Methods. The National Inpatient Sample (NIS) was used to identify all hospitalizations during 2002 to 2014; all primary and secondary diagnoses were searched to identify resistant infection that utilized the ICD-9 code “V09.” All hospitalizations were stratified based on the indication of resistant infection, and comparisons were made with the chi-square test and linear regression for categorical and continuous variables, respectively. A multivariable binary logistic regression model was used to examine survival for those with ESBL infection. All analyses were conducted with SAS version 9.4. P < 0.005 was considered significant.

Results. The analysis identified 320,885,511 hospitalizations with 17,732 identified with ESBL infection. Significant differences for those with and without an ESBL infection were found based on the US region with the pertinent results as follows: Northeast: 19.95% vs. 23.30%, Midwest: 14.71% vs. 16.81%, South: 25.14% vs. 40.53%, and West: 40.20% vs. 19.35%; P < 0.001. Results indicated the US region as a significant predictor of mortality for those with ESBL infection. Regions identified in Figure 1. Conclusion. Notable findings from this study include a statistically significant variation in mortality risk between US regions. Comparatively lower risk of mortality as related to ESBL infection was noted in the Midwest region when compared with the West region. A greater understanding of the regional epidemiology of β-lactamases is needed to clarify why this disparity exists.

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1196. Serratia marcescens Strains Carrying bladaKPC-2 and bladaKPC-3 Carbenapenemase Associated With Chronic Mechanical Ventilation
Matthew Fisher, MD, Elizabeth Diago-Navarro, PhD, Olga Kaplan, MD, Eric Sin, MD, and Bettina C. Fries, MD, FIDSA
1Infectious Diseases, Stony Brook University Hospital, Stony Brook, New York, 2Department of Medicine (Division of Infectious Disease), Stony Brook University Hospital, Stony Brook, New York, 3Stony Brook University, Stony Brook, New York

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Background. Carbapenem resistance (CR) in Enterobacteriaceae is a growing concern which the CDC has designated as an urgent threat. At our institution we have noted emergence of CR strains in clinical isolates including a growing number of Serratia marcescens. CR in Serratia marcescens in the United States is mostly reported to be encoded by the SME family of chromosomally encoded carbapenemases, while Serratia marcescens.

S. marcescens.

S. marcescens.

S. marcescens.

S. marcescens.

1197. Microbiological Surveillance of Duodenoscopes Before and After High-Level Disinfection Following Endoscopic Retrograde Cholangiopancreatography (ERCP)
Ben K. Loprandi, MD, FIDSA1,2, Tasha Fernley, BS1,3, Jana Coombs, BS1,3, Michaela A. Gazdik, PhD1,5, Lori Smit, RN, MS1,3, Kristin K. Dascomb, MD, PhD1,3, and John Burke, MD, FIDSA, FSHEA1,2
1Clinical Epidemiology and Infectious Diseases, Intermountain Medical Center, Murray, Utah, 2Division of Infectious Diseases, University of Utah School of Medicine, Salt Lake City, Utah, 3Biology, Utah Valley University, Orem, Utah, 4Endoscopy Laboratory, Intermountain Medical Center, Murray, Utah, 5LDS Hospital and University of Utah, Salt Lake City, Utah

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Background. Transmission of antibiotic-resistant bacteria during endoscopic retrograde cholangiopancreatography (ERCP) has been linked to the complex design of the duodenoscope (scope) elevator channel and cantilever. We implemented a scope cleaning program to monitor the efficacy of disinfection and to identify frequency of pre-disinfection exposure to antibiotic-resistant bacteria.

Methods. Facilities performing ERCPs within the Intermountain Healthcare system voluntarily submit scope cultures to the Infectious Diseases Epidemiology Laboratory. Cultures are collected at designated intervals based on procedure volumes at each site. Samples are submitted by endoscopy techs trained to collect flush and swab samples of the distal end of the scope using a previously described method before (PRE) and after (POST) high-level disinfection. Selective media is used to screen for Gram-negative bacilli-resistant to third generation cephalosporins (ESBL) and vancomycin-resistant Enterococcus (VRE).

Results. Between March 7, 2016 and April 18, 2018, 1,255 scope samples from 10 facilities were cultured (533 PRE samples and 722 POST samples). 483 (90.6%) PRE samples were positive, with 75 (15.5%) screening positive for an antibiotic-resistant organism (60 ESBL and 15 VRE). 19 (2.6%) POST samples were positive, with 4 (21.1%) screening positive for ESBL. One of the four ESBL positive POST samples had a corresponding PRE sample for comparison; E. coli and Klebsiella variicola were isolated in both indicating residual contamination. Two of the ESBL-positive POST cultures did not have corresponding PRE samples and one had a PRE culture negative for ESBL.

No POST samples contained VRE. Endoscopy personnel were contacted for each positive POST culture and endoscopy reprocesing practices were reviewed. Additionally, scopes were quarantined, reprocessed and re-cultured. Scopes were returned to use once POST cultures were negative.

Conclusion. Conformations of scopes with antibiotic-resistant bacteria during ERCP is common. High-level disinfection is effective at reducing bacterial burden but is imperfect. Routine surveillance for post-reprocessing bacterial colonization has been helpful to minimize patient exposure and to maintain focus on the importance of reprocesing.

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1198. Clinical Characteristics and Outcomes of Klebsiella pneumoniae Infections in Service Members Who Sustained Trauma in Iraq and Afghanistan
John Oke, MD, PhD, Katrin Mende, PhD, Susan J. Kaiser, BS1, Leigh Carson, MS1,3, Dan Z. Lu, MS1,3, Timothy J. Whitman, DO1,3, Joseph L. Petfield, MD1,3, David R. Trible, MD, DPh1,3 and Dana M. Blyth, MD1,3
1Infectious Disease, San Antonio Military Medical Center, San Antonio, Texas, 2Infectious Diseases Clinical Research Program, Department of Preventive Medicine (Biostatistics), Uniformed Services University of the Health Sciences, Bethesda, Maryland, 3Preventive Medicine and Biostatistics, Infectious Disease Clinical Research Program, Uniformed Services University of the Health Sciences, Bethesda, Maryland, 4Walter Reed National Military Medical Center, Bethesda, Maryland, 5Landstuhl Regional Medical Center, Landstuhl, Germany, 6Infectious Disease Clinical Research Program, Uniformed Services University, Bethesda, Maryland, 7Department of Medicine, Brooke Army Medical Center, Fort Sam Houston, Texas

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Background. Klebsiella pneumoniae infections present a challenge to the clinician due to increasing resistance. K. pneumoniae was the third most common species of multdrug-resistant (MDR) Gram-negative organism in trauma patients sustaining injuries in Iraq and Afghanistan from 2009 to 2014. This study aims to elucidate the epidemiology of these infections by characterizing clinical aspects, risk for MDR infections, and outcomes.

Methods. All initial and serial (27 days from prior isolate) infecting K. pneumoniae isolates were collected from the Trauma Infectious Disease Outcomes Study (TIDOS) (6/09-12/14). Antimicrobial susceptibilities were determined using the BD Phoenix Automated Microbiology System and CLSI criteria. MDR was defined as resistant to one or more of 23 classes of antimicrobials, β-lactamases, carbapenems and/or fluoroquinolones or production of an ESBL or KPC.

Results. Of 588 K. pneumoniae isolates in the TIDOS registry, 141 infecting isolates (98 initial) from 51 patients met inclusion criteria. Initial isolates were respiratory (31%), wound (25%), blood (20%), urine (10%), intra-abdominal (8%) and other (6%). All patients were male with a median age of 23 years (IQR 21–28). The majority

represents a clonal expansion and whether the blαKPC-2 plasmid was transferred from Klebsiella or Enterobacter to Serratia in one of the patients.

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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

Alfredo J. Mena Lora, MD1,2; Rita Rojas Fermin, MD; Anel Guzman, MS; Scott Borgetti, MD and Susan C. Blesdale, MD,1 Division of Infectious Diseases, University of Illinois at Chicago, Chicago, Illinois,2 Department of Infectious Diseases, Hospital General Plaza de la Salud, Santo Domingo, Dominican Republic, 3Microbiology Laboratory, Hospital General Plaza de la Salud, Santo Domingo, 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 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 (59%) and CH (62%) while blood was most common at DRH (62.5%). CRKP isolates from DRH were susceptible to colistin at varying rates (AC=85%, CH = 63%, DRH = 80%). Sixteen patients died compared with 1 of 35 patients without serial isolates.**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 curtail 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

Tomas Divic, MD, PhD1; Miroslav Mestrovic, MD, PhD2; Tatjana Brezak Tatic, MD, PhD2; Maja Bogdan, MD; 3Daniela Bandic-Pavlovic, MD, PhD; Gordana Cavric, MD, PhD; Domago Jurevics, MD, PhD2; Katharina Bernadette Srieter, MD; Ana Bencic, MD in training; Sandra Saradic, MD, PhD2; and Branka Bedenic, MD, PhD2,3. 1Clinical Microbiology and Parasitology Unit, Polyclinic Dr. Zora Profozic, Zagreb, Croatia, 2University Centre Varazdin, University North, Varazdin, Croatia, 3Department of Laboratory Diagnostics, Children’s Hospital Zagreb, Zagreb, Croatia, 4University of Zagreb, School of Medicine, Zagreb, Croatia, 5Microbiology Service, Institute of Public Health for the Osijek-Baranja County, Osijek, Croatia, 6University Hospital Centre Zagreb, Zagreb, Croatia, 7Internal Medicine Department, Clinical Hospital Merkur, Zagreb, Croatia, 8Josip Juraj Strossmayer University of Osijek, School of Medicine, Osijek, Croatia, 9Clinical Hospital Centre Osijek, Osijek, Croatia, 10Clinical Hospital Centre “Sestre Milosrdnice” Zagreb, Croatia, 11Clinical Hospital Centre Split, Split, Croatia

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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 is 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 mobilization were interrogated by conjugal mating and PCR mapping, respectively. Plasmids were characterized by conjugation and transformation experiments, as well as PCR-based replication 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 IS6052 was found upstream of blaCMY-2 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-lactamase 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 Aminoglycoside Resistance

Takuya Yamagishi, MD, PhD1; 2Marti Matsui, MD, PhD; 2Teyoshi Sekuruka, PhD; 2Masayuki Ito, PhD; 2Munehisa Fukusumi, MD, PhD; 2Tomoko Uchida, MD, PhD; 2Miyuki Tsubokura, RN; 2Akio Tawa, MD, PhD; 2Shoji Nakamori, MD, PhD; 2Atsushi Miyamoto, MD, PhD; 2Hideki Yoshida, MD, PhD; 2Satowa Suzuki, MD, PhD; 2Kengo Shibayama, MD, PhD, PhD; 2Makoto Kuroda, PhD; 2Tamano Matsui, MD, PhD; 2and Kanaoru Oishi, MD, PhD; 2Infectious Disease Surveillance Center, National Institute of Infectious Diseases, Tokyo, Japan, 3Antimicrobial Resistance Research Center, National Institute of Infectious Diseases, Tokyo, Japan, 4Patologen Genomics Center, National Institute of Infectious Diseases, Tokyo, Japan, 5Department of Paediatrics, Kameda Medical Center, Kamogawa, Chiba, Japan, 6Department of Infectious Diseases, National Hospital Organization Osaka National Hospital, Osaka, Japan, 7Infection Control Team, National Hospital Organization Osaka National Hospital, Osaka, Japan, 8Department of Paediatrics, National Hospital Organization Osaka National Hospital, Osaka, Japan, 9Department of Surgery, National Hospital Organization Osaka National Hospital, Osaka, Japan, 10Osaka City Public Health Office, Osaka, Japan, 11Department of Bacteriology II, National Institute of Infectious Diseases, Musashimurayama, Tokyo, Japan