

Table 2: Organism, Multilocus Sequence Type (MLST) and Carbapenemases Present

Organism and MLST	Total Isolates	
	(n=131)	Carbapenemase Present (No.)
<i>K. pneumoniae</i> ST-258	17	KPC-2 (2); KPC-3 (13)
<i>E. coli</i> ST-113	14	NDM-1; OXA-48
<i>E. coli</i> ST-131	14	NDM-1; OXA-48
<i>E. coli</i> ST-405	9	NDM-5 (2)
<i>E. cloacae</i> ST-116	7	KPC-2 (2)
<i>K. pneumoniae</i> ST-45	4	KPC-2
<i>K. pneumoniae</i> ST-11	3	NDM-1 (2); NDM-7
<i>E. coli</i> ST-69	3	NDM-5
<i>K. pneumoniae</i> ST-35	3	KPC-2 (2); NDM-5
<i>E. coli</i> ST-10	2	NDM-5 (2)
<i>K. pneumoniae</i> ST-16	2	KPC-2
<i>K. pneumoniae</i> ST-37	2	KPC-2 (2)
<i>K. pneumoniae</i> ST-147	2	NDM-5 (2)
<i>E. coli</i> ST-156	2	OXA-181
<i>E. coli</i> ST-410	2	OXA-181
<i>E. coli</i> ST-167	2	NDM-5
<i>E. hormaechei</i> ST-901	1	IMI-1
<i>E. cloacae</i> ST-484	1	KPC-2
<i>E. cloacae</i> ST-729	1	KPC-2
<i>E. cloacae</i> ST-359	1	NDM-5
<i>E. coli</i> ST-6870	1	NDM-5
<i>K. pneumoniae</i> ST-2970	1	KPC-2
<i>K. pneumoniae</i> ST-395	1	NDM-5 & OXA-232
<i>K. pneumoniae</i> ST-1043	1	NDM-1
<i>E. coli</i> ST-1316	1	NDM-7
<i>K. pneumoniae</i> ST-193	1	KPC-3
<i>K. pneumoniae</i> ST-268	1	KPC-2
<i>E. coli</i> ST-648	1	OXA-48
<i>E. coli</i> ST-73	1	NDM-5
<i>E. coli</i> ST-443	1	OXA-181
Unknown Sequence Type	27	IMI-3; KPC-2; NDM-1; OXA-181

**Conclusion:** Compared to US data, Alameda County *Klebsiella* spp. were nearly half as likely to produce any carbapenemase, and *E. coli* were three times more likely to produce an NDM carbapenemase. CP-CRE represented a wide array of MLST, with the globally distributed KPC-producing outbreak strain ST-258 being the most frequently identified. Two strains that have been associated with hypervirulent and multidrug resistant infections in Asia, *K. pneumoniae* ST-35 and ST-11, were also reported.

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**1433. Promoting Vaccination of Vaccine Preventable Diseases in Newly Employed Nurses and Doctors Guided by Serological Study**

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**Background.** Vaccination after serological evaluation of healthcare workers is key component of vaccine preventable diseases (VPDs) preparedness in hospital. The aim of this study is to determine the seroprevalence of VPDs and the vaccination rates among newly employed nurses and doctors.

**Methods.** A cross-sectional study was conducted at a referral university hospital in the Republic of Korea. All newly employed nurses and doctors without immunity were recommended to have the hepatitis B virus (HBV), varicella zoster virus (VZV), measles, mumps, and rubella (MMR), hepatitis A virus (HAV) and tetanus-diphtheria-pertussis (Tdap) vaccination. HBV, VZV, MMR vaccinations were financially supported and Tdap vaccination was recommended without testing. We investigated the seroprevalence of HAV, HBV, and VZV and vaccination rate of recommended vaccination (HAV, HBV, MMR, VZV, and Tdap) from Jan 1<sup>st</sup>, 2017 to March 31<sup>st</sup>, 2020.

**Results.** A total of 668 (527 female, 141 male) newly employed nurses and doctors were identified. The median age (IQR) is 25 (24-27). Seroprevalence were 59.1% (95%

confidence interval [CI] 55.4-62.8) for HAV, 86.1% (95% CI 83.5-88.7) for HBV, and 92.4% (95% CI 90.4-94.4) for VZV. Vaccination rate of recommended vaccination were 24.5% (95% CI 18.5-30.5) for HAV, 23.3% (95% CI 13.6-33.0) for HBV, 48.7% (95% CI 33.0-64.4) for VZV, 30.0% (95% CI 25.5-34.5) for MMR and 33.1% (95% CI 29.0-37.2) for Tdap respectively.

**Conclusion.** Seroprevalence of HAV was lower than HBV and varicella in newly employed nurses and doctors. Although persistent effort to improve the healthcare worker's vaccination, the actual rates were low. Further strategy promoting vaccination of newly employed nurses and doctors are needed.

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**1434. Rickettsial Infections Complicated With Acute Renal Failure**

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**Background.** Rickettsiosis, an acute febrile illness, is generally considered as a benign disease. However, severe cases were reported, among which acute renal failure (ARF) represented 13 to 18% of the cases. We aimed to study the clinical and evolutionary features of rickettsiosis complicated with ARF, when compared with all rickettsial infections.

**Methods.** We conducted a retrospective study including all patients hospitalized for rickettsiosis in the infectious diseases department between 1995 and 2018. The diagnosis was confirmed by serologies (seroconversion).

**Results.** Overall, we encountered 28 patients (6.4%) with ARF among 440 patients with rickettsiosis. There were 19 males (67.9%). Patients with ARF were significantly older (53±16 vs 38±17 years; p< 0.001). They consulted for eruptive fever (78.6%), febrile cephalalgia (10.7%) or isolated fever (10.7%). Arthralgia and vomiting were noted in 75% and 35.7% of the cases, respectively. There were 4 cases (14.3%) of meningitis and 2 cases (7.1%) of meningoencephalitis. The mean creatinine levels were 158 µmol/L [120-444 µmol/L]. In comparison with all rickettsial infections, eschars were more frequently noted among patients with ARF (46.4% vs 23.8%; p=0.008). They were more frequently diagnosed with septic shock (14.3% vs 0.5%; p< 0.001) and retinitis (10.7% vs 1.5%; p=0.015). Comparison of the disease evolution showed that death was significantly more frequent among cases with ARF (7.1% vs 0.2%; p=0.011). The mean length of hospital stay was significantly longer among patients with ARF (8.7±4.7 vs 5.3±3.5 days; p=0.001). As to gender and the revealing symptoms, no significant difference was noted.

**Conclusion.** Rickettsial infections complicated with ARF had a poor prognosis, especially among the elderly. Prompt empiric antibiotic therapy might improve the prognosis.

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**1436. Use of Whole Genome Sequencing to Characterize Antimicrobial-resistant Salmonella Berta Isolates from Clinical and Retail Meat Sources**

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**Background.** Antimicrobial resistance (AMR) in foodborne pathogens of animal origin, including non-typhoidal *Salmonella* (NTS) are a public health concern. Pennsylvania conducts integrated surveillance for AMR in NTS isolates from human and animal sources in collaboration with the National Antimicrobial Resistance Monitoring System (NARMS).

**Methods.** During 2009-2014, *Salmonella enterica* isolates from various types of meat purchased from randomly selected retail outlets in southeastern Pennsylvania were analyzed by pulsed-field gel electrophoresis (PFGE). We compared PFGE patterns from meat with clinical isolates in the Pennsylvania surveillance database. All meat isolates and a subset of matched clinical isolates were tested for susceptibility to antimicrobial agents. Eleven isolates with indistinguishable PFGE patterns were analyzed by whole genome sequencing (WGS). Sequence data were uploaded to the FDA's GalaxyTrakr platform for quality assessment, genome assembly, AMR gene detection, and phylogenetic inference via single-nucleotide polymorphism (SNP) analysis.

**Results.** PFGE patterns of 86 (48.6%) of 177 meat isolates had PFGE matches to 1,665 clinical isolates; 40 distinct PFGE patterns were represented among the shared patterns. Seventeen (43%) of the 40 shared PFGE patterns (with ≥1 isolate(s) from both sources) were considered multi-drug resistant (MDR). Among the 48 *S. Berta* pattern JAXX01.0001 isolates, 5 (10.9%) and 2 (100%) from human and meat sources respectively were MDR including resistance to amoxicillin and ceftriaxone. WGS analysis of one isolate from ground turkey meat (PNUSAS061602) was genetically related to clinical isolates including two within 9 and 11 SNPs [Figure]. Presence of genes that hydrolyze extended spectrum cephalosporins (ESC), [blaCMY, blaHERA, or blaTEM], was identified in eight (two meat and six clinical) isolates. One meat isolate was resistant to six antibiotics including ceftriaxone.

Figure 2. Single nucleotide polymorphism (SNP) distance matrix showing relatedness in non-typhoidal *Salmonella* isolates from retail meat (n=2) and human (n=9) sources — Pennsylvania, 2010-2014. One *S. Berta* from retail meat was separated from two clinical two clinical isolates by 9 and 11 SNPs. Second isolate from meat