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 infection 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.

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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Session: 136. Healthcare Epidemiology: MDRGram Negative Infections
Friday, October 5, 2018: 12:30 PM

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 CRKP in three contrasting settings, a 49-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) (Figure 1). Diabetes and end-stage renal disease were common comorbidities at all settings. Charleston Comorbidity Index (CCI) score was highest at AC (6.6) (Figure 1). Diabetes and end-stage renal disease were common comorbidities at all settings.

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.

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

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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 cephalosporinases 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 LTCFs and from outpatients between 2015 and 2017, 1.23% of them were resistant to third generation 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 determinants and genetic plasmidic genes were interrogated by conjugal mating and PCR mapping, respectively. Plasmidic metalloenzymes are conjugated and transformation experiments, as well as PCR-based replication typing.

Results. High-level resistance to amoxicillin, co-amoxiclav, first, second and third generation 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 IS6609 was found upstream of blaCTX-M-8 genes. CTX-M positive strains harbored IncK plasmid, whereas AmpC-positive strains were negative for known plasmidic 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.

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 CRKP in three contrasting settings, a 49-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 CH (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%).

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.
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. Gene-based screening is a tool to detect and track multi-drug-resistant organisms (MDROs) in hospitalized patients. MDRD 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 ICU 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), carbapenemase-producing organisms or CPOs (OXA-23, OXA-51) and CREs (KPC,NDM,VIM, IMP, OXA-48) were tested on swabs by the Acutas-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 nonvalueable. Subjects had a mean age 67.5 ± 12.0 years (26-94 years) and 39% were females. Subjects were admitted for a 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 (72.4 ± 10 years, P = 0.03); more likely to have had 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 serial 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.

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

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Session: 136. Healthcare Epidemiology: MDR-Gram Negative Infections

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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<sup>KPC</sup>-3 carbapenemase in April–May 2017 that are nearly identical to a strain from 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 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 each 2017 isolate, with 13 SNPs common to all four. Each C. freundii isolate harbored wild-type <i>bla<KPC</i>-3. Despite the close relationship among the 2017 cluster, the plasmids harboring the <i>bla<KPC</i>-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 <i>blaKPC-3</i>. No transmission chains were found between any of the affected patients.

Conclusion. WGS confirmed clonality among four contemporaneous <i>bla<KPC</i>-3-containing C. freundii isolates, and marked similarity with a 2014 isolate, within the same institution, differing only 13–16 SNPs and 2017 isolates suggests durable persistence of the <i>bla<KPC</i>-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.

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