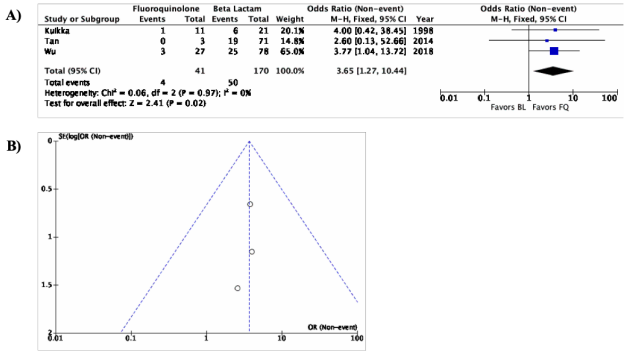


Figure 2. A) Forest plot showing FQ monotherapy is associated with increased survival compared to BL monotherapy using a fixed-effects model. **B)** Funnel plot showing the studies included in the meta-analysis.

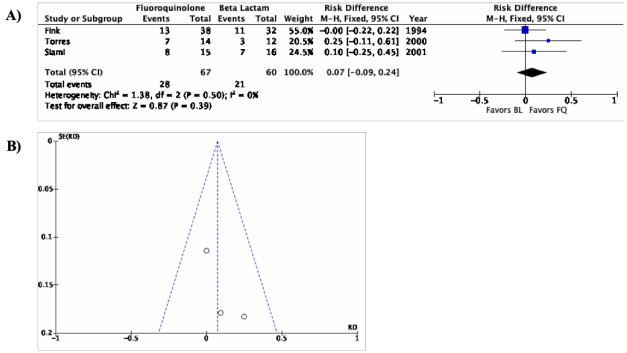


Figure 3. A) Forest plot showing FQ monotherapy is associated with similar bacteriological eradication rates compared to BL monotherapy using a fixed-effects model. **B)** Funnel plot showing the studies included in the meta-analysis.

Conclusion: The data appear to suggest FQ monotherapy is significantly associated with increased survival in PA bacteremia and associated with similar rates of bacteriological eradication in pneumonia and skin and soft tissue infection caused by PA compared to BL monotherapy. However, more research is needed to make meaningful clinical recommendations.

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

130. increase in Multidrug Resistance (2011–2018) and the Emergence of Extensive Drug Resistance (2020) in shigella Sonnei in the United States

Naeemah Z. Logan, MD[1]; Beth E. Karp, DVM, MPH[1]; Kaitlin A. Tagg, PhD[2]; Claire Burns-Lynch, MPH[3]; Jessica Chen, PhD[2]; Amanda Garcia-Williams, PhD[1]; Zachary A. Marsh, MPH[2]; Kevin O'Laughlin, MD[1]; Ian D. Plumb, MBBS, MSc[1]; Morgan N. Schroeder, MPH[2]; Hattie E. Webb, PhD[1]; Hannah Zenas, MPH[1]; Jenny Draper, PhD[4]; Andrew Ginn, PhD[4]; Elena Martinez, PhD[4]; Sally R. Partridge, PhD[5]; Eby Sim, PhD[4]; Vitali Sintchenko, MBBS, PhD[4]; Jonathan Iredell, MBBS, PhD[6]; Louise Francois Watkins, MD, MPH[7]; [1]Division of Foodborne, Waterborne, and Environmental Diseases, Centers for Disease Control and Prevention, Atlanta, GA, Atlanta, Georgia; [2]Centers for Disease Control and Prevention, Atlanta, Georgia; [3]Emory University Rollins School of Public Health, Atlanta, Georgia; [4] (2) Microbial Genomics Reference Laboratory, Centre for Infectious Diseases and Microbiology Laboratory Services, NSW Health Pathology, ICPMR Westmead, NSW Australia; [3] University of Sydney, Sydney, NSW Australia, Westmead, New South Wales, Australia [5] (3) University of Sydney, Sydney, NSW Australia; [4]Centre for Infectious Diseases and Microbiology, The Westmead Institute for Medical Research, Westmead Hospital, NSW Australia, Westmead, New South Wales, Australia; [6] (2) Microbial Genomics Reference Laboratory, Centre for Infectious Diseases and Microbiology Laboratory Services, NSW Health Pathology, ICPMR Westmead, NSW Australia; [3]University of Sydney, Sydney, NSW Australia; [4]Centre for Infectious Diseases and Microbiology, The Westmead Institute for Medical Research, Westmead Hospital, NSW Australia, Westmead, New South Wales, Australia; [7]Division of Foodborne, Waterborne, and Environmental Diseases, Centers for Disease Control and Prevention, Atlanta, Georgia

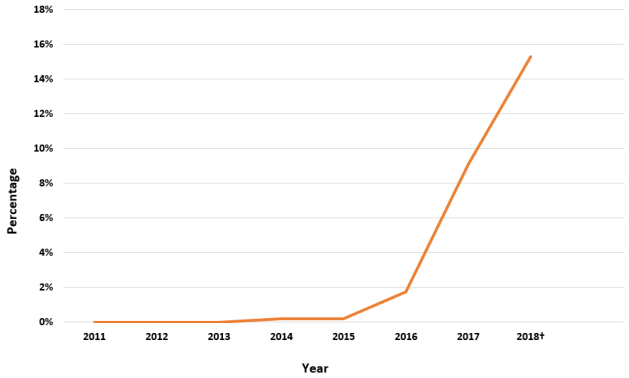
Session: O-25. Hot Topics in Bacteria and Viral Infections

Background: Multidrug-resistant (MDR) *Shigella sonnei* infections are a serious public health threat, and outbreaks are common among men who have sex with men (MSM). In February 2020, Australia's Department of Health notified CDC of extensively drug-resistant (XDR) *S. sonnei* in 2 Australian residents linked to a cruise that departed from Florida. We describe an international outbreak of XDR *S. sonnei and* report on trends in MDR among *S. sonnei* in the United States.

Methods: Health departments (HDs) submit every 20th *Shigella* isolate to CDC's National Antimicrobial Resistance Monitoring System (NARMS) laboratory for susceptibility testing. We defined MDR as decreased susceptibility to azithromycin (MIC ≥32 µg/mL) with resistance to ampicillin, ciprofloxacin, and cotrimoxazole, and XDR as MDR with additional resistance to ceftriaxone. We used PulseNet, the national subtyping network for enteric disease surveillance, to identify US isolates related to the Australian XDR isolates by short-read whole genome sequencing. We screened these isolates for resistance determinants (ResFinder v3.0) and plasmid replicons (PlasmidFinder) and obtained patient histories from HDs. We used long-read sequencing to generate closed plasmid sequences for 2 XDR isolates.

Results: NARMS tested 2,781 *S. sonnei* surveillance isolates during 2011–2018; 80 (2.9%) were MDR, including 1 (0.04%) that was XDR. MDR isolates were from men (87%), women (9%), and children (4%). MDR increased from 0% in 2011 to 15.3% in 2018 (Figure). In 2020, we identified XDR isolates from 3 US residents on the same cruise as the Australians. The US residents were 41–42 year-old men; 2 with available information were MSM. The US and Australian isolates were highly related (0–1 alleles). Short-read sequence data from all 3 US isolates mapped to the $bla_{CTX\text{-}M\text{-}27}$ harboring IncFII plasmids from the 2 Australian isolates with >99% nucleotide identity. $bla_{CTX\text{-}M\text{-}27}$ genes confer ceftriaxone resistance.

Increase in Percentage of Shigella sonnei Isolates with Multidrug Resistance* in the United States, 2011–2018†



* Multidrug resistance defined as decreased susceptibility to azithromycin (MIC ≥32 µg/mL) with resistance to ampicillin, ciprofloxacin, and cotrimoxazole.

† Data from 2018 is preliminary.

Conclusion: MDR *S. sonnei* is increasing and is most often identified among men. XDR *S. sonnei* infections are emerging and are resistant to all recommended antibiotics, making them difficult to treat without IV antibiotics. This outbreak illustrates the alarming capacity for XDR *S. sonnei* to disseminate globally among at-risk populations, such as MSM.

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

131. The Protective Role of Mucosal Interferons in Infants with Respiratory Syncytial Virus (RSV) Infection

Jeanette Taveras, DO[1]; Cristina Garcia-Maurino, MD[2]; Melissa Moore-Clingenpeel, MA, MAS[3]; Sara Mertz, BS[1]; Mark E. Peeples, PhD[4]; Octavio Ramilo, MD[1]; Asuncion Mejias, MD, PhD, MsCS[1]; [1]Nationwide Children's Hospital, Grandview Heights, Ohio; [2]Center for Vaccines and Immunity, The Research Institute at Nationwide Children's Hospital, Columbus, Ohio; [3]The Research Institute at Nationwide Children's Hospital, Columbus, Ohio; [4]The Ohio State University, Columbus, Ohio

Session: O-25. Hot Topics in Bacteria and Viral Infections

Background: Despite the high burden associated with RSV infection in young children the factors that determine disease severity are not well understood. The objective of this study was to assess the association of mucosal cytokine profiles, RSV loads (VL) and RSV disease severity.

Methods: Single-center, prospective study in previously healthy infants with mild (outpatients; OP), moderate (inpatient-IP; ward) or severe (IP-PICU) RSV infection. Mid-turbinate swabs were obtained to measure VL by PCR, and cytokine concentrations (conc.) using a 13-plex panel that included type I (IFN-α2), II (IFN-γ), and III (IFN-λ2/λ3) interferons (IFN), and inflammatory cytokines. Multivariable analyses were performed to identify factors predictive of disease severity.

Results: From 2014 to 2019 we enrolled 219 infants: 78 with mild RSV infection (OP; median [IQR] age, 6 [3.4–10.5] mo.), 101 with moderate disease (3.5 [1.3–8.3] mo.), and 40 with severe disease (2.3 [1.5–5.7] mo.). Duration of symptoms at enrollment was 4 (3–5) days and comparable between OP and IP, yet RSV VL in OP were significantly higher than in IP (8.1 [7.4–8.6] vs 7.4 [6.4–8.1] $\log_{10}$ copies/mL; p< 0.01) with no differences between ward and PICU infants. Median conc. of IFN-α2, IFN-γ, and IFN-λ2/λ3 were significantly higher in OP vs IP irrespective of hospitalization unit (Table 1). IP-10 conc. were also higher in OP and in ward patients vs PICU patients (p< 0.0001) and were independently associated with lower odds of supplemental O_2 needs (OR, 95% CI: 0.4 [0.22–0.69]; p< 0.01) and PICU admission (0.4 [0.23–0.67]; p=0.001). In addition, higher IFN-λ2/λ3 conc. were nearly associated with lower odds of prolonged O_2 use (OR: 0.35 [0.11–1.07]; p=0.07), and prolonged hospitalization (OR: 0.42 [0.16–1.03]; p=0.06).

Table 1. Mucosal cytokine concentrations in children with RSV infection

	RSV-OP(n=78)	RSV-IP (n=141)	RSV-Ward (n=101)	RSV-PICU (n=40)	OP vs Ward vs PICU (p-value)
Type-I IFN					
IFN-α2	1.6 (0.9-2.2)	0.7 (0.3-1.2)	0.7 (0.5-1.2)	0.7 (0.1-1.2)	<0.0001
IFN-β	3.6 (1.5-7.9)	2.4 (1.1-5.8)	2.4 (1.8-6.0)	1.8 (0.7-3.9)	0.1
Type-II IFN					
IP-10	268.6 (118.5-825.6)	87.6 (15.3-221.2)	116.2 (28.4-234.9)	34.8 (4.5-124)	<0.0001
IFN-γ	1.6 (0.8-3.5)	1.2 (0.5-1.9)	1.2 (0.7-2.3)	1.1 (0.4-1.3)	0.05
Type-III IFN					
IFN-λ1	5.2 (2-14.1)	3.4 (1.9-9.1)	3.4 (1.9-9.1)	3.3 (1.9-9.1)	0.2
IFN-λ2/λ3	14.3 (4.4-24.8)	8.9 (3.4-12.7)	8.9 (3.7-12.7)	8.9 (1.4-12.7)	0.0007

IP: inpatients; OP: outpatients. Values represent absolute numbers and medians (25%-75% interquartile range-IQR). Cytokine conc. expressed in pg/mL. Mann-Whitney test was used to determine differences between two groups; Kruskal-Wallis was used to determine differences between three groups (p-values*).

Conclusion: Infants with mild RSV infection had higher RSV VL and higher conc. of IP-10 and type-I, III IFN than those hospitalized with severe disease. These findings suggest that IP-10 and mucosal IFNs are associated with protection against severe RSV disease and could be used as biomarkers for patient stratification in the clinical setting.

Disclosures: **Octavio Ramilo, MD**, **Bill & Melinda Gates Foundation** (Grant/Research Support)**Janssen** (Grant/Research Support, Advisor or Review Panel member)**Medimmune** (Grant/Research Support)**Merck** (Advisor or Review Panel member)**NIH/NIAID** (Grant/Research Support)**Pfizer** (Consultant, Advisor or Review Panel member)**Sanofi/Medimmune** (Consultant, Advisor or Review Panel member) **Asuncion Mejias, MD, PhD, MsCS**, **Janssen** (Grant/Research Support, Advisor or Review Panel member)**Merck** (Advisor or Review Panel member)**Roche** (Advisor or Review Panel member)

132. Emergence and Spread of Multidrug-resistant salmonella Serotype Infantis Infections in the United States, 2003–2018

Felicita Medalla, MD, MS[1]; Daniel C. Payne, PhD, MSPH[2]; Preethi Sundararaman, MPH[1]; Meseret Birhane, MPH, MAS[1]; Andrew Classon, MPH[1]; Hayat Caidi, PhD[1]; Jason Folster, PhD[1]; Cindy R. Friedman, MD[2]; Louise Francois Watkins, MD, MPH[3]; [1]Division of Foodborne, Waterborne, and Environmental Diseases, Centers for Disease Control and Prevention, Atlanta, GA, Atlanta, Georgia; [2]Centers for Disease Control and Prevention, Atlanta, Georgia; [3]Division of Foodborne, Waterborne, and Environmental Diseases, Centers for Disease Control and Prevention, Atlanta, Georgia

Session: O-25. Hot Topics in Bacteria and Viral Infections

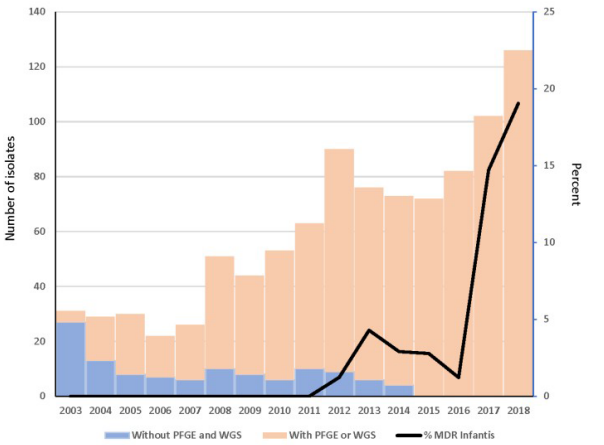
Background: Infantis re-emerged as a leading *Salmonella* serotype when a multidrug-resistant (MDR) strain with a rare extended spectrum β-lactamase (ESBL) $bla_{\text{CTX-M-65}}$ gene emerged among returned travelers from Peru in 2012 and then spread domestically. This strain has been isolated from chickens at slaughter and retail, and humans in outbreaks traced to chicken. We reviewed national surveillance data to determine incidence trends and antibiotic resistance among Infantis infections.

Methods: We reviewed data from 2003–2018 from the Foodborne Diseases Active Surveillance Network to determine the incidence and epidemiology of infections in 10 sites under surveillance; PulseNet to determine pulsed-field gel electrophoresis (PFGE) patterns; and National Antimicrobial Resistance Monitoring System (NARMS) to determine antimicrobial susceptibility testing (AST) results and resistance genes of isolates identified by whole genome sequencing (WGS). We defined MDR Infantis as having ceftriaxone resistance by AST and either the $bla_{\text{CTX-M-65}}$ gene or one of 18 PFGE patterns linked to that gene by WGS.

Results: The 2,154 patients with Infantis infection had a median age of 36 years and 57% were female; 86% had isolates from stool, 9% from urine, and 3% from blood. Only 10% reported foreign travel and 27% were hospitalized. The incidence of infections began increasing in 2010 and by 2017–2018 was 2-fold higher than the average during 2003–2009. During 2003–2018, 856 (88%) of 970 NARMS isolates had PFGE or WGS data; 48 isolates were MDR Infantis, and in addition to ceftriaxone and ampicillin resistance (by definition), all 48 were resistant to 3 or more antibiotic classes, 94% had decreased susceptibility to ciprofloxacin, and 67% were resistant to cotrimoxazole. During 2012–2016, 2% of isolates were MDR Infantis; this increased to 17% during 2017–2018 (Figure).

Conclusion: During the past decade, the incidence of Infantis infections markedly increased. This was likely driven by the emergence of an ESBL-producing strain that was initially associated with travel, and is now mostly domestically acquired and associated with consuming chicken. MDR Infantis now accounts for 1 in 5 Infantis infections. Public health strategies to reduce *Salmonella* contamination of chicken could help prevent these infections.

Number of *Salmonella enterica* Infantis isolates and percentage MDR Infantis* by year—United States, 2003–2018†



*MDR Infantis isolates were defined as having ceftriaxone resistance by antimicrobial susceptibility testing and either the $bla_{\text{CTX-M-65}}$ gene or one of 18 pulsed-field gel electrophoresis (PFGE) patterns linked to that gene; % MDR Infantis was calculated among isolates with PFGE or whole-genome sequence (WGS) data.

†Since 2003, 50 state and 3–4 local health departments have participated in the National Antimicrobial Resistance Monitoring System. Isolates were tested for antimicrobial susceptibility, PFGE, and WGS (since 2014).

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

133. validation of a Global Respiratory Severity Score in Infants with Primary RSV Infection

Xing Qiu, PhD[1]; Lu Wang, MS[1]; Edward E. Walsh, MD[2]; Mary T. Caserta, MD[1]; [1]University of Rochester Medical Center, Rochester, New York [2]University of Rochester, Rochester, New York

Session: O-25. Hot Topics in Bacteria and Viral Infections

Background: We recently developed a global respiratory severity score (GRSS) as a research tool from (n=139) infants with primary respiratory syncytial virus (RSV) infection enrolled prospectively in the Assessing Predictors of Infant RSV Effects and Severity (AsPIRES) study. The objective of the present study was to validate our original findings that the GRSS correlates well with clinical outcomes including hospitalization and length of stay (LOS) utilizing an independent cohort.

Methods: Clinical and demographic data on infants with primary RSV infection were abstracted from the electronic medical record. The GRSS was calculated by applying the original training data formula to the new data set. We compared the mean GRSS between the hospitalized and non-hospitalized group with Welch two sample t-test, and correlated it with hospitalization and LOS using Pearson's correlation test.

Results: A total of 184 (98 hospitalized and 86 non-hospitalized) subjects were enrolled. The hospitalized and non-hospitalized infants were different in general appearance, the percentage with rales, retractions, lethargy, respiratory rate and oxygen saturation. The hospitalized group had a significantly ($t=9.334$, $p< 0.0001$) higher GRSS (4.20±2.10) than the non-hospitalized group (1.76±1.41). Using GRSS ≤3.5 as the classification criterion, we correctly predicted the hospitalization status of 131 (71.2%) subjects. The area under the ROC curve of the GRSS as a classifier of hospitalization is AUC=0.8265 ($p< 0.0001$). Pearson correlation between the GRSS and LOS is ($p< 0.0001$).

Area under the ROC curve of the GRSS