOR = 0.8 95% CI 0.2–4.2). With a bundled infection control with Osaka City Public Health Office, the outbreak was contained in July 2016.

Conclusion. Dissemination of carbapenemase gene by transmissible plasmid can play a critical role to complicate epidemiology of CPE outbreak and made it difficult to control. Plasmid analysis using WGS technology is a promising tool to untangle it.

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

1202. Multimodal Sequencing of a Clonal Case Cluster of Carbapenem-Resistant Citrobacter Reveals Unexpectedly Rapid Dynamics of KPC3-Containing Plasmids

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Background. Carbapenem-resistant *Enterobacteriaceae* (CRE) are a major public health threat. We report four clonally related *Citrobacter freundii* isolates harboring the bla^{KPC-3} carbapenemase in April–May 2017 that are nearly identical to a strain from 2014 at the same institution. Despite differing by ≤5 single nucleotide polymorphisms (SNPs), these isolates exhibited dramatic differences in carbapenemase plasmid architecture.

Methods. We sequenced four carbapenem-resistant *C. freundii* isolates from 2017 and compared them with an ongoing CRE surveillance project at our institution. SNPs were identified from Illumina MiSeq data aligned to a reference genome using the variant caller Pilon. Plasmids were assembled from Illumina and Oxford Nanopore sequencing data using Unicycler.

Results. The four 2017 isolates differed from one another by 0–5 chromosomal SNPs; two were identical. With one exception, these isolates differed by >38,000 SNPs from 25 *C. freundii* isolates sequenced from 2013 to 2017 at the same institution for CRE surveillance. The exception was a 2014 isolate that differed by 13–16 SNPs from each 2017 isolate, with 13 SNPs common to all four. Each *C. freundii* isolate harbored wild-type bla^{KPC-3}. Despite the close relationship among the 2017 cluster, the plasmids harboring the bla^{KPC-3} genes differed dramatically: the carbapenemase occurred in one of the two different plasmids, with rearrangements between these plasmids across isolates. The related 2014 isolate harbored both plasmids, each with a separate copy of *blaKPC-3*. No transmission chains were found between any of the affected patients.

Conclusion. WGS confirmed clonality among four contemporaneous bla^{KPC-3}-containing *C. freundii* isolates, and marked similarity with a 2014 isolate, within an institution. That only 13–16 SNPs varied between the 2014 and 2017 isolates suggests durable persistence of the bla^{KPC-3} gene within this lineage in a hospital ecosystem. The plasmids harboring these carbapenemase genes proved remarkably plastic, with plasmid loss and rearrangements occurring on the same time scale as two to three chromosomal point mutations. Combining short and long-read sequencing in a case cluster uniquely revealed unexpectedly rapid dynamics of carbapenemase plasmids, providing critical insight into their manner of spread.

Disclosures. **M. J. Ferraro**, SeLux Diagnostics: Scientific Advisor and Shareholder, Consulting fee. **D. C. Hooper**, SeLux Diagnostics: Scientific Advisor, Consulting fee.

1203. Molecular Screening for Multi-Drug Resistance Genes in Hospitalized Veterans

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Background. Gene-based screening is a tool to detect and track multi-drug-resistant organisms (MDROs) in hospitalized patients. MDRO acquisition and colonization during the duration of a hospital stay and their persistence over time are not well described.

Methods. A peri-anal swab was collected within 48 hours of admission from patients on medical wards and the MICU at the Washington DC VA Medical Center and repeat swabs were obtained day 7 and 14 on patients consenting to participate. Clinical and laboratory data from admission to 12mo post discharge was reviewed. Genes associated with VRE (VanA), ESBL (CTX-M), carbapenase-producing organisms or CPOs (OXA-23, OXA-51) and CREs (KPC,NDM,VIM, IMP, OXA-48) were tested on swabs by the Acuitas-MDRO Test (OpGen, Inc.).

Results. Between July 2015 and August 2016, 565 hospitalized patients were screened with 210 swabs collected from 182 subjects. One swab was nonevaluable. Subjects had a mean age 67.5 ± 12.0 years (26–94 years, 38% ≥70 years) and 39% received empiric antibiotics at admission. Subjects were hospitalized for 1037 cumulative bed-days (1–81 days) with median LOS of 3 days; 84% (152/182) had a stay of a week or less. Among those who remained hospitalized long enough for serial testing, 45% were willing or able to provide >1 swab. Those with >1 swab were significantly older (+4.9 years, $P = 0.03$), more likely to have to have been admitted for an infectious diagnosis (48% vs. 24%, $P = 0.02$). All subjects negative for MDRO genes on admission with >1 swab remained negative on serial sampling. Sixteen subjects (8.8%) had one or more genes present on screening and all three with >1 swab had persistence of that gene on repeat sampling. Genes harbored included CTX-M (4.4%), VanA (4.4%), OXA-51(0.6%), KPC (0.6%).

Conclusion. The rate of occult MDRO colonization was low in our predominately elderly hospitalized patients. The majority of consenting participants were discharged before swabs could be repeated. Serial sampling revealed that results of swabs persisted over time in the same subject despite treatments received during hospitalization, including exposures to antibiotics. The identification of occult MDRO carriage during a hospitalization, even when obtained after admission, may have utility in guiding treatment for providers.

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

1204. The MDR Upon Admission Score for Shortening Time to Initiation of Appropriate Antimicrobial Therapy in the Era of Widespread Resistance to Antimicrobials

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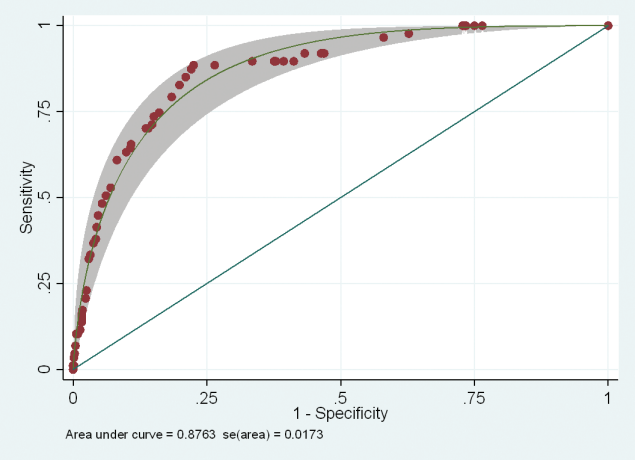
Background. Multi-drug-resistant organisms (MDRO) pose a growing burden, including in non-hospital settings. Delay in initiation of appropriate antimicrobial therapy (DAAT) upon admission to an acute care hospital is common and is associated with worse outcomes. The aim of this study was to develop a prediction score for MDRO infection upon admission, in order to improve patients' outcomes and avoid misuse of broad-spectrum antimicrobials.

Methods. A retrospective case–control analysis was conducted at Assaf Harofeh Medical Center, Israel, comparing adult patients with MDRO infections diagnosed in the first 48 hours of hospitalization to patients presenting with non-MDRO sepsis (i.e., patients with microbiologically confirmed non-MDRO infection, or patients with non-microbiologically confirmed sepsis). MDROs were determined by clinical laboratory testing. Patients were identified over four consecutive months (August–December 2016). A multivariable logistic regression of predictors for MDRO infection upon admission was used to develop the prediction score.

Results. Ninety-five of 818 total patients (11.6%) had MDRO infection. The final score included 10 parameters: (1) home therapy (IV therapy, wound care, or specialized nursing care, 16 points), (2) routine (at least weekly) outpatient clinic visits in the past 3 months (15 points), (3) history (2 years) of past MDRO colonization (14 points), (4) any antibiotics in the preceding 3 months (12 points), (5) invasive procedure in the past 6 months (11 points), (6) elderly (≥65 years old, 10 points), (7) hemiplegia or paraplegia (8 points), (8) resident of long-term care facility (7 points), (9) severe sepsis (i.e., severe sepsis, septic shock, or multi-organ failure, 6 points), and (10) acute kidney injury (5 points). A cutoff of ≥24 points had a sensitivity of 90%, a specificity of 73% and an ROC AUC = 0.88 (figure).

Conclusion. This study presents the development of a new prediction score for MDRO infection upon admission, based on parameters that could easily be extracted

at bedside for patients admitted with sepsis. A future prospective interventional study is needed in order to validate the score, captured at bedside electronically, in terms of improving patients' outcomes.



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

1205. Emergence of Carbapenemase Producing *Enterobacteriaceae* in South Central Ontario, Canada

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Background. The spread of CPE is an increasing global threat to patient safety. We describe the introduction and evolution of CPE in south-central Ontario, Canada.

Methods. The Toronto Invasive Bacterial Diseases Network has performed population based surveillance for CPE in metropolitan Toronto and Peel region from first identified isolates in 2007. All laboratories test/refer all carbapenem non-susceptible Enterobacterial isolates for PCR testing for carbapenemases. Demographic and medical data and travel history are collected from chart review and patient/physician interview.

Results. Since 2007, 659 patients have been identified as colonized/infected with CPE; 362, 57%) have at least one clinical isolate. Annual incidence has increased from 0 in 2006 to 1.3 per 100,000 in 2016/17 (Figure 1). First bacteremia occurred in 2010, the incidence in 2017 was 0.14 per 100,000 population. 388 (59%) patients were male, median age was 70 years (range 3 months–100 years). Most common genes among first isolates were NDM (306, 46%), OX48 (149, 23%), KPC (122, 19%). Most common species were *K. pneumoniae* (268, 41%) and *E. coli* (259, 39%). Over time, second species/same gene were identified in 113 (16%) patients. In addition, 34/xxx patients with isolates with NDM and/or OXA-48 subsequently had a second isolate with a different gene/gene combination. Of 518 patients whose travel and hospitalization history are available, patients with VIM were less likely than other patients to have a foreign hospitalization or travel history (9/28 vs. 341/490, $P < 0.0001$). Patients with KPC were more likely to have a hospitalization history outside Canada and the Indian subcontinent (25/70, 36%), in Canada (47/164,29%) than to have no hospitalization in the last year (13/93, 14%), or a history of hospitalization in the Indian subcontinent (2/191, 1%) ($P < 0.001$). The number of incident patients with different hospitalization and travel history over time is shown in Figure 2.

Conclusion. CPE is increasingly recognized in southern Ontario, both in patients with a history of exposure in healthcare in other countries, and to healthcare in Canada. Intensification of control programs is urgently needed.

Figure 1. Incidence of clinical isolates of CPE over time.

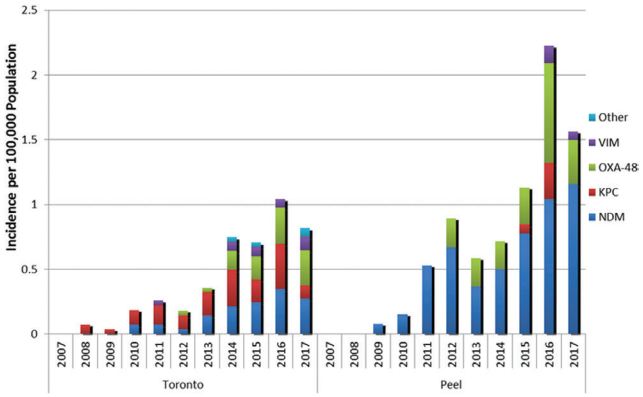
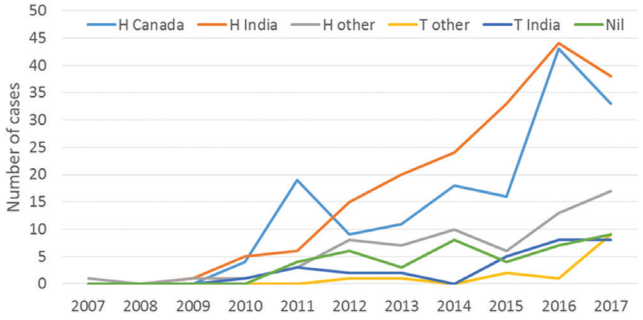


Figure 2. Number of incident CPE cases with different hospitalization (H) and travel (T) history over time.



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1206. Risk Factors of Antibiotic Resistance in *E. coli* Isolated from the MAL-ED Birth Cohort Study in Rural Tanzania

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Background. The emergence and spread of antimicrobial resistance is a serious global public health crisis. Drug-resistant Gram-negative bacteria, like *Escherichia coli*, are particularly concerning given their significant morbidity and mortality. Despite the increasing prevalence of drug-resistant Gram-negative bacteria worldwide, there are significant knowledge gaps in low resource countries. We aimed to characterize the prevalence, phenotypes, and risk factors of drug-resistant *E. coli* carriage in children up to age 5 from stool collected in the Etiology, Risk Factors, and Interactions of Enteric Infections and Malnutrition and the Consequences for Child Health and Development (MAL-ED) birth cohort study in rural Tanzania.

Methods. Two hundred sixty-two children were enrolled in the MAL-ED Tanzania site. We randomly selected 100 children who had *E. coli* specimens archived every 6 months through 60 months. Up to five lactose-fermenting colonies were selected from growth on MacConkey agar. Drug susceptibility testing of 18 antibiotics was performed by disk diffusion. CLSI interpretive criteria were used for determination of resistance. Generalized estimating equations were used to create a multivariate Poisson regression model for drug resistance risk factors.

Results. Eight hundred twenty-three *E. coli* specimens were available for testing. The highest rates of resistance were to ampicillin, cefazolin, and cotrimoxazole, respectively. No carbapenem resistance was found. 1.8% met criteria for extended-spectrum β-lactamase production based on combination disk testing. 696 (84.6%) specimens met criteria for multi-drug resistance (nonsusceptible to at least 1 drug in at least three drug categories). In terms of dynamic risk factors, there was no association between antibiotic use or episodes of diarrhea and antibiotic resistance. For static risk factors, there was an association between higher income and increased antibiotic resistance.