**1184. Resistance Patterns and Susceptibility Analysis of *Klebsiella pneumoniae* Infections in Service Members Who Sustained Trauma in Iraq and Afghanistan**

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***Background.*** *Klebsiella pneumoniae* was the third most common species of multidrug-resistant (MDR) Gram-negative organism in military trauma patients injured in Iraq and Afghanistan (2009–2014). This study aims to characterize the antimicrobial susceptibility and resistance patterns of *K. pneumoniae* isolates in these patients.

***Methods.*** All infecting *K. pneumoniae* isolates (IKpI) archived by the Trauma Infectious Disease Outcomes Study (TIDOS) and 96 colonizing isolates (CKpI) from groin swabs were included (6/09-12/14). All CKpI linked with IKpI were included; the remainder to total 50 MDR and 46 non-MDR CKpI were chosen randomly. Antimicrobial identification and susceptibilities were determined by CLSI criteria using the BD Phoenix Automated Microbiology System. MDR was defined as either resistance to ≥3 classes of aminoglycosides, β-lactams, carbapenems, and/or fluoroquinolones or production of an ESBL or KPC.

***Results.*** Of 588 *K. pneumoniae* archived isolates, 237 isolates were included in the analysis (141 IKpI and 96 CKpI). IKpI sources were 40% wound, 22% respiratory, 20% blood, 9% urine, and 9% other. Antibiotic susceptibilities for IKpI were: cefazolin (CFZ) 20%, ceftriaxone 30%, levofloxacin 62%, piperacillin–tazobactam (PTZ) 41%, meropenem 96%, and amikacin 89%. MDR IKpI and CKpI were more likely to have had prior fluoroquinolone (82% vs. 18%, $P < 0.01$) or anti-pseudomonal penicillin (53% vs. 47%, $P < 0.01$) exposure. Seventeen patients had CKpI cultured at a median of 5 days (IQR 2–17) before a subsequent IKpI with 11 (65%) having MDR CKpI. All IKpI isolated after MDR CKpI were also MDR. Among IKpI recovered after non-MDR CKpI, new resistance was noted in 1 IKpI to gentamicin (200 days post-CKpI), 1 IKpI to ertapenem (7 days post-CKpI), two IKpI to CFZ (10 days and 17 days, respectively), and 1 IKpI to PTZ (19 days post-CKpI). Serial isolates of IKpI had similar MDR status (63% initial IKpI were MDR, whereas 76% of subsequent IKpI were MDR).

***Conclusion.*** *K. pneumoniae* isolates in military trauma patients from Iraq and Afghanistan had challenging resistance patterns. Prior exposure to fluoroquinolones and anti-pseudomonal penicillins were associated with MDR *K. pneumoniae* isolation. MDR status of CKpI predicted subsequent IKpI MDR status.

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**1185. Impact of Bloodstream Infections Caused by Multidrug-resistant Organisms on Performance Status: A KARS-Net Study**

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***Background.*** Infections caused by multidrug-resistant (MDR) organisms are associated with poorer clinical outcomes and higher economic burden. However, there has been limited data on the impact of MDR infection on the performance status of patients.

***Methods.*** Patients with bloodstream infections by *S. aureus, E. faecium, E. coli, K. pneumoniae, P. aeruginosa,* and *A. baumannii* have been identified prospectively as a part of a multicenter nationwide surveillance for antimicrobial resistance. Medical records of the patients enrolled from July 2015 through December 2016 were reviewed for demographic, clinical, microbiologic characteristics, and patient outcome. MDR was defined as MRSA, VRE, and nonsusceptibility to one or more agents in three or more different classes of antibiotics for Gram-negative bacteria. Performance status was evaluated by Eastern Cooperative Oncology Group (ECOG) Performance Status before admission and at discharge. Primary outcome was any decline in ECOG at discharge. Multiple logistic regression was used to identify independent risk factors for ECOG decline.

***Results.*** A total of 19 hospitals participated to the network. The numbers of subjects were 410 for *S. aureus*, 392 for *E. faecium*, 708 for *E. coli* and *K. pneumoniae*, and 678 for *P. aeruginosa* and *A. baumannii*. In univariate analysis, bacteremia by MDR organisms was associated with ECOG decline only in patients with *P. aeruginosa* (18.4% vs. 10.3%, OR 1.962, 95% CI 1.132–3.399) and *A. baumannii* (27.6% vs. 11.8%, OR 2.834, 95% CI 1.328–6.045) infections. Patients with MDR *K. pneumoniae* infection had lower risk of ECOG decline (6.6% vs. 15.8%, OR 0.378, 95% CI 0.183–0.780). Multivariable analysis also showed that infection by MDR organism was independently associated with ECOG decline in patients with *P. aeruginosa* or *A. baumannii* infections (OR 2.068, 95% CI 1.478–2.895), but not with other MDR organisms. Comorbidities and initial ECOG showed higher effect size in patients with *S. aureus* and *E. faecium* infections.

***Conclusion.*** In this large multicenter nationwide study, bloodstream infections caused by MDR *P. aeruginosa* and *A. baumannii* were associated with higher risk of decline in performance status at discharge. MDR status did not show association in infections by other species.

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**1186. Prevalence of Carbapenemase-Producing *Enterobacteriaceae* (CPE) in Hospital Drains in Southern Ontario**

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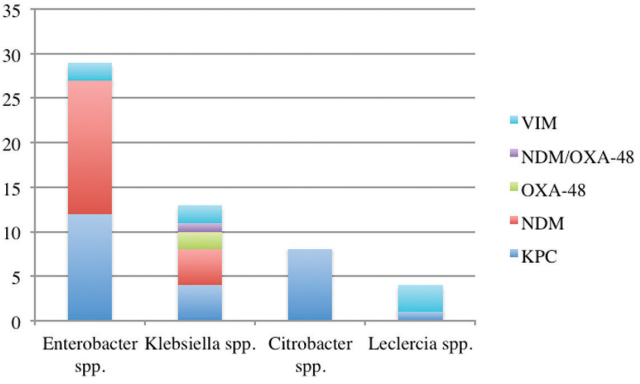
***Background.*** Hospital waste water systems are an emerging reservoir for CPE. We aimed to describe the prevalence of CPE in hospital drains in southern Ontario, where patients are rarely colonized/infected by CPE.

***Methods.*** Ten Ontario hospitals identified rooms occupied by CPE+ inpatients from 2007 to 2017. Drain swabs from patient rooms and communal shower rooms were inoculated into BHI + 10% Dey-Engley neutralizing broth and incubated overnight, then PCR on enriched broth for carbapenemase genes as well as culture on McPOD/McMEM were performed.

***Results.*** Over 10 years in 10 hospitals, 343 CPE+ inpatients exposed 1,205 drains (852 sinks, 353 bathtub/shower drains) in 501 patient rooms and 71 communal shower rooms. 53 (4%) drains in 40 (8%) patient rooms and 10 (14%) communal shower rooms were CPE+ by PCR and culture. CPE+ drains were from 15/475 (3%) hand hygiene sinks, 4/352 (1%) bathroom sinks, 23/272 (9%) bathtubs/showers, and 11/81 (13.6%) communal showers. Eleven (21%) of the CPE+ drains contained 31 CPE gene/species combinations. Patient room drain CPE gene/species combinations are shown in Figure 1: eight (15%) matched the CPE gene/species combination of a room occupant, 23 (43%) matched gene only, and 23 (43%) did not match. 54% of drain isolates were *Enterobacter* spp. but 9% of patient isolates were *Enterobacter* spp. There were 155 (13%) additional drains with one or more genes detected by PCR but not culture; 94 (61%) contained VIM (88 bathtub, one bathroom sink, and five hand hygiene sink drains), 33 GES, 17 OXA, 16 IMP, 10 KPC, and five NDM. There were six drains where one or more genes were detected by culture but not PCR; four (67%) were bathtub/shower drains containing an OXA, one bathtub/shower drain containing an NDM, and one hand hygiene sink drain containing a KPC.

***Conclusion.*** Hospital drains may become a reservoir for CPE, which may persist for years. Sensitivity of PCR and culture for detection of CPE and CP organisms may differ. The presence of "unmatched" drains suggests undetected patient colonization. Risk of transmission from drains to room occupants requires investigation.

**Figure 1.** Patient room CPE drain isolate gene/species combinations ($N = 54$).

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