Themes and key clinical questions asked during outbreaks of SARS and MERS

Theme	Key question(s)	Objective
Clinical characterisation	What is the clinical presentation and spectrum of disease?	Determine symptomology, progression of disease, laboratory findings, and radiological features in different patient groups (adults vs. children, immunosuppressed patients) and identify early presenting symptoms
Prognosis	What are the risk factors for death or severe illness?	Identify factors such as comorbidities, demographic factors, test parameters, etc. that predict death, ICU admission, etc.
Clinical management	What treatments are effective for MERS/SARS patients? What is the role of antivirals in treatment? What is the role of steroids in treatment?	Determine the role of antiviral treatments, steroid treatments, or combination in comparison to supportive therapy
Diagnosis	What is the optimal diagnostic test for detecting the virus?	Evaluate sensitivity/specificity/positive predictive value/negative predictive value of different diagnostic assays such as real-time RT-PCR and ELISA
Viral pathogenesis	What is the duration of viral shedding?	Determine the viral shedding profiles over time and in different body fluids
Epidemiological characterisation	What characteristics define a "case"?	Develop criteria for suspected, probable, and confirmed cases
Infection prevention and control / Transmission	What are the risk factors which pre-dispose health care workers to infection or transmission?	Determine the activities or prevention measures that are correlated with protection or infection in health care workers
Susceptibility	What are the risk factors for infection? (patient population)	Determine the risk factors for patient infection, in the community and health care setting
Psychosocial	What are the psychosocial consequences of infection with the virus?	Determine effect of illness, treatment, and isolation procedures on the psychological and social well-being of those infected

Conclusion: The thematic analysis was used to identify the key clinical research questions asked during outbreaks of SARS-CoV and MERS-CoV and study designs were recommended to answer these questions. By defining the key clinical research questions, this study provides a first step in creating standardized clinical research protocols and defining core data variables to be collected during future outbreaks of respiratory coronaviruses.

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

1428. Lyme Disease Treatment in the United States: Prescribing Patterns from a Nationwide Commercial Insurance Database, 2016-2018

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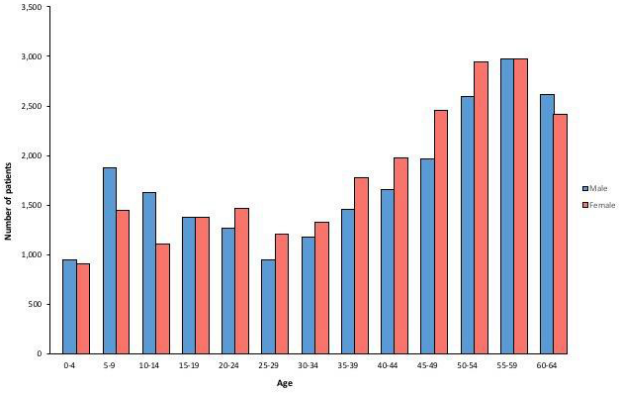
Background. Lyme disease (LD) is the most common vector-borne disease in the United States and is a significant public health problem. The use of non-standard antibiotic treatment regimens for LD has been associated with adverse effects; however, the overall landscape of treatment has not been described previously. We aimed to describe real-world antibiotic prescribing patterns for LD.

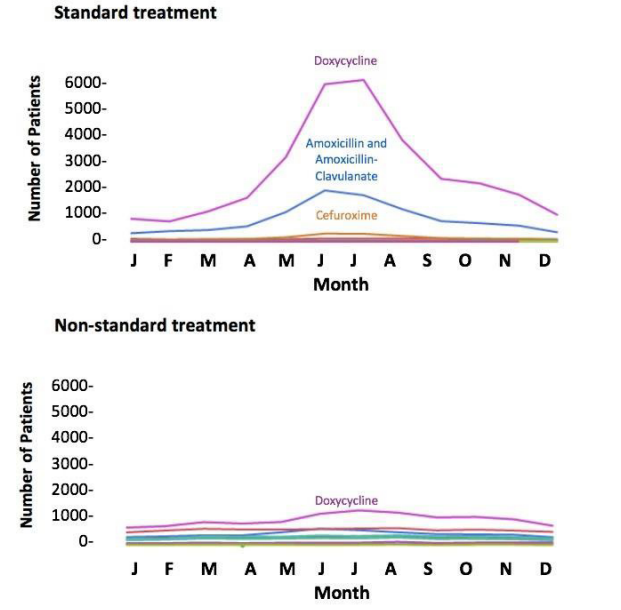
Methods. We performed a retrospective analysis of the MarketScan commercial claims database of outpatient encounters from 2016-2018 in the United States. We identified all individuals with a visit that included an LD diagnosis code and a prescription within 30 days of the visit for one or more of 12 antibiotics that may be prescribed for LD. We then categorized each individual as having received either standard or non-standard treatment during the two-year period. Standard treatment was defined as treatment with a first, second or third-line antibiotic for LD, for no longer than 30 days, and for no more than two episodes during the study period. Descriptive and multivariable analyses were performed to compare characteristics of people who received standard vs non-standard treatment for LD.

Results. A total of 84,769 prescriptions met criteria for inclusion, written for 45,926 unique patients. The mean duration of prescriptions was 21.4 days (SD 10.8). Most individuals (84.5%) treated for LD received standard treatment during the study period. Female gender (OR 1.5, p< 0.0001) and age 19-45 (p=0.0003) were significantly associated with being prescribed non-standard LD treatment. Treatment in low-incidence states (OR 2.2 compared to high-incidence states, p< 0.0001) and during non-summer months (OR 2.2, p< 0.0001) was more likely to be non-standard.

Age distribution of patients receiving treatment for Lyme disease, by gender and age at first prescription



Seasonality of standard versus non-standard treatment of Lyme disease



Conclusion: In this population of employed, young, and insured patients, young and middle-aged women were at the highest risk of receiving non-standard LD treatment. Treatments prescribed in states with low incidence of LD or during non-summer months were also more likely to be non-standard, a trend which likely reflects misdiagnosis or overtreatment of LD. Future studies are needed to further define prescriber and patient factors associated with non-standard LD treatment and related adverse outcomes.

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1429. Meningococcal Disease Outbreak in a Refugee Reception Identification Center in Greece and Administration of Mass Antibiotic Prophylaxis

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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 septicaemia. 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

		KPC (n=32)		NDM (n=21)*			OXA-48-like (n=7)*			IMI (n=2)		ESBL (n=100)**		Other β-lactamase (n=157)**	
Organism	Isolates (%)	KPC-2	KPC-3	NDM-1	NDM-5	NDM-7	OXA-48	OXA-181	OXA-232	IMI-1	IMI-3	SHV-group	CTX-M-group	TEM-1	AmpC-type
Enterobacter spp.	71 (31)	7	0	0	1	0	0	0	0	1	1	5	1	11	53
E. coli	60 (27)	0	0	1	9	1	2	4	0	0	0	1	32	24	25
Klebsiella spp.	95 (42)	11	14	4	4	1	0	0	1	0	0	59	22	41	21
TOTAL	226	18	14	5	14	2	2	4	1	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)