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

Organism and MLST	Total Isolates (n=131)	Carbapenemase Present (No.)
K. pneumoniae ST-258	17	KPC-2 (2); KPC-3 (13)
E. coli ST-113	14	NDM-1; OXA-48
E. coli ST-131	14	NDM-1; OXA-48
E. coli ST-405	9	NDM-5 (2)
E. cloacae ST-116	7	KPC-2 (2)
K. pneumoniae ST-45	4	KPC-2
K. pneumoniae ST-11	3	NDM-1 (2); NDM-7
E. coli ST-69	3	NDM-5
K. pneumoniae ST-35	3	KPC-2 (2); NDM-5
E. coli ST-10	2	NDM-5 (2)
K. pneumoniae ST-16	2	KPC-2
K. pneumoniae ST-37	2	KPC-2 (2)
K. pneumoniae ST-147	2	NDM-5 (2)
E. coli ST-156	2	OXA-181
E. coli ST-410	2	OXA-181
E. coli ST-167	2	NDM-5
E. hormaechei ST-901	1	IMI-1
E. cloacae ST-484	1	KPC-2
E. cloacae ST-729	1	KPC-2
E. cloacae ST-359	1	NDM-5
E. coli ST-6870	1	NDM-5
K. pneumoniae ST-2970	1	KPC-2
K. pneumoniae ST-395	1	NDM-5 & OXA-232
K. pneumoniae ST-1043	1	NDM-1
E. coli ST-1316	1	NDM-7
K. pneumoniae ST-193	1	KPC-3
K. pneumoniae ST-268	1	KPC-2
E. coli ST-648	1	OXA-48
E. coli ST-73	1	NDM-5
E. col 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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Session: P-65. Public Health

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 1st, 2017 to March 31th, 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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Session: P-65. Public Health

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.

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

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

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Session: P-65. Public Health

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

was separated from those associated with human infections by 14 (n=1), 17 (n=1) and ≥20 (n=7).

	M1002588 3001A	M1100987 3001A	M1202244 7001A	PNUSAS0 61600	PNUSAS0 61601	PNUSAS0 61602	PNUSAS0 61603	PNUSAS0 61606	PNUSAS0 61608	PNUSAS0 62053	PNUSAS0 62054	SRR8137 075
M10025883 001A	1	32	43	38	31	33	31	34	25	38	33	130
M11009873 001A	32	1	22	23	11	9	26	19	30	23	42	130
M12022447 001A	43	22	1	32	17	24	35	29	39	35	51	139
PNUSAS06 1600	38	23	32	0	21	25	21	14	36	30	37	134
PNUSAS06 1601	31	11	17	21	0	14	24	17	27	23	40	128
PNUSAS06 1602	33	9	24	25	14	0	28	20	32	24	44	129
PNUSAS06 1603	31	26	35	21	24	28	0	17	29	23	30	127
PNUSAS06 1606	34	19	29	14	17	20	17	0	32	24	32	129
PNUSAS06 1608	25	30	39	36	27	32	29	32	0	28	16	122
PNUSAS06 2053	38	23	35	30	23	24	23	24	28	0	36	134
PNUSAS06 2054	33	42	51	37	40	44	30	32	16	36	0	129
SRR813707 5	130	130	139	134	128	129	127	129	122	134	129	0

Conclusion. WGS analysis revealed clinically relevant ESCs genes in closely related *S.* Berta isolates from human and animal sources. Presence of these genes in NTS highlights the need for enhanced One-Health surveillance and judicious use of antibiotics in humans and food-animal production.

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1437. Biochemical characterization of L1 and L2 β-lactamases from clinical isolates of Stenotrophomonas maltophilia

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Session: P-66. Resistance Mechanisms

Background. *Stenotrophomonas maltophilia* is a Gram-negative, non-fermenting opportunistic pathogen. Two β-lactamases provide intrinsic resistance to β-lactams: a class B Metallo- β-lactamase L1, and a class A serine β-lactamase (SβL) L2. Recently, we described novel variants of the L1 and L2 in a collection of clinical *S. maltophilia* isolates collected in the US, and showed through analyses of the amino acid sequences that L1 and L2 grouped into 4 (A-D, B, C, and E) and 2 (A and D) clades, respectively. We aimed to characterize the new L1 and L2 clinical variants biochemically.

Methods. Representative *bla*L1 and *bla*L2 genes from each of the identified clades were cloned into pBC-SK and pET24 vectors and transformed into *E. coli* DH10B and BL21 (DE3) cells, respectively. Minimal inhibitory concentrations (MICs) were determined using CLSI approved methods. Cell-based assays and biochemical characterization performed on purified enzymes, including circular dichroism (CD), thermal stability, and steady-state kinetics assays, were performed.

Results. Susceptibility testing results using DH10-B *E. coli* strains expressing the L1 and L2 variants are shown in Table 1. Remarkably, while all L1 variants confer the same level of resistance to carbapenems, L2B conferred higher MICs to 3rd gen cephalosporins and aztreonam than L2D. Kinetics assays confirmed differences in the *k*cat of both enzymes to ceftazidime (32s-1 for L2B vs. 7s-1 for L2D) and avibactam inhibition constant *Ki* (1.7 μM for L2B vs. 4.5 μM for L2D). Structurally, L2B and L2D present distinctive CD spectra and thermal stabilities (*Δ*Tm 5°C).

Table 1

Table 1. Minimum inhibitory concentrations of *E. coli* pBC SK (+) producing L1 and L2 variants.

	TAZ	TAX	FEP	PIP	ATM	TZP	TIM	SAM	CZA	IPM	MEM
pBCSK+	0.5	0.125	0.06	4	0.25	≤2	≤16	≤16	≤0.5	0.5	≤0.125
L1a	512	64	4	2048	0.25	2048	>4096	4096	>128	32	32
L1b	512	64	4	2048	0.25	2048	>4096	4096	>128	16	16
L1c	512	128	4	2048	0.25	1024	>4096	4096	>128	16	16
L1d	512	64	4	1024	0.25	1024	>4096	4096	>128	**8**	16
L1e	**16**	**16**	**0.5**	1024	0.25	1024	>4096	4096	**16**	32	32
L2b	128	32	2	512	2048	512	256	64	0.5	0.5	0.125
L2d	**8**	**8**	2	512	**512**	256	128	128	0.25	0.5	0.125

TAZ: ceftazidime; TAX: cefotaxime; FEP: cefepime; PIP: piperacillin; ATM: aztreonam; TZP: piperacillin tazobactam; TIM: ticarcillin clavulanate; SAM: ampicillin sulbactam; IPM: imipenem; MEM: meropenem. Values in red represent ≥ 2 folds difference in the MIC value.

Conclusion. As opposed to the L2 variants, our results suggest that the L1 variants may not be functionally nor structurally different. Differences between L2B and L2D might have arisen due to the use of cephalosporins and SβL inhibitors. Further experiments are on the way to determine the structural basis of these observations and the implication of these for the design of novel β-lactamase inhibitors.

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1438. Dissecting the Multifaceted Nature of Antibiotic Resistance in Clinical Isolates of Neisseria gonorrhoeae by Natural Transformation

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Session: P-66. Resistance Mechanisms

Background. *Neisseria gonorrhoeae* (NG) causes the sexually transmitted disease gonorrhea. It has developed resistance to every antibiotic introduced for gonorrhea treatment such that NG clinical isolates with multidrug resistance (MDR) are increasingly common. We hypothesize that natural transformation could be used to transfer genetic determinants of antibiotic resistance from drug-resistant NG clinical isolates without pre-knowledge of the genetic determinants to a new background under antibiotic selection to generate isogenic transformants for further characterization.

Methods. Natural transformation, PCR amplification and DNA sequencing, and antibiotic susceptibility testing were used in the studies.

Results. We have validated the hypothesis using genomic DNA from an MDR including ciprofloxacin-resistant NG clinical isolate as a donor and a ciprofloxacin-susceptible NG isolate as a recipient under the selective pressure of ciprofloxacin. This led to a series of transformants that contain single or multiple genetic resistance determinants being generated depending on the resistance levels and transformation frequencies. Antibiotic susceptibility testing and genetic characterization of the transformants allowed us to (i) identify ciprofloxacin resistance determinants including efflux mutation $mtrR_{-79}$ and target mutations GyrA S91F D95G and ParC D86N, (ii) quantify the contribution of each genetic determinant responsible for the ciprofloxacin resistance and (iii) regenerate the ciprofloxacin resistance phenotype of the donor isolate to detect multiple paths of possible resistance development for ciprofloxacin. Furthermore, we also validated the hypothesis with a novel antibiotic gepotidacin to identify pre-existing genetic determinants contributing to varying susceptibility to this antibiotic. Finally, we envision that, along with whole genome sequencing, natural transformation could be used to identify and quantify novel genetic resistance determinants to current or novel antibiotics in drug-resistant NG clinical isolates.

Conclusion. We demonstrated the utility of natural transformation in dissecting the multifaceted nature of antibiotic resistance in NG clinical isolates.

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1439. High Rates of Drug Resistance in Escherichia coli from a Pilot Antimicrobial Resistance Surveillance System in Cambodia

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Session: P-66. Resistance Mechanisms

Background. Antimicrobial resistance (AMR) is a major and growing global public health problem. The Cambodia Ministry of Health established a pilot laboratory-based AMR surveillance system for blood specimens in 2017. The objective of this study is to characterize AMR among pathogenic isolates from blood samples.

Methods. A retrospective analysis was performed using one year of data from a pilot AMR Surveillance system in Cambodia. Four blood culture isolate pathogens were included: *Escherichia coli, Klebsiella pneumoniae*, *Salmonella Typhi /Salmonella Paratyphi A* and *Staphylococcus aureus*. Blood culture isolates that were referred from eleven sentinel sites were analyzed at the National Public Health Laboratory for identification. Antibiotic susceptibility testing (AST) was done using disk diffusion, minimum inhibitory concentration method following Clinical Laboratory Standard Institute (CLSI) guidelines.

Results. Among 214 pathogenic isolates from blood samples, *E.coli* was the most common (56.1%), followed by *Salmonella Typhi*/*Salmonella Paratyphi* A (18.7%), *Staphylococcus aureus* (13.5%), and *Klebsiella pneumoniae* (11.7%). Methicillin Resistance *Staphylococcus aureus* (MRSA) was detected in half of the isolates. E.coli was resistant to ampicillin (94.4%), trimethoprim-sulfamethoxazole (84.5%), and ceftriaxone (79.2%). *Salmonella Typhi* was resistant to ampicillin (73.3%) and trimethoprim-sulfamethoxazole (60.0%) and *Salmonella Paratyphi A* were resistant to fluoroquinolones (91.7%). For last resort antibiotics, *E.coli* was resistant to carbapenem groups (3.2% for imipenem, 4.9% for meropenem, and 5.0% for ertapenem). *Klebsiella pneumoniae* was not resistant to any groups.

Conclusion. *E.coli* was found at high rates in blood samples and was resistant to common antibiotics used in Cambodia. These pilot data show the importance of establishing a national AMR surveillance system in Cambodia to monitor AMR trends following GLASS guidelines.

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