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**Background.** An increased likelihood of transmission of communicable diseases such as invasive meningococcal disease (IMD) exists in refugee camps. Herein, we describe an outbreak investigation of 5 IMD cases among immigrants in Greece.

**Methods.** Epidemiological, clinical and laboratory data (culture and molecular identification) as well as the public health management concerning an outbreak of meningococcal disease in a refugee Reception Identification Center (RIC), are described.

**Results.** During the period 17<sup>th</sup> January - 17<sup>th</sup> February 2020, five cases of IMD in refugees were reported to the National Public Health Organization (NPHO). Four cases were from Afghanistan and resided in the RIC of Lesvos Island; two females aged 2 yo and 21 yo and two males 13 yo and 6 yo. The fifth case, a 4 month old male of Syrian nationality, exhibited symptoms after moving to an inland accommodation center (AC) from Lesvos RIC, on December 2019. Four of the cases presented with meningitis and septicemia. All cases recovered and had no common exposure other than shared geographic space. *Neisseria meningitidis* was identified by molecular typing (mPCR, PorA, MLST, WGS) in all cases at the National Meningitis Reference Laboratory; 3/5 cases were identified as MenB, porA 7-2,4, and ST-3129 (new clone) while 2/5 (21 yo female, 13 yo male) as MenY, porA: 5.2, ST-22cc. To prevent secondary cases, antimicrobial chemoprophylaxis via Directly Observed Therapy (DOT) was administered to 4.024 Afgan close contacts (26.7% of the total Afgan population). MenACWY and MenB vaccination was recommended in response to outbreak among persons aged < 20 years old. No new IMD case occurred in the RIC during a follow-up period of 4 months.

**Conclusion.** The detection of a new clone in Greece of Chinese and Taiwanese origin through migrants, further underlines the need of enhanced surveillance for early detection, molecular typing, immediate intervention with antibiotic prophylaxis and/or supplemental vaccination in order to prevent IMD in refugee camps.

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**1430. Novel Transmission of Burkholderia pseudomallei from a Freshwater Aquarium to a Human — Maryland, 2019**

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**Background.** Nearly all U.S. cases of melioidosis, a potentially fatal disease caused by *Burkholderia pseudomallei*, are associated with travel to endemic areas. In September 2019, a patient in Maryland with no international travel history developed melioidosis and whole genome sequencing (WGS) of the patient's clinical isolate showed it clustered most closely with isolates from Southeast Asia. CDC and Maryland Department of Health (MDH) investigated possible sources of *B. pseudomallei* exposure to identify the source and route of transmission and evaluate risk to others.

**Methods.** MDH interviewed the patient and household members during October–December 2019. In consultation with CDC, MDH conducted environmental sampling of the patient's home including drains, faucets, potted and ground soil, imported products, and two freshwater aquariums. Samples were tested for *B. pseudomallei* at CDC by PCR and culture. *B. pseudomallei* isolates underwent WGS and were analyzed along with a reference panel of geographically diverse, publicly available genomes.

**Results.** Three environmental samples, all from aquarium #2, were positive for *B. pseudomallei*. These isolates matched the patient's clinical isolate by WGS, suggesting the aquarium was the source of exposure. According to interviews, the patient set up both aquariums in July 2019 and all the fish in aquarium #2 died in August 2019. The patient recalled reaching her bare hands and arms into the aquarium in August 2019, one month prior to illness onset.

**Conclusion.** This investigation led to the first documentation of transmission of *B. pseudomallei* from a freshwater aquarium to a human. Many freshwater ornamental fish are imported from Southeast Asia, so this newly recognized transmission route may have significant implications for the freshwater aquatics trade. Further investigations are underway at the retail location that sold the fish and the commercial vendors that supplied the freshwater animals and plants imported from Southeast Asia.

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**1431. Occurrence of Sporadic Human Ascariasis in Non-Endemic Regions: The Importance of Zoonotic Transmission from Swine**

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**Background.** Ascariasis in developed countries occurs only sporadically, and usually in travelers or in children in rural settings with exposure to *Ascaris suum* from swine. Reciprocal transmission between humans and swine is possible given *A. suum* and *A. lumbricoides* are considered conspecific based on published mtDNA and nuclear ribosomal ITS-1 studies with recognized phenotypic/genotypic differences reflecting host-specific adaptive changes. Here we evaluated 15 cases of human ascariasis detected over 6 a year period in a non-endemic region of the Upper Midwest USA.

**Methods.** Helminth specimens (n=15) spontaneously passed per rectum were submitted for laboratory identification during 2013-19 and identified morphologically as *A. lumbricoides/suum* (undifferentiated). All patients attended local clinics and brought specimens in for identification. Clinical records were available for 13 patients.

**Results.** Ages ranged from 14 months to 41 years with 13 cases (87%) occurring in children < =12 years and 2 (13%) >30 years; 9 patients (60%) were female. Thirteen (87%) of the *A. lumbricoides/suum* specimens were adults and 2 (13%) were juveniles. Individuals with records available either lived on or had visited a farm (5) or hobby farm (2) where pigs were currently or likely historically present; lived at a rural address (4); used animal manure for gardening (1); or lacked discernable farm connections though was active outdoors (1). International travel history was lacking in all cases. One 2-year old child from a rural address had passed 2 worms 6 months apart. All 13 patients were treated with albendazole per guideline without complication.

**Conclusion.** Ascariasis attributable to poor sanitation has been largely eradicated from the USA since the early 1980s. Sporadic infections in non-travelers have continued to be recognized and likely represent zoonotic transmission from domesticated swine. While human and pig *Ascaris* have long been considered distinct species, recently published molecular and cross-transmission experiments point to conspecificity. This case series is a reminder of the zoonotic disease risks posed by swine-origin *Ascaris*, especially in young children, and reinforces the need for proper herd management and attention to personal hygiene for at-risk individuals.

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**1432. Population-based Surveillance of Carbapenem-Resistant Enterobacteriaceae (CRE) in Alameda County, 2017-2020**

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**Background.** Infections caused by carbapenem-resistant Enterobacteriaceae (CRE), especially those that are carbapenemase-producing (CP), are difficult to treat and result in high mortality—the Centers for Disease Control and Prevention (CDC) designates CRE an urgent level threat to public health. Alameda, a northern California county with 1.67 million residents, mandates submission of all carbapenem-resistant isolates *Escherichia coli*, *Klebsiella* spp., and *Enterobacter* spp. We assessed the genetic profiles of CRE isolates and compared to aggregate US data from the same time period.

**Methods.** Isolates are submitted to the Alameda County Public Health Laboratory (ACPHL), where antimicrobial resistance genetic markers are identified by whole genome sequencing (WGS) using single-end, 150-cycle reactions in a MiSeq (Illumina). Resistance genes were identified using pipelines built in Geneious and confirmed with Resfinder. All epidemiological analyses were conducted using R (Version 4.0).

**Results.** ACPHL performed WGS on 226 CRE isolates submitted between June 2017 and February 2020. A total of 34/95 (36%) *Klebsiella* spp., 17/60 (28%) *E. coli*, and 10/71 (14%) *Enterobacter* spp. a carbapenemase enzyme. Among all Enterobacteriaceae, 21/226 (9%) produced the New Delhi-metallo-β-lactamase (NDM) carbapenemase (Table 1). Among all CRE, 17/226 (8%) were *Klebsiella pneumoniae* with the multilocus sequence type (MLST) of ST-258. All six *Klebsiella pneumoniae* ST-35 and ST-11 isolates produced a carbapenemase (Table 2).

Table 1: Carbapenemases, Extended Spectrum β-Lactamases (ESBL) and Other β-Lactamases by Organism

Organism	Isolates (%)	KPC (n=23)		NDM (n=21) <sup>*</sup>			OXA-48 like (n=7) <sup>*</sup>		IMI (n=2)		ESBL (n=100) <sup>**</sup>		Other β lactamase (n=57) <sup>**</sup>	
		KPC-2	KPC-3	NDM-1	NDM-5	NDM-7	OXA-48	OXA-181	OXA-232	IMI-1	IMI-3	SHV	CTX-M6	TEM-1
Enterobacter spp.	71 (33)	7	0	0	1	0	0	0	1	1	5	1	11	55
E. coli	60 (27)	0	0	1	9	1	2	4	0	0	1	32	24	25
Klebsiella spp.	95 (42)	11	14	4	4	1	0	1	0	0	59	22	41	21
TOTAL	226	18	14	5	14	2	2	4	1	1	65	55	76	99

<sup>\*</sup>One isolate with NDM-5 and OXA-232

<sup>\*\*</sup>Isolates may contain multiple genes in category (e.g. SHV and CTX-M gene)

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