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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 17th January - 17th 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

Patrick Dawson, PhD, MPH¹; Monique M. Duwell, MD, MPH²; Ruth J. Thompson, n/a²; David A. Crum, DVM, MPH²; David Blythe, MD, MPH²; Ruth Jacobs, MD³; Mindy G. Elrod, n/a¹; Jay E. Gee, PhD¹; Lindy Liu, MPH¹; David D. Blaney, MD¹; Zachary Weiner, PhD¹; William A. Bower, MD¹; Alex R. Hoffmaster, PhD¹; Johanna S. Salzer, DVM, PhD¹; ¹CDC, Atlanta, Georgia; ²Maryland Department of Health, Baltimore, Maryland; ³Holy Cross Germantown Hospital, Germantown, Maryland

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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

Thomas R. Fritsche, MD, PhD¹; Jennifer K. Meece, PhD¹; Susan K. Meyer, BS, MT¹; Kelly L. Ortega, AD, MLT¹; Nicolette S. Wolff, BS, MT¹; Matthew C. Hall, MD²

¹Marshfield Clinic Health System, Marshfield, Wisconsin; ²Ascension Medical Group, Weston, Wisconsin

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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

Sam Horwich-Scholefield, MPH CIC¹; Tyler Lloyd, BS²; Vici Varghese, Ph.D²; Emily Yette, PhD MPH¹; Sandra Huang, MD¹; Mark Pandori, PhD HCLD(ABB)³; ¹Alameda County Public Health Department, Oakland, California; ²Alameda County Public Health Laboratory, Oakland, California; ³Nevada State Public Health Laboratory, Reno, Nevada

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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) [*]			OXA-48 like (n=7) [*]		IMI (n=2)		ESBL (n=100) ^{**}		Other β lactamase (n=57) ^{**}	
		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

^{*}One isolate with NDM-5 and OXA-232
^{**}Isolates may contain multiple genes in category (e.g. SHV and CTX-M gene)