of patients (82%) suffered blast injuries; of which, 88% were from improvised explosive devices. Patients had a median injury severity score (ISS) of 38 (IQR 30–45) and time from injury to first infecting *K. pneumoniae* isolate was 15 days (IQR 8–31). The median hospital stay was 49 days (IQR 28–70) and four patients died. All patients had received antibiotics prior to diagnosis. Twenty-three (46%) patients had initial isolates classified as MDR. There was no difference in age, ISS, or time from injury to first isolation among those who did and did not have initial MDR isolates. Sixteen patients had 64 serial isolates, of which 24 were wound, 20 respiratory, 14 blood and six urine. Three of these 16 patients died compared with 1 of 35 patients without serial isolates.

Conclusion. *K. pneumoniae* infections are common among combat casualties. Patients with *K. pneumoniae* infections were severely injured and almost half of initial infecting isolates were MDR, complicating treatment.

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

1199. Epidemiology of Carbapenem-Resistant *Klebsiella pneumoniae:* A Comparative Study Between Facilities in the United States and the Dominican Republic

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Background. The prevalence of multi-drug-resistant organisms (MDRO) is on the rise globally. MDRO infections carry high morbidity and mortality. There is a paucity of data on Carbapenem-resistant *Klebsiella pneumoniae* (CRKp) in the Dominican Republic (DR). Evaluating CRKp in various settings will provide data on contrasting epidemiologic risk factors. We evaluated the epidemiology of CKRp in three contrasting settings, a 495-bed urban academic center (AC), a 151-bed urban community hospital (CH) and a 200 bed teaching hospital in the DR (DRH).

Methods. We performed a retrospective cohort study of patients with CRKp cultures from 2014 to 2016 from AC, CH and DRH. A comparative evaluation of the epidemiology of CRKp between the cohorts was performed. Demographics, co-morbid conditions, antibiotic sensitivity, and outcomes were compared between hospital cohorts.

Results. Cohort AC had 64 patients, compared with eight from CH and eight from DRH. AC (59%) and CH (62%) cohorts included more men than the DRH cohort (25%). Average age was 62, 66, and 51, respectively. History of MDRO, antibiotic use in the past 6 months and hospitalization within the past year were common risk factors (Figure 1). Diabetes and end-stage renal disease were common comorbidities at all facilities (Figure 2). Charleston Comorbidity Index (CCI) score was highest at AC (6.6) and DRH (6.4) compared with CH (4). Mortality was highest in DRH (63%, 6/8) and AC (11%, 7/64) while CH had no deaths. Urine was the most common source at AC (67%) and CH (75%) while blood was most common at DRH (62.5%). CRKp isolates were susceptible to colistin at varying rates (AC=85%, CH = 63%, DRH = 80%).

Figure 1. Common risk factors for CRKp between facilities.

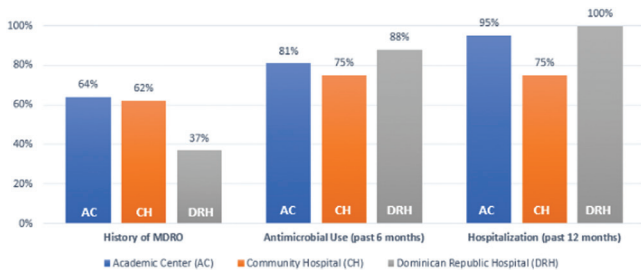
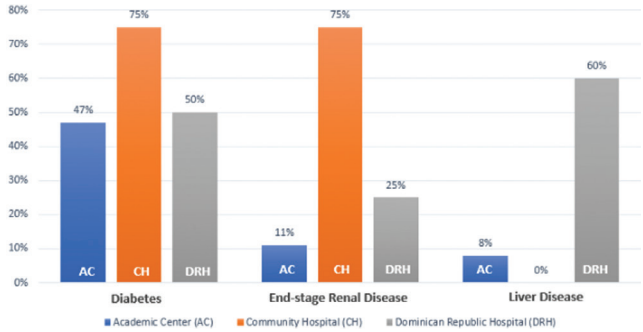


Figure 2. Common patient comorbidities for CRKp between facilities.



Conclusion. Prior antibiotic use and hospitalization were common risk factors in all settings. Mortality and CCI scores for CRKp was highest at AC and DRH, which are tertiary referral centers. CH had less overall mortality and higher rates of colistin resistance. Further studies are needed to understand these risk factors. Strengthening antimicrobial stewardship and infection control practices in the United States and abroad may help curb the spread of resistance in different clinical settings.

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

1200. Molecular Epidemiology of Cephalosporinases and Extended Spectrum β-Lactamases (ESBLs) in *Proteus mirabilis* Isolates From Croatia: Following the Spread of Resistance Determinants Between Long-Term Care Facilities and the Community

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Background. Previous studies on *P. mirabilis* strains isolated from Croatian healthcare institutions revealed the predominance of TEM-52 extended spectrum β-lactamase (ESBL), as well as the emergence of plasmid AmpC β-lactamases. Our aim was to molecularly characterize cefalosporinases in *P. mirabilis* isolates from long-term care facilities (LTCFs) and to compare their resistance profile and dynamics with community isolates.

Methods. From a total of 3,321 *P. mirabilis* isolates collected from two LCTFs and from outpatients between 2015 and 2017, 1.23% of them were resistant to third generation of cephalosporins. Antimicrobial sensitivity was tested by broth microdilution method. ESBLs and plasmid-mediated AmpC β-lactamases were detected with phenotypic inhibitor-based tests and polymerase chain reaction (PCR). Antibiotic resistance dissemination and genetic context of *bla* genes were interrogated by conjugal mating and PCR mapping, respectively. Plasmids were characterized by conjugation and transformation experiments, as well as PCR-based replicon typing.

Results. High-level of resistance to amoxicillin, co-amoxiclav, first, second and third generation of cephalosporins was found in all isolates. Three isolates tested positive in inhibitor-based test with clavulanic acid, and 38 both in Hodge test and combined disk test with phenylboronic acid, indicating the production of ESBLs and plasmid-mediated AmpC β-lactamases, respectively. Two ESBL-positive organisms yielded amplicons with primers for CTX-M β-lactamase of group 1 and one for TEM. All AmpC-positive organisms were identified by PCR as CMY (with an additional TEM). Insert sequence IS^{Ecp-1} was found upstream of bla^{CMY}i bla^{CTX-M} genes. CTX-M positive strains harbored IncK plasmid, whereas AmpC-positive strains were negative for known plasmid types. This is also a first description of *P. mirabilis* harboring CTX-M-15 β-lactamase in Croatia.

Conclusion. Our study showed the persistence of CMY β-lactamases in one LTCF, but also the dissemination of characteristic resistance determinants to another LTCF and the community. Similar to some other studies, there was a clear trend of cephalosporinase dynamic switch from TEM variants to CMY and CTX-M, with impending consequences for treatment decisions.

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

1201. A Prolonged Multispecies Outbreak of Carbapenemase-Producing Enterobacteriaceae Due to Transmissible Plasmid With Carbapenemase Gene

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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